



262

# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 202292

TO: Jane Zara  
Location: REM-2A59&2C18  
Art Unit: 1635  
Monday, October 02, 2006  
Case Serial Number: 10/642946

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen 1a69  
Phone: 571-272-2518

*BOB*  
barbara.obryen@uspto.gov

### Search Notes

Hi Jane,

For the score over length search, neither fragment had hits in the EST database, so no EST results are included with the S/L output.

Barb

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ACCESS DB #

202292

PLEASE PRINT CLEARLY

9-981

Scientific and Technical Information Center

# SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77572 Date: 9/19/06  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/642,946  
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: ISOLATED Genomic polynuc's ... chrom 7  
Inventors (please provide full names): JW RYAN

Earliest Priority Date: 028800 9-24-01 CYRE

## Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- ① Please Search ~~Seq~~ Seq ID No: 3  
Nucleic Acid DATA BASES only  
~~028800~~  
No size limits
- ② Please Search Seq ID No: 6  
Between nucleotides 1967-2208  
Between nucleotides 3002-3237  
~~Between 40-60~~  
Length Limit To 50 NTS.  
3-1150AA  
6-45980NA  
Score over Length For ② only  
70% Homology size 10-241 nt

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GenCore version 5.1.9  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: September 30, 2006, 23:28:37 ; Search time 13965 Seconds

(without alignments)  
7953.933 Million cell updates/sec

Title: US-10-642-946-3

Perfect score: 6272  
Sequence: 1 MAANVAGAPLISCLIALALAC.....TCGAPFTTVERTYTNFGDF 1158

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame.p2n.model -DEV=xlp  
-Q=/abs/ABSGWEP.apool/US10642946/runat\_29092006\_125308\_12482/bpp\_query.fasta\_1  
-DB=GenEmbl -QFMT=fasta -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45  
-POCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p  
-USER=US10642946@CGN\_1\_10799@runat\_29092006\_125308\_12482 -MCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

GenEmbl:.\*  
1: gb\_env:.\*  
2: gb\_pat:.\*  
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4: gb\_pl:.\*  
5: gb\_pr:.\*  
6: gb\_ro:.\*  
7: gb\_sta:.\*  
8: gb\_sy:.\*  
9: gb\_un:.\*  
10: gb\_vl:.\*  
11: gb\_ov:.\*  
12: gb\_ncg:.\*  
13: gb\_in:.\*  
14: gb\_om:.\*  
15: gb\_ba:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6272	100.0	3935	2	AR240603	Sequence
2	6272	100.0	3935	2	AX578006	Sequence
3	6272	100.0	3935	5	AF053944	Homo sapi

4	6264	99.9	4125	5	BC038588	BC038588 Homo sapi
5	6263	99.7	4038	5	AB209744	AB209744 Homo sapi
6	6246	99.6	3913	2	CQ716956	CQ716956 Sequence
7	5080	81.0	3909	6	AK128980	AK128980 Mus muscu
8	5079	81.0	3869	6	BC082577	BC082577 Mus muscu
9	5077	80.9	3790	6	AF053943	AF053943 Mus muscu
10	5054	80.6	3728	2	E07353	E07353 cdna encodi
11	5054	80.6	3728	2	I15213	I15213 Sequence 1
12	4791	76.4	16161	2	AX473127	AX473127 Sequence
13	4771	76.1	153303	5	AC006454	AC006454 Homo sapi
14	4551	72.6	2839	5	D86479	D86479 Homo sapien
15	4003	63.8	2759	14	AF043942	AF043942 Bos tauru
16	3639.5	58.0	195129	6	AL627069	AL627069 Mouse DNA
17	3632.5	57.9	22581	6	MMAEBP1	MMAEBP1
18	3621	57.7	22245	12	AC095141	AC095141 Rattus no
19	3598	57.4	2571	2	CQ850412	CQ850412 Sequence
20	3598	57.4	2571	5	AK127541	AK127541 Homo sapi
21	3488.5	55.6	2168	2	AX577931	AX577931 Sequence
22	2974	47.4	2172	5	AK090931	AK090931 Homo sapi
23	2881	45.9	205220	12	AC150911	AC150911 Pan trogl
24	2171.5	34.6	3772	2	AR252414	AR252414 Sequence
25	2171.5	34.6	3772	2	AR693304	AR693304 Sequence
26	2171.5	34.6	3772	2	AR705856	AR705856 Sequence
27	2171.5	34.6	3772	2	AR757229	AR757229 Sequence
28	2171.5	34.6	3772	2	AR758729	AR758729 Sequence
29	2171.5	34.6	3772	2	AR776043	AR776043 Sequence
30	2171.5	34.6	3772	2	AX403174	AX403174 Sequence
31	2171.5	34.6	3772	2	AX464258	AX464258 Sequence
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33	2135.5	34.0	3574	5	BC036789	BC036789 Homo sapi
34	2106.5	33.6	3441	2	AX338496	AX338496 Sequence
35	2106.5	33.6	3470	2	AR447746	AR447746 Sequence
36	2066	32.9	2490	2	AX82239	AX82239 Sequence
37	2066	32.9	2490	6	AF017639	AF017639 Mus muscu
38	2053.5	32.7	2430	6	BC021444	BC021444 Mus muscu
39	2015	32.1	2392	2	AX254979	AX254979 Sequence
40	2006.5	32.0	1868	2	C0729493	C0729493 Sequence
41	1811.5	28.9	125384	12	AC135546	AC135546 Tetraodon
42	1767.5	28.2	2379	2	CS208029	CS208029 Sequence
43	1767.5	28.2	2379	6	AF077738	AF077738 Mus muscu
44	1766	28.2	2368	6	BC003713	BC003713 Mus muscu
45	1748.5	27.9	2382	2	AR219252	AR219252 Sequence

## ALIGNMENTS

RESULT 1  
AR240603  
LOCUS AR240603 3935 bp DNA  
DEFINITION Sequence 1 from patent US 6468766.  
ACCESSION AR240603  
VERSION AR240603.1 GI:27285699  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3935)  
AUTHORS Lee, M.-E., Layne, M.D., and Yet, S.-F.  
TITLE Aortic carboxypeptidase-like polypeptide  
JOURNAL Patent: US 6468766-A 1 22-OCT-2002;  
President and Fellows of Harvard College; Cambridge, MA  
FEATURES  
source location/Qualifiers  
1..3935  
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/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 0  
Score: 6272.00 Length: 3935  
Percent Similarity: 100.0% Matches: 1158  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0

DB:	2	Gaps:	0
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QY	1 MetAlaIaValArgGlyValProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys	20	
Db	140 ATGGCGGCGGTGGCGGGGGCGCCCTGCTCAGCTGCTCTTGCGCTTGGCTGTGC	199	
QY	21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40	
Db	200 CCGAGAGGGCGCCCGCAGACGGGTGCTGACCGAGACGAGATGAGAGGATTCCTCCAGGGCG	259	
QY	41 PheLeuSerGluLeuGluProGluProArgGluLeuAspAspValGluAlaProProProPo	60	
Db	260 TTCCTGTCTGAGACTGAGAACCTTGAGCCCGGGAGAGACGATGAGAGCCCGCGCTCTCC	319	
QY	61 GluProThrProArgValArgIysAlaGlnAlaGlyIysAspProGlyIysAspArgProGly	80	
Db	320 GAGCCACCCCGGGGTCCGAAAAGCCGAGCGGGGGGCAAGCAGAGGAAGCGCCAGGG	379	
QY	81 ThrAlaAlaGluValProProGluIysThrIysAspIysGlyIysIysGlyIysIysAsp	100	
Db	380 ACGGCGCGAGAAAGTGTCTCGGAAAAGCAAAAGACAAAGAGGAAGAAAGCAAAAGAC	439	
QY	101 IysGlyIysProIysValProIysGluSerLeuGluGlySerProArgProProIysIysGly	120	
Db	440 AAAGGCCCAAGGTGCCAAGGAGTCTCTTGAGGGGTCTCCCAAGCGCCGCCCAAGAGGGCG	499	
QY	121 IysGluIysProProIysAlaThrIysIysAspIysProIysGluIysProProIysAlaThrIys	140	
Db	500 AAGGAAAGAACCCACCCAGAGCCACCAAGAAAGCCCAAGAAAGCACCTAAAGGCACCAAG	559	
QY	141 IysProIysGluGluProProIysAlaThrIysIysProIysGluIysProProIysAla	160	
Db	560 AAGCCCAAGAGAGAGCCACCAAGGCCACCAAGAGCCCAAGAGAGAGCCACCAAGAGCC	619	
QY	161 ThrIysIysProProSerGlyIysValArgProProIleLeuAlaProSerGluThrLeuGlu	180	
Db	620 ACCAAGAAACCCCGCTCAGGAGAAAGAGCCCGCCCATCTGGCTCTCCCAAGAAACCTCGAG	679	
QY	181 ThrProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyVala	200	
Db	680 TGGCCACTGCCCCCAGCCCCCAGCCCTGGGCCCCGAGAGAGCTACCCAGAGAGGAGGGGCG	739	
QY	201 ProLeuSerAspAsnIleProGluIysProGlyGluGluThrHisValGluAlaGluGluHis	220	
Db	740 CCCCTCTCAAAATTAACCTGGCAGAAATCCAGAGAGAGAACCCCATGTGAGGACACAGAGCAG	799	
QY	221 GlnProGluProGluGluGluThrGluGluProThrLeuAspIysIleAspGluIleGlu	240	
Db	800 CAGCCTGAGACCCGAGAGAGAGACCCGAGCAACCACTGAGCTAACAATGACAGATCGAG	859	
QY	241 ArgGluAspIysGluAspPheGluIleIleArgArgGluIysGluIleProArgProProPro	260	
Db	860 AAGGAGGACTTAAGAGACTTTAGTACATTCGCGCCAGAAAGCAACCCAGCCACCCCA	919	
QY	261 SerArgArgArgArgProGluIysValIleProGluIleProGluGluIysIysAlaProAla	280	
Db	920 AGCAGAAAGAGAGAGCGCCAGCGGCTGTGGCCAGAGCCCTCTAGAGAGAAAGCGCCGCGC	979	
QY	281 ProAlaProGluGluIysGluIleGluProProValIysProLeuLeuProProLeuProPro	300	
Db	980 CCAGCCCCCGAGAGAGATTGAGCTCTCTGTGAACCTCTGCTGCCCCCGCTGCCCT	103	
QY	301 AspIysIysIysAspGlyIysIysValIleProAlaIysIysAspAspMetCAspIysIysPheGlyPro	320	
Db	1040 GACTATGAGTGAAGTTCATCTGATCCCAACTACGATGAGATGACATTAATCTTGGGCT	109	
QY	321 ProProProProGluIysProAspAlaGluIysGluIleThrAspGluGluIysGluIysLeuIys	340	
Db	1100 CCTCGGCCCCAGAGCCCATGCTGAGCGCCAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG	115	
QY	341 IysProIysIysGluIysAspSerProIysGluGluIleThrAspIysIysIysIysIysIysIys	360	

Db	1160	AAACCCAAAAGAGAGACAGCAGCCCAAGGAGAGACCGAACAAGTGGCAGTGGAGAAAG	121
QY	361	GIYLYASPHIIGLYSGIUPROARGLYSGIUGIULEGIUGIUGIUTPRThProThr	380
Db	1220	GGCAAGAGACACAAAGAGCCCGGAAGGGCGAGAGTTGGAGAGAGATGCAGCGCTACG	127
QY	381	GIULYVALIYCYAPROPROILEGIYMETGIUSERHISARGLIGIUNASPHANGIILE	400
Db	1280	GAGAAAGTCAAGTGTCCCCCATTTGGAGTGGAGTACACCCGTATTGAGGACAAACGAGATC	133
QY	401	ARGAIAASERSEMELIENRGIIGIYLENGIYALIGIINARGLIARGLEUNSMETGIN	420
Db	1340	CGAGGCTCTTCATGCTGGCGACAGCGCTGGGGGACAGCGGGCGGCTCAACATGCAAG	139
QY	421	THRGIALAETHRGIUABSPAPITRYTRAPSGIYALATPRCYALAGIUNASPAALARY	440
Db	1400	ACCGGTGCCACTGAGAGACACTACATATGATGGTGGGTGTGCCGAGAGACATGCCAG	145
QY	441	THRGINTPRIIGIULVALIAPTHRARGARGTHTHRARGPHETHGIYVALLIETHRGIN	460
Db	1460	ACCCAGTGGATAGAGGTGACACCAAGAGAGACTACCCGGTTACAGGCGCTCATACCCAG	151
QY	461	GIYARGASERSEIRLEHISAPAPHPHEVALITPRTHRPHENVALGIYPHESEARAN	480
Db	1520	GGCAGAGACTCCAGCATCATACCAATTTGTGACCACCTTGTGGGGCTTCAGCAAT	157
QY	481	AAPSERGINTHRTIPVALMETYTRHRANGIYTRGIUGIUMETTHRPHENIISGLIYAN	500
Db	1580	GACAGCGCAGACATGGGTGATGTRACACCAAGCGCTATGAGGAATGACCTTATAGGAAAC	163
QY	501	VALIAPLYASPTH-PROVALIENUSERGULEUPROGIUPROVALIALAARGPHEILE	520
Db	1640	GTGGACAAAGACACACCGGTGCTGATGAGACTCCACAGACCGGTGATGGCTGTTTCAATC	169
QY	521	ARGIIETYPROLEUTHRTIPRASNGLYSERLEUCYMERARGLEUGIULIENGUYCY	540
Db	1700	CGCATCTTACCACCTACCTCGAATGGCAGCGCTGATGCGCTGGAGGTGCTGGGGTGC	175
QY	541	SERVALIAPROVALITYSERITYTRYALAGIINANGIULVALIATHRASAPPLEU	560
Db	1760	TCTGTGGCCCTGTCTACAGCTACTACGACAGATGAGGTGGTGGCCACCGATGACCTG	181
QY	561	AAPPHENRGIHISERTYRLIYASPHWETARGIINLEMETLYVALIANGIUGIU	580
Db	1820	GATTTCCGGCACACAGCTAACAGGACAGCGCCAGCTCATGAAGTGGTGAACGAGGAG	187
QY	581	CYBPROTHIILETHRARGTHRTRYSERLENGUYLYSSESERARGIYLEUYSIIETYP	600
Db	1880	TGCCCCACCATCAACCGCACTTACAGCGCTGGGCAAGAGCTCACGAGCGCTCAAGATCTAT	193
QY	601	ALAMETGIUIESERAPASNPROGIYGIUNHISGLIULEGIUGIUPROGIUPHEARTYR	620
Db	1940	GCCATGGAATCTTCAGACAACTCTGGGAGACATGAATCGGGGAGACCCGAGTTCCGCTAC	199
QY	621	THRIAGIYIIEHISGLIYANGIULVALIENGUYARGIUGIULEULEULEULEUNMETGIN	640
Db	2000	ACTGGCTGGGATCATGCGCAACGAGGTGCTGGGCGCAGAGACTGTGGCTGCCTCATGCAG	205
QY	641	TYRLEUCYARGIULTRYARGAPGIYANP-ROARGVALIARGSERLEUVALIGIINAPTHR	660
Db	2060	TACCTGTGGCGAGAGTACCGCATGGGAAACCAACGTGTGCGGAGCTGTGTGACGAGCAACA	211
QY	661	ARGIIEHISLEUVALI-PROSERLEUNP-ROAPSGIYTRYGIULVALIALAAGIINMETGIY	680
Db	2120	CGCATCACCTGGTGCCTCATCTGAACCTTGATGGCTACGAGAGTGGCAGCGCAGATGGGC	217
QY	681	SERGIUPHEGIYASNTIPALALEUGIYLEUTPRTHRGIUGIUGIYPHEASPIIEPHGIU	700
Db	2180	TGAGAGTTTGGGACATCGGCGCTGGGACGTGTGACAGGAGGAGGCTTTGACATCTTTGAA	223
QY	701	AAPPHETROASPLEUNSERVALIENUTPRIYALIGIUGIULARGLYSTPRVALI-PROIYR	720

Db	2240	GATTTCCGGGATCTCACTCTGTGCTTGGGGAGCTGAGAGAGGAAATGGGTCCCTTAC	2239
Qy	721	ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal	740
Db	2300	CGGGTCCCGCAACATTAATCTGGCCATCCGTGAAGCTTACCTTTGGCCAGATGCCAGGTA	2359
Qy	741	SerThrGluValArgAlaIleIleAlaTrpMetGluValAsnProPheValLeuGluVala	760
Db	2360	TCCAGGGAGGTCTCGGGCCATCTTCCCTGGAGGAGGAAGAACCCCTTGCTGTGGAGCA	2419
Qy	761	AsnLeuAsnGluGluGluValArgLeuValSerTyrProTyrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAACCGCGCGGAGCGGCTAGTATCTTACCCCTTACGATATGAGCCCGCACGCTACC	2479
Qy	781	GlnGlnGlnLeuLeuAlaIleAlaMetAlaAlaIleArgGluValAspGluValAspGluVal	800
Db	2480	CAGAGCAGCTGTGCTGGCCGAGCCATGGGAGAGCCCGGGGGAGAGATGAGGAGAGGTC	2539
Qy	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGGCCCGAGACATCCAGACCAACGACCATCTTCCGCTGGCTTGCATCTCTCCGC	2599
Qy	821	SerAlaHisLeuThrLeuThrGluProTyrArgGluGluGluValAlaGlnAspTyrThr	840
Db	2600	TCCGCACACTTCACCTTACCGAGCCCTTACCGGGAGGCTGCAGAGCCCAAGACTACACC	2659
Qy	841	GlyGlyMetGlyIleValaIleAsnGluValaIleTyrTrpAsnProArgThrGlyThrIleAsnAsp	860
Db	2660	GGCGGCATGGGGATGTCTACCGGGGCCAAGTGGAAACCCCGGACCGGGAATTTCAATAC	2719
Qy	861	PheSerTyrLeuHisTrpAsnCysLeuGluLeuSerPheTyrLeuGluCysAspIlePhe	880
Db	2720	TTTCAGTTTACCTGCATACCAACACTGCTGGAGCTCTCTTCTACCTGGCTGTGACAAAGTTC	2779
Qy	881	ProHisGluSerGluLeuProArgGluTrpGluAsnAsnGluAlaLeuLeuThrPhe	900
Db	2780	CCTCATGAGAGTGAAGCTGCCCCCGCAGTGGAGAACCAAGAGAGCGCTCTCACTTC	2839
Qy	901	MetGlnGlnValaHisArgGlyIleLeuGluValaValaThrAspGlnGlnIleProIle	920
Db	2840	ATGAGAGCAGGTGACACCGCGGCATTTAAGGGGGTGGTGAAGACAGACAGACGATCCCATTT	2899
Qy	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHisGluValaIleThrAlaSerGlyGly	940
Db	2900	GCCAAAGCCACCATCTGTGTGAGTGGCATTTATCAACGCGCTGAGAGACAGCCAGTGTGTT	2959
Qy	941	AspTyrTrpArgGluLeuAsnProGluTyrIleArgValaIleThrAlaHisGluGlyTyr	960
Db	2960	GATTACTGGCGAATCTTGAACCCGGGTGAAGTACCCCGTGAAGCCCAAGCGGAGGGCTTAC	3019
Qy	961	ThrProSerAlaLeuThrCysAsnValaAspTyrAspIleGluValaIleThrGlnCysAsnPhe	980
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Qy	981	IleLeuAlaArgSerAsnTrpValaArgIleArgGluIleMetAlaMetAsnGluValaArg	1000
Db	3080	ATCTGCTGCTGCTCAACTGGAGGCGATCCGGGAGATCATGGCATGAAGGGAAACGG	3139
Qy	1001	ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLeuGlnGln	1020
Db	3140	CCTATCCCAACATAGACCATTCGGCGCTTATGACCCCAACAGCGACGCTCTCAGACAG	3199
Qy	1021	ArgArgLeuGlnHisArgLeuArgLeuArgIleGlnMetArgLeuArgArgLeuAsnAla	1040
Db	3200	CGAGCGCTTACAACACCGCTGCGCTTGGGGACAGATCGGCTGCGGCGCTCAAGCC	3259
Qy	1041	ThrThrThrLeuGlyProHisThrValaProProThrLeuProProAlaProAlaThrThr	1060
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Qy	1061	LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTyrGluGlu	1080
Db	3320	CTGACACTTACCATATGAGCCCTGGGGCTTCTATACCGCCAAACACCGCTGTGGAGAGAG	3379

Qy	1081	SerglunThrguThrTrTyrrThgUvaValThrcUluPhegThrgUvaGluProglu	1100
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Qy	1101	PheglThrUysValGluProglUphgUluThrgUluLeugUluProglUphgUluThrGln	1120
Db	3440	TTTGGGACCAAGGTGGAGCCCGAGTTTGAAGCCAGTTGGAGCCTGAGTTGACACCCAG	3499
Qy	1121	LeugUluProglUphgUluGluGluGluGluGluGluGluUlysGluGluGluUlleaThrGly	1140
Db	3500	CTGGAAACCGAGTTTGAGGAAGAGAGAGAGAGGAAGAAAGAGAGAGATAGCACTGGC	3559
Qy	1141	GlnAlaPheProPheThrThrValGluThrTyrrThrValAsnPheGlyAspPhe	1158
Db	3560	CAGGCATTCCTCTTCAACAAGTAGAGCTTACACAGTAGAATTGTGGGACTTC	3613
RESULT 2			
AX578006		3935 bp	DNA
LOCUS			linear
DEFINITION	Sequence 128 from Patent WO02081745.		PAT 08-JAN-2003
ACCESSION	AX578006		
VERSION	AX578006.1		GI:27647214
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Garcia,T., roman Roman,S., Baron,R., Calli,K., Theilhaber,J., Connolly,T., Jackson,A., Bushnell,S.E. and Rawadi,G.		
JOURNAL	Genes involved in osteogenesis, and methods of use		
Patent:	WO 02081745-A 128 17-Oct-2002;		
Avantis Pharma S.A. (FR)			
FEATURES	location/Qualifiers		
source	1..3935		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Alignment Scores:			
Pred. No.:	0	Length:	3935
Score:	6272.00	Matches:	1158
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatch:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0
US-10-642-946-3 (1-1158) x AX578006 (1-3935)			
Qy	1	MetAlaAlaValAlaArgGlyAlaProLeuIleuSerCysLeuLeuAlaLeuLeuAlaLeuCys	20
Db	140	ATGCGGCGCGTGGCGCGGGGCGCCCTGCTCAGCTGCTCTGCGGTGGTGGCCCTGTGC	199
Qy	21	ProGlyGlyAlaArgProGlnInThrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40
Db	200	CTGTAGAGCGCCCGCAGACGCTGCTCAGACGACGACGATCGAGGGTCTTCGAGGGC	259
Qy	41	PheLeuSerGluLeuGluProGluProGluProArgGluAspAspValGlnAlaProProProPro	60
Db	260	TTCTGTGTAGAGCTTAGAACCTGAGCCCCCGGAGAGACACGTGAGAGGCCCGCGCTCCC	319
Qy	61	GluProThrProArgValAlaArgValAlaGlnAlaGlyGlyLysProGlyLysArgProGly	80
Db	320	GAGCCCAACCCCGCGGTGTCGAAAAGCCCGAGCGGGGCAAGCCAGGGAAGCGCGCACGGG	379
Qy	81	ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp	100
Db	380	ACGGCCGAGAAAGTCTCCGAAAGAACCAAGACCAAGGGAAGAAAGCGAAGAAAGAC	439
Qy	101	LysGlyProLysValProLysGluSerLeuGluGluGlySerProArgProProLysGly	120

Db	440	AAAGGCCCCCAAGGTCCCAAGAGATCTCTTGAGGGGTCCGCCAGGCGCCCAAGAAAGGG	499
Qy	121	LySGluLySPProProGluYsAlaThrLySlySPProLySGluLySPProProGluYsAlaThrLyS	140
Db	500	AAAGGAAAGCCCAAGGCCCAAGGCCCAAGAAAGCCCAAGAAAGCCCAAGGCCCAAGGCCCAAG	559
Qy	141	LySPProLySGluGluProProGluYsAlaThrLySlySPProLySGluGluProProGluYsAla	160
Db	560	AAAGCCCAAGAGAGAGCCCAAGGCCCAAGAAAGCCCAAGAAAGCCCAAGAAAGCCCAAGAGCC	619
Qy	161	ThrLySlySPProProSerGlyLySArgProProIleLeuAlaProSerGluThrLeuGlu	180
Db	620	ACCAAGAAAGCCCCCGTCAGAGGAAAGGCCCCCAATCTGGCTCCCTCAAGAAACCTCGAG	679
Qy	181	TRPProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyAla	200
Db	680	TGGCCACTGGCCCCCAAGCCCCCAAGCCTGGCCCCCAAGAACTACCCAGAGAGGAGGGGGCG	739
Qy	201	ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGluGluHis	220
Db	740	CCCTCTCAAAATACCTGGCAGAAATCCAGAGAGAGAACCACTGTGGAGGCACAGAGAC	799
Qy	221	GlnProGluProGluGluGluGluThrGluGlnProThrLeuAspTyrsAsnAspGlnIleGlu	240
Db	800	CAGCCTGAGCCCGAGAGAGAGACCGAGCAACCACTGACTACATACCAAGATCGAG	859
Qy	241	ArgGluAspTrpGluAspPheGluTrpIleArgArgGluGluGlnProArgProProPro	260
Db	860	AGGAGGAGACTTGAAGACTTGTGATGATCTGGCGCCAGAGAACCAAGCCAGCCACCCCA	919
Qy	261	SetArgArgArgArgProGluArgValITrpProGluProProGluGluYsAlaProAla	280
Db	920	ACCAAGAAAGAGAGGCCCGAGGGGCTGGCCAGAACCCCTGAGAGAAAGGCCCGGGCC	979
Qy	281	ProAlaProGluGluArgIleGluProProValLySPProLeuLeuProProLeuProPro	300
Db	980	CCAGCCCCGAGAGAGAGATTGAGCCTCTGTGAAACCTCTGTCGCCCGCGGCCCT	1039
Qy	301	AspTyTrpGlyAspGluITyrValIleProAsnTyTrpAspAspMetAspTyTrpPheGlyPro	320
Db	1040	GACTATGAGTAGGTATACGTATCCCAACTAGATGACATGACATTAATTAATTTGGGCT	1099
Qy	321	ProProProGluGluLySPProAspAlaGluArgGlnThrAspGluGluGluGluLeuLyS	340
Db	1100	CCTCCGCCCCAGAGGCCGATGCTGAGCCCGACGAGAGAGAAAGAGAGAGAGCTGAAG	1159
Qy	341	LySPProLySGluAspSerSerProLySGluGluThrAspLyTrpAlaValGluLyS	360
Db	1160	AAACCCAAAAGAGAGACAGAGCCCAAGAGAGAGAACCGACAAGTGGCGACGTGGAGAG	1219
Qy	361	GlyLySAspHisLySGluProArgLySGluGluGluGluGluGluGluGluGluGluGluGlu	380
Db	1220	GGCAAGAGACCAAAAGGCCCGAAAGGGCGAGAGACTGGAGAGAGAGTGAAGCTTAAG	1279
Qy	381	GluLySValLySCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle	400
Db	1280	GAGAAAGTAAAGTGTCCCCCATTTGGGATGGAGTCAACCGTATTGAGACAAACAGATC	1339
Qy	401	ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln	420
Db	1340	CGAGCTCTCCATGCTGGCGCCACGCGCTGGGGGACAGCGCGCGGCTCAACATGACAG	1399
Qy	421	ThrGlyAlaIThrGluAspAspTyTrpArgGlyAlaITrpCysAlaGluAspAspAlaArg	440
Db	1400	ACCGGTGCCACTGAGAGACATCATATGATGTGGCTGTGGTCCAGAGCATGTCCAGG	1459
Qy	441	ThrGlnITrpIleGluValAspTrpArgArgTrpThrArgPheThrGlyAlaIThrGln	460
Db	1460	ACCCAGTGAATAGGTGACACCAAGAGAGACTACCCGCTTCAAGCGCTCATCACCCAG	1519
Qy	461	GlyArgAspSerSerIleHisAspAspPheValIThrThrPhePheValGlyPheSerAsn	480

Db	1520	GGCAGAGACTCCAGATTCATGACGATTTTGTGACCACTTCTTCGTGGGCTTCAGCAAT	1579
Qy	481	AspSerGlnThrTrpValMetYrTrhAsnGlyTrGluMetThrPheHisGlyAsn	500
Db	1580	GACAGCCAGCATGGTGGTATGTATCACCAAGGCTATAGAGAAATGACTTTTCATGGGAAC	1639
Qy	501	ValAspIysAspThrTrpProValLeuSerGluLeuLeuProGluProValValAspPheIle	520
Db	1640	GTGACAGAGGACACACCCTGGCTAGAGAGCTCCCAAGCCGGGTGGTGGCTTCGTTTCATC	1699
Qy	521	ArgIleYrProLeuThrTrpAsnGlySerLeuGlyMetCArgLeuGluValLeuGlyCys	540
Db	1700	CGCATCTACCACTCACCTGGAAATGGACGCTGTGCATTCGGCTCGGAGAGTCTGGGGTCC	1759
Qy	541	SerValAlaProValYrYrSerYrYrAlaGlnAsnGluValAlaThrAspAspLeu	560
Db	1760	TCTGTGGCCCTGTCTACAGCTACTTAGCACAGAAATAGGGTGGGCCACGATGACTGT	1819
Qy	561	AspPheArgHisHisSerYrYrLysAspMetCArgGlnLeuMetLysValValAsnGluGlu	580
Db	1820	GATTTCCTGGGACCAACAGCTACAGAGACATGGCCAGCTCATGAAAGGTGTGAAGAGAG	1879
Qy	581	CysProThrIleThrArgTrhYrYrSerLeuGlyLysSerSerAspArgYrLeuLysIleYr	600
Db	1880	TGCCCAACATACCCCGACTTACAGCTTGCGGCAGAGAGCTCAGAGGCTTCAGATCTAT	1939
Qy	601	AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgYr	620
Db	1940	GGCATGGAGATCTCAGACCAACCTGTGGGAGCATGACTGGGGGAGCCCGAGTTCCGCTAC	1999
Qy	621	ThrAlaGlyIleHisGlyAsnGluValLeuGlyLysArgGluLeuLeuLeuLeuMetGln	640
Db	2000	ACTGTGTGGATCCATGGCAGAGAGAGTCTGGGCGAGAGCTGTTCCTGCTCATGACG	2059
Qy	641	TyrLeuCysArgGlyLysYrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr	660
Db	2060	TACCTGTCCAGAGATACCGGATGGGAGAACCCACGTGTGGCCAGCTGTGTACAGACACA	2119
Qy	661	ArgIleHisIleValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly	680
Db	2120	CGCATCCACCTGGTGCCTCACTGACCACTGATGGCTACAGAGTGGGACGGCAGATGGGC	2179
Qy	681	SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCAGAGTTGGGAACTGGGGCTGTGGGACTGTGGACTGGAGGGGCTTTGACATCTTGA	2239
Qy	701	AspPheProAspLeuAsnSerValLeuTrpGlyValGluGluValGlyLysTrpValProYr	720
Db	2240	GATTTCCCGGATCTCAACTGTGTCTCTGGGAGACTGAGGAGAGAAATGGGTCCCTCAC	2299
Qy	721	ArgValProAsnAsnAsnLeuProIleProGluArgYrLeuSerProAspAlaThrVal	740
Db	2300	CGGGTCCCCAACAAATTAATTGCCATCCCTGAAGCTACCTTTGGCCAGATGCCACGGTA	2359
Qy	741	SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyValA	760
Db	2360	TCCAGGAGGTCCGGGCGCATATTGGCTGTGATGAGAGAAACCCCTTCGTCTGTGGAGCA	2419
Qy	761	AsnLeuAsnGlyGlyGluArgLeuValSerYrProYrAspMetAlaArgThrProThr	780
Db	2420	AATCGAAACGGGGGAGACCGGTGTGATATCTTACCCCTACGATATAGGCCCGGACGCTTAC	2479
Qy	781	GlnGluGlnLeuLeuAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal	800
Db	2480	CAGGAGCAGCTGTGTGGCCGACCATGCGACACACCGGGGGGAGAGATGAGAGAGAGTTC	2539
Qy	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGCCACGAGAGACTCCAGAACCAACGCCATCTTCCGGTGGCTTGCCATCTCTCCGC	2599
Qy	821	SerAlaHisIleLeuThrLeuThrGluProYrTrhArgGlyGlyCysGlnAlaGlnAspYrThr	840
Db	2600	TCCGACACCTTCACTTACCGAGCGCTTACCGCGGAGGCTTCCAGAGCCACAGACTTACAC	2659



Db 260 TTCCTGTACAGCTAGAACCTGAGCCCGGGAGAGACGAGCTGAGGCGCCCGCTCC 319  
 QY 61 GIUProThrProArgValArgValAGlnAlaGlyGlyLeuProGlyLeuArgProGly 80  
 Db 320 GAGCCACCCCGGGGTCCGAAAAAGCCAGGCGGGGGCAAGCCAGGAGGCGGCCAGG 379  
 QY 81 ThrAlaAlaGluValProProGluLeuThrLeuAspGlyLeuLeuGlyLeuLeuAsp 100  
 Db 380 AGGCGCGAGAAAGTGCCTCCGGAAAAAGACCMAAGAGAGAGAGAAAGCAAGAAAGAC 439  
 QY 101 LysGlyProLeuValProLysGlySerLeuGluGlySerProArgProLysGly 120  
 Db 440 AAAGCGCCCAAGGTGCCCCAAGAGTCTTGAGAGGGTCCCCAGGCGCGCCAAAGAGGG 499  
 QY 121 LysGluLeuProProLysAlaThrLeuLysProLysGluLeuProLysAlaThrLys 140  
 Db 500 AAGGAAACACCAACCCAGGACCAAGAAAGCCCAAGAGAGACCACTAAGGACCAAG 559  
 QY 141 LysProLysGluGluProProLysAlaThrLeuLysProLysGluLeuProLysAla 160  
 Db 560 AAGCCCAAGAGAGAGCCCAACAGGACCAAGAGACCAAGAGAGCCCAAGAGCC 619  
 QY 161 ThrLeuLysProProSerGlyLysArgProProLeuLeuAlaProSerGluThrLeuGlu 180  
 Db 620 ACCAAGAGCGCCCGTCAGGAGAGAGCGCCCGCATTCGTGCTCCCTCAGAAACCTGAG 679  
 QY 181 ThrProLeuProProProProSerProGlyProGluLeuProGluGluGlyAla 200  
 Db 680 TGGCCACTGCCCCCAGCCCGGAGCGCTGCGCCGAGAGACTACCCAGAGAGGAGGGG 739  
 QY 201 ProLeuSerAspAsnThrProGluAsnProGluGluGluThrHisValGluAlaGluHis 220  
 Db 740 CCCCTCTCAATACTGCGAGAAATCCAGAGAGAGAACCATGTGAGGACAGAGGAC 799  
 QY 221 GlnProGluProGluGluGluThrGluGluProThrLeuAspTyrAsnAspGlnLeu 240  
 Db 800 CAGCTGAGCGCGAGAGAGAGACCGAGCAACCCAGCTGAGCTACATGACGATCGAG 859  
 QY 241 ArgGluAspTyrGluAspPheGluTyrLeuArgGlnLysGlnProArgProProPro 260  
 Db 860 AGGAGAGACTATGAGACTTGTGATCATTCGCGCAGAGCAACCCAGGCCACCCCA 919  
 QY 261 SerArgArgArgArgProGluArgValTyrProGluProProGluGluLysAlaProAla 280  
 Db 920 AGCAGAAAGAGAGGCCCCAGCGGGTCTGGCCAGAGCCCCCTTAGAGAGAGGCCCG 979  
 QY 281 ProAlaProGluGluGluGluGluProProValLysProLeuLeuProProLeuProPro 300  
 Db 980 CCAAGCCCCGAGAGAGATGAGCTCTGTAAGCTCTGCTGCCCGCGCTGCCCT 1039  
 QY 301 AspTyrGlyAspGlyTyrValLeuProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320  
 Db 1040 GACTATGGTGTATGATACGTGATCCCACTACGATGACATGACATTAATTTGGGCT 1099  
 QY 321 ProProProGluLysProAspAlaGluArgGlnThrAspGluGluLysGluLeuLys 340  
 Db 1100 CTTCCGCCCGAGAGAGCCGATGCTGAGCGCCAGACGAGAGAGAGAGAGCTGAAG 1159  
 QY 341 LysProLysLeuGluAspSerSerProLysGluGluGluThrAspLysTyrAlaGluLys 360  
 Db 1160 AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219  
 QY 361 GlyLeuAspHisLeuGluProArgGlyGlyGluGluGluGluGluGluGluGluGlu 380  
 Db 1220 GGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279  
 QY 381 GlnLeuValLysCysProProLeuGlyMetGlySerHisArgTLeuLysAspGlnLeu 400  
 Db 1280 GAGAAAGTCAAGTCTCCCTCCATTTGGATGAGTCAACCTGTTAGAGAGAGAGAGAT 1339  
 QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420  
 Db 1340 CGAGCTCTCTCATGTGCGCACGAGCTGGGGGACAGCGCGGCGGCTCAACATGACG 1399

QY 421 ThrGluAlaThrGluAspAspTyrTyrAspGlyAlaTyrCysAlaGluAspAlaArg 440  
 Db 1400 ACCGGTGCACATGAGAGAGACACTATATAGTGTGCTGTGGCCAGAGACATGCTCAG 1459  
 QY 441 ThrGlnTyrLeuGluValAspThrArgArgThrThrArgPheThrGlyValLeuThrGln 460  
 Db 1460 ACCGATGATAGAGTGGAGACACAGAGAGACTACCGGTTACAGGGGTATCAACCCAG 1519  
 QY 461 GlyArgAspSerSerLeuHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480  
 Db 1520 GGCAGAGACTCCAGCATCATGACATTTGTGACACACTTCTTGTGGGCTTCAGCAT 1579  
 QY 481 AspSerGlnThrThrValMetThrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500  
 Db 1580 GACAGCCAGACATGGGTGATGATACCAAGGAGCTATGAGAAATATACCTTTATGGAGAC 1639  
 QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheLe 520  
 Db 1640 GTGACAAAGAGACACCGGTGCTGATGAGTCCAGAGCGGTGTGGCTCGTTTCATC 1699  
 QY 521 ArgTyrTyrProLeuThrThrAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540  
 Db 1700 CCGATCTACCACTCAGCTGAGATGAGAGCTGTGCATGCGCTGAGAGGTGCTGAGG 1759  
 QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaThrAspAspLeu 560  
 Db 1760 TTTGTGGCCCTGTCTTACAGTACTACGACAGAAATGAGTGTGGCCACCATGACCTG 1819  
 QY 561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValAlaAsnGluGlu 580  
 Db 1820 GATTTCCGACACACAGCTACAGAGACATGCGCCAGCTCATGATAGTGTGAAAGAGAG 1879  
 QY 581 CysProThrThrThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysTyr 600  
 Db 1880 TCCCCACCATCACCAGCTTACAGCTGTGGCAAGAGCTCACAGGCTTCAAGATCTAT 1939  
 QY 601 AlaMetGluLeuSerAspAsnProGluGluGluGluLeuGluGluProGluPheArgTyr 620  
 Db 1940 GCGATGAGATTTCAACACACCTGGGAGCATGAACTGGGGAGCCGAGATTCGCTAC 1999  
 QY 621 ThrAlaGlyLeuHisGlyAsnGluValLeuGluArgGluLeuLeuLeuLeuMetGln 640  
 Db 2000 ACTGCTGGGATCATGAGGACAGAGGTGCTGGGCCAGAGCTGTGCTGCTCATGACG 2059  
 QY 641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
 Db 2060 TACTGTGCCGAGAGTACCGCATGAGAACCCAGCTGTGCGAGCTGTGAGAGACACA 2119  
 QY 661 ArgTyrHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680  
 Db 2120 CCGATTCACCTGTGCTGCTCATGAACTGTATGCTGACAGAGTGCAGAGTGGCC 2179  
 QY 681 SerGluPheGlyAsnTyrAlaLeuGluTyrLeuThrGluGluGlyPheAspLeuPheGlu 700  
 Db 2180 TCAGATTTGGGAACTGGGCGCTGGGACTGTGAGCTGAGAGAGGCTTTGACATCTTGA 2239  
 QY 701 AspPheProAspLeuAsnSerValLeuTyrGlyAlaGluGluLysGlyTyrValProTyr 720  
 Db 2240 GATTTCCCGATCTCAACTGTGCTGTGGAGCTGAGAGAGAGAGAGAGAGAGAGAG 2299  
 QY 721 ArgValProAsnAspAsnLeuProLeuProGluArgTyrLeuSerProAspAlaThrVal 740  
 Db 2300 CCGGTCCCAACAAATACCTTGGCCATCTCTGAACGCTACCTTTCCGAGATGCCAGT 2359  
 QY 741 SerThrGluValArgAlaLeuLeuAlaTyrMetGluLysAsnProPheValLeuGlyAla 760  
 Db 2360 TCAGAGAGAGTCCGGGCGCATTCGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2419  
 QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
 Db 2420 AATCTGAAAGGGGGAGAGGCTATGATTCACCTTACGATATGAGCCGACGCTTACC 2479



[illegible]

Db	3560	CAGGCACTTCCCTTCAACAAGTACGACCTTACACAGTGAACCTTTGGGACCTTC	3613
RESULT 4			
LOCUS	BC038588		
DEFINITION	Homo sapiens AE binding protein 1, mRNA (CDNA clone MGC:46180		
ACCESSION	BC038588		
VERSION	BC038588.1		
KEYWORDS	MG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 4125)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klusner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hale, F., Ditchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stadton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kaha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McEran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viall, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bonfield, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmutz, J., Myers, R.M., Buetow, L.Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 4125)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:gcgaps-remail.nih.gov">gcgaps-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:ayec_mgc@hgrl.nih.gov">ayec_mgc@hgrl.nih.gov</a> Ahtler, N., Nysle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karllins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Maiello, C., Makari, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Skattipod, S., Thomas, P.J., Touchman, J.W., Taugson, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		



QY 461 GYArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480  
 DB 1686 GCGAGAGATCCAGCATCCATGACGATTTTGTACCACTCTTCTGGGCTTCAACAT 1745  
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 DB 1806 GTGGACAGAGACACACCGGTGATGAGCTCCAGAGCCGGTGGTGGCTCTTTTCATC 1865  
 QY 521 ArgIleTyrrProLeuThrTrpAsnGlySerLeuCyMetArgLeuGlnValLeuGlyCyV 540  
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 QY 541 SerValAlaProValTyrrSerTyrrValaGlnAsnGlnValValAlaThrAspAspLeu 560  
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 QY 561 AspPheArgHisHisSerTyrrTyrrValAspMetArgGlnLeuMetLeuValValaAngGlu 580  
 DB 1986 GATTTCCGGCACACAGCTTACAGAGCAATGCCCGCACTCATGAAAGGTGGTGAACGAGAG 2045  
 QY 581 CyProThrIleThrArgThrTyrrSerLeuGlyLeuSerSerArgGlyLeuLeuValIleTy 600  
 DB 2046 TGGCCCACTACACCGGCACTTACAGCTGGGGAAAGCTCACAGAGCCCTCAAGATCTAT 2105  
 QY 601 AlaMetGlnIleSerAspAsnProGlyGlnHisGlnLeuGlyGluProGluPheArgTy 620  
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 QY 621 ThrAlaGlyIleHisGlyValAngGlnValLeuGlyValArgGlnLeuLeuLeuMetGln 640  
 DB 2166 ACTGGTGGGATCCATGGCAACGAGGTGGCTGGGGCGAGAGCTGTGGCTGCTCAATG 2225  
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 QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrrGlnValAlaIleGlnMetGly 680  
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 QY 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGlnGluGlyPheAspIlePheGlu 700  
 DB 2346 TCAGAGTTTGGAACTGGCGGTGGGACTGTGGACTGAGAGGGCTTTGACATCTTTGAA 2405  
 QY 701 AspPheProAspLeuAsnSerValLeuTrpGlyValaGlnGluArgTyrrTrpValProTy 720  
 DB 2406 GATTTCCCGGATCTCACTGTGTCTGTGGAGCTGAGAGAGAGAAATGGGTCCCTTAC 2465  
 QY 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrrLeuSerProAspAlaThrVal 740  
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 QY 781 GlnGluGlnLeuLeuAlaAlaMetAlaAlaAlaArgGlyGluAspGluValAla 800  
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DB 2766 TCCGACACCTTACCTTGAACCAAGCCCTTACCGCGAGGCTGCCAAGCCCAAGACATCAC 2825  
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REFERENCE  
 AUTHORS  
 1 Kanehori, K., Ishibashi, T., Chiba, Y., Ono, Y., Fujimori, K., Hirooka, S.,  
 Tanai, H., Watanabe, S., Ishida, S., Ota, Y., Hotuka, T., Watanabe, M.,  
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A.,  
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 Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K.,  
 Masuno, Y., Nagai, K. and Isogai, T.  
 NEDO cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 3909)  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Isogai, T. and Yamamoto, J.  
 TITLE  
 Direct Submission  
 Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: fil-cdna@hifcy.com, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO cDNA sequencing project supported by Ministry of Economy,  
 Trade and Industry of Japan: cDNA full insert sequencing: Research  
 Association for Biotechnology (RAB); cDNA library construction:  
 Helix Research Institute (HRI) (supported by Japan Key Technology  
 Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and  
 Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.

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US-10-642-946-3 (1-1158) x AKI28980 (1-3909)

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 QY AsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyValGlnArgGlyArgLeu 417  
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RESULT 8  
LOCUS BC082577 3869 bp mRNA linear ROD 16-SEP-2004  
DEFINITION Mus musculus AE binding protein 1, mRNA (cdna clone MGC:100139  
IMAGE:30648530), complete cds.  
ACCESSION BC082577  
VERSION BC082577.1 GI:52139026  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Scurionathi; Muroidae; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 3869)  
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
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human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 3869)  
Director MGC Project.  
DIRECTOR MGC Project.  
TITLE Director MGC Project.  
AUTHORS Director MGC Project.  
JOURNAL Submitted (15-SEP-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.  
Thomas L. Casavant.  
Web site: <http://genome.uiowa.edu>  
Contact: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu); [tom-casavant@uiowa.edu](mailto:tom-casavant@uiowa.edu)  
Bonaldi,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,  
Fisher,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,  
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,  
Casavant,T., Soares,M.B.  
Clone distribution: MGC clone distribution information can be found  
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DB 503 AAGGACAAAGGCCCAAGGCCCAAA---CCCTGGAGGGCTCTACCGAGGCCCAAG 559  
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QY	478	PheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPhe	497
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QY	498	HisGlyAsnValAspLyvAspThrProValLeuSerGluLeuProGluProValVala	517

Db	1679	TATGAAATGTGGACAGAGACACCTGTGTGGACAGCTCCCTGGACCACTTGTGACC	1738
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Db	1739	COTTTCATCCGCATCTATCCATCACTCACTGGACGGTAGCTGTGTCAATGCGCTGGAGGTG	1798
Qy	538	LeuGlyCySerValAlaProValTySerTyTriYalaglnaengluValAlaThr	557
Db	1799	CTAGAGCTCCCGGTGACCCCTGTCTCTACAGCTACTACGACAGATGAGGTGTAACTACT	1858
Qy	558	AspAspLeuAspPheAspGhiHisSerTyIlyAspMetArglnLeuMetIysValVal	577
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Qy	578	AengluGluCySPProThrIleThrArgThrTySerLeuGlyLysSerSerArgGlyLeu	597
Db	1919	AATGAGAGTGTCCCAACATCACTCGACATACAGCTCGGGCAGAAATTCAACAGAGGCTC	1978
Qy	598	LysIleTyAlaMetGluIleSerAspAspProGlyLglnHisgluLeuGlyGluProGlu	617
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Qy	618	PheArgTyTriThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeu	637
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Qy	658	GlnAspThrArgIleHisLeuValProSerLeuAspProAspGlyTyTriGluValAlaAla	677
Db	2159	CAGAGCACGCCATCCACCTGTGTCCCTCGCTGTAACCTATGTGCTATGAGGTGGACGC	2218
Qy	678	GlnMetGlySerGluPheGlyAsnTriPAlaLeuGlyLeuTriPThrGluGluGlyPheAsp	697
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Qy	818	SerPheAlaSerAlaHisIleLeuThrLeuThrGluProTyTriArgGlyGlyCySglnAlaGln	837
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Qy	1137	IleAlaThrGlyGlnAlaPheProPheThrThrValGluThrTrpValAsnPheGly		1156							
Db	3533	ATGACACAGCGCTTACATTTCCATCTACACACAGTGCAGACTTACACAGTAACTTTGGG		3592							
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Db	3593	GACTTC 3598									
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ACCESSION	AF053943	complete cds.									
VERSION	AF053943.1	GI:3288913									
KEYWORDS											
SOURCE	Mus musculus (house mouse)										
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										

REFERENCE	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
AUTHORS	Sotgiougnath; Muroidae; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 3790)
JOURNAL	Layne,M.D., Endege,W.O., Jain,M.K., Yet,S.-F., Hsieh,C.M., Chin,M.T., Perrella,M.A., Blanan,M.A., Haber,E. and Lee,M.E. Aortic carboxypeptidase-like protein, a novel protein with discoidin and carboxypeptidase-like domains, is up-regulated during vascular smooth muscle cell differentiation
PUBMED	J Biol. Chem. 273 (25), 15654-15660 (1998) 9624159
REFERENCES	2 (bases 1 to 3790) Layne,M.D., Endege,W.O., Jain,M.K., Yet,S.-F., Hsieh,C.M., Chin,M.T., Perrella,M.A., Blanan,M.A., Haber,E. and Lee,M.E. Direct Submission Submitted (16-MAR-1998) Cardiovascular Biology Laboratory, Harvard School of Public Health, 677 Huntington Ave, Boston, MA 02115, USA
TITLE	Location/Qualifiers
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VERSION E07353.1 GI:2175493
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ORGANISM Mus sp.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 3728)
AUTHORS Kawai,S., Takeshita,A., Okazaki,M. and Aman,E.
TITLE BONE-RELATED CARBOXYPEPTIDASE-LIKE PROTEIN AND ITS PRODUCTION
JOURNAL Patent: JP 1994121682-A 1 06-MAY-1994;
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OS Mus sp. (mouse)
PN JP 1994121682-A/1
PD 06-MAY-1994
PF 03-DEC-1992 JP 1992324033
PR 28-AUG-1992 JP 92P 230029
PI KAWAI SHINJI, TAKESHITA ATSUSHI, OKAZAKI MAKOTO, AMAN EGON PC
C12N9/48,A61K37/02,A61K39/395,A61K39/395,C07K13/00, PC
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Best Local Similarity: 82.3% Mismatches: 112
Query Match: 80.6% Indels: 38
DB: 2 Gaps: 9
US-10-642-946-3 (1-1158) x E07353 (1-3728)
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Qy 638 LeuMetGlnTrpLeuCysArgGluTrpArgAspGlyLysAspProArgValArgSerLeuVal 657  
Db 1953 CTCATGCAATACCTTATGCGAGAGTACCGGATGGAAACCGAAGATGGCGCAACTGGTGTG 2012  
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QY      1018  LeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArg 1037
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QY      1057  ProAlaThrThrLeuSerThrThrIleGlnProTyrGlyLeuIleProProThrThrAla 1076
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QY      1077  GlyTyrGlnGlnSerGlnThrGlnThrTyrThrGlnValValThrGlnPheGlyThrGln 1096
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QY      1097  ValGlnProGlnPheGlyThrLysValGlnProGlnPheGlnThrGlnLeuGlnProGln 1116
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Db      3387  ATGACACAGGCGCTTACATTCTCACTCACAACAGTGGAGACTTACAGTGAATTGGG 3446
QY      1157  AspPhe 1158
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RESULT 11
LOCUS      115213
DEFINITION Sequence 1 from patent US 5460951.
ACCESSION 115213
VERSION    115213.1 GI:1250121
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 3728)
AUTHORS   Kawai,S., Takeshita,S., Okazaki,M. and Amann,E.
TITLE      Bone-related carboxypeptidase-like protein and process for its
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JOURNAL    Patent: US 5460951-A 1 24-OCT-1995;
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Alignment Scores:
Pred. No.: 0
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Percent Similarity: 87.14
Best Local Similarity: 82.34
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QY      21  ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGlnGlnPheLeuGlnGly 40
Db      129  CCTGAGGGGAAACCCACAGCGGTGCTGACGAGCGAGATGAGGAGTTCTTCGAAAGC 188
QY      41  PheLeuSerGlnLeuGlnProLys-----ProArgGluAspAspValGlnAlaProPro 58
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QY      59  ProProGlnProThrProArgValaArgLysAlaGlnAlaGlyGlyLysProGlyLysArg 78
Db      249  CTTCCGAAACCCACCAAGCGTCCCGCAAAATCCAAAGCGAGGGGCAAG----- 296
QY      79  ProGlyThrAlaAlaGlnValaProProGlnLysThrLysAspLysGlyLysLysGlyLys 98
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QY      99  LysAspLysGlyProLysValaProLysGlnSerLeuGlnGlySerProArgProProLys 118
Db      357  AAGGACAAAGGCCCCAAAGCCACAA---CCCTGGAGGCTTTCAGGCCCAACCAAG 413
QY      119  LysGlyLysGlnLysProProLysAlaThrLysLysProLysGlnLysProProLysAla 138
Db      414  AAACCAAGAGAGAGCCCAAGGCCCAAGGACCAAGAGGCCCAAGAGAAACCAACCAAGGCC 473
QY      139  ThrLysLysProLysGlnGlnProProLysAlaThrLysLysProLysGlnLysProPro 158
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Qy	978	CysAsnPheIleLeuAlaArgSerAsnTrpIlyAspIleArgGluIleMetAlaMetAsn	997
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Qy	1057	ProAlaThrThrLeuSerThrThrThrIleGluProTrpGlyLeuIleProProThrThrAla	1076
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VERSION	AX473127.1	GI:22207848	
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ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Ryan, J. W.		

TITLE	Isolated genomic polynucleotide fragments from chromosome 7			
JOURNAL	Patent: WO 0224741-A 8 28-MAR-2002; Ryan, James W. (US)			
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QY	41	PheLeuSerGluLeuGluProGluProArgGluAspValGluAlaProProProPro	60	
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QY	84	-----	84	
Db	10533	TGGCTTACTAATCGACCGACGCCAGATGCCTGGAGGAGCCCTGTAGCCGAGGT	10474	
QY	84	-----	84	
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Db	7354	ACCTGCTGTCCCTGCTGTCCCTGCGTGCACACCCAGCAAGCTGCTGTCTCTGTC	7295
QY	313	-----	313
Db	7294	CTCAGAGCTGTCTTCTTGGCCGCTTCCCTGTGTTCTGTGGCTGTGACCCCAAG	7235
QY	313	-----	313
Db	7234	GGTGTCCTAGGCAACACTGACCTGTACACCATGTGGGTTCCAGCCTCCAGTCT	7175
QY	313	-----	313
Db	7174	GTGCTTAACGTGGCTTCCCGCTGCTGTGGCACTGCCCACTCTTCAGGAGCCCG	7115
QY	313	-----	313
Db	7114	AGGGCTTTTGCTCCTCTGTGTCTATGCCCCGTGCTCCCTGAGCCCTCAGTTCCCTT	7055
QY	313	-----	313
Db	7054	CCTCTGGGTGAGCCGCTGATGCATTTCTCTGCCCCCAGGTCCCATCATGTGCT	6995
QY	313	-----	313
Db	6994	CCAATGTCTCCCAATCTACACCCCAAGCCCGAACCCAGGACAGGTGCAATTGTCC	6935
QY	313	-----	313
Db	6934	TCCAGGCTTTTCCATGCCCCCTGGGCTGAGTCTTTCCCAAGCCAGATCTCTGGAA	6875
QY	313	-----	313
Db	6874	GGCCGGGCTGTGACTTACAGAGGCTTTGTCTCAAGCTGCCCTGTAGCTCGGAGTGTCTCT	6815

[illegible]

Db 5734 GCTCTGGCCCTGGCTTTGAGTCCATTCCAGGTGGGCTGTGTGACAGGGCAACAGGGAGCCAC 5675  
Qy 383 ----- 383  
Db 5674 CAGCTGACAGAGCTGCCCTCTGACTGTGCCCGATGTGCGGGAGTGGGCTCTGGGCT 5615  
Qy 383 ----- 383  
Db 5614 CTTGGTCTTGGGTTGGTGGAGGAAGATGAGCTAGTGAGCCATTCTGGGGTAC 5555  
Qy 384 -----Lys-CysProProlIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400  
5554 GCCTCCCTCAGAGTGTCCCCCATTTGGATGAGTGCACACCTGATTGAGGCAACAGATC 5495  
Qy 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyValGlnArgGlyArgLeuAsnMet--- 419  
5494 CGAGCCTCCTCATGTGTGCGCCACAGCGCTGGGGGCAAGCGCGGCTCAACATGTCAG 5435  
Qy 419 ----- 419  
Db 5434 GTGGGATTTGGGATGGGCCCATCTCCCACTGGGATTAAGGAACTCTCCGCCATGCTCA 5375  
Qy 420 -----GlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTr 433  
5374 GCCTCCCTGCCCTGGACAGACCGGTGCCACTGAGGACGACTACTATGATGTGTG 5315  
Qy 433 PCyValIleGluAspAspAlaArgThrGlnTyrIleGluValAspThrArgThrThrAr 453  
5314 GTGTGCCAGAGAGCATGTCCAGAGACCCAGTGATAGAGTGAGACCCAGAGAGCATACCG 5255  
Qy 453 gPheThrGlyValIleThrGlnGlyArgAspSerSerIleHis----- 467  
5254 GTTCACAGGGGTATCATCCAGAGGACAGACTCCAGATCAGTGTGCGTGCAGGCTCAT 5195  
Qy 467 ----- 467  
Db 5194 GATATGTTGGCAAGGGAGATGGCTACATAGGCATGTGTGTCCATTAAAGAGATT 5135  
Qy 467 ----- 467  
Db 5134 CCAGTGGGCCCTTTCTTTGGCCAGCCAAAGAGGCCAAAAGATCAGTAGAGGATCACC 5075  
Qy 467 ----- 467  
Db 5074 CTGGCCATCCCACTCTCAGCTGTGCTAGTCAAGCCCTGTGTCTGTATGACATGAGT 5015  
Qy 467 ----- 467  
Db 5014 TTAGGACAGATCACTGCCCATGTGCTATGTGACGGGCAATAGACCCAGGCTCAACACT 4955  
Qy 467 ----- 467  
Db 4954 GGGCCGTGACAGCAACACCTGTAGCTTTAAATTCTTGGGGCTCGGAAGAAGGAGGCTC 4895  
Qy 467 ----- 467  
Db 4894 AGGCCACTGAGGGCCTGGAGGGGGAAGAACCTTGTCTGACCACTGTCCACTCCACAG 4835  
Qy 468 -AspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTyrValMet 487  
4834 TGACGATTTTGTGACCACTTTCTTGTGGGCTTCAGCAATGACCAAGCCAGATGGGTGAT 4775  
Qy 487 cTyrThrAsnGlyTyrGluGluMet----- 495  
4774 GTACACCAACGGCTATGAGAAATGTGTGGGACCAATGCCAGGCTTGTGCTGTGCC 4715  
Qy 495 ----- 495  
Db 4714 ATTGTCTGGGCGAGGGGTGGCTCTCAGAGGGGCTGGCACTGCTCTGAGGCTTGCTT 4655  
Qy 496 -----ThrPheHisGlyAsnValAspIleAspThrProValLeuSerGluLeuProG 513

Db 4654 CTCGCCAGACCTTTCAATGGGAACGTGGACAAAGGACACACCCGCTGTGATGAGTCCCAAG 4595  
Qy 513 IuProValValAlaArgPheIleArgIleTyrProLeuThrTyrPheAsnGlySerLeuCysM 533  
4594 AGCCGGTGGGTGCTCCTTTTCATCCGATCTACCCACTCACTGGAATGAGCAGCTGTGCA 4535  
Qy 533 ePheArgLeuGluValLeuGlyCysSerVal----- 542  
4534 TGCCTCTGAGAGTGTGGGTGTCTGTGTGACCCGTGATGTGGAGGCTGGCAGGGGCTC 4475  
Qy 542 ----- 542  
Db 4474 TGAGTGAAGTGGGTGCTAGGTGGGCCAGCCGGGCAACCAAGTAAAGCAACCCCGCT 4415  
Qy 543 -----AlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeu 561  
4414 CCCTTGACGTGTCTACAGTACTACGACAGAAATAGGTGTGGCCACGATGACCTGG 4355  
Qy 561 sPheArgHisHisSerTyrTyrAspMet----- 570  
4354 ATTTCCGGACCAACAGCTACAAAGACATGCGCAGGTTGGAGCATATATCTTGGGGCTG 4295  
Qy 570 ----- 570  
Db 4294 GGGGTGGACCTGTCTGTGTGCTGACGGGAGTGTGTGCTGTGTCTTGTCACTGGGGCC 4235  
Qy 570 ----- 570  
Db 4234 AGTCCCTACTGTTCCAGGAGATGTGCTGTCCCTCACTTAGAAGAAGCCAGTACT 4175  
Qy 570 ----- 570  
Db 4174 GGGGGCTGCTGAAGGGGTATGATGCCGCTCTCCATAGAGAGGCCCTGAAATGGAA 4115  
Qy 571 -----ArgG 572  
4114 GGGGATGTGACAGGGGGAGCGATTCATGATTAATTCACAGTCTCTCCCTCTGTGCCC 4055  
Qy 572 IuLeuMetIysValValIleAsnGluGlyCysProThrIleThrArgThrTyrSerLeuGly 592  
4054 AGCTCATGAAGGTGTGGAACGAGAGATGCCCCACATCAACCCGACTTACAGCTGGGCA 3995  
Qy 592 ySerSerArgGlyLeuIysValIleTyrAlaMetGluIleSerAspAsnProGlyIuHisG 612  
3994 AGAGCTTCAGAGGCTCAAGATCTTATGCAATGAGATCTCAACAACTCTGGGAGACATG 3935  
Qy 612 IuLeu----- 613  
3934 AACTGGGGAGAGGTCTGTGGGGCCAGCAGTGTGCTGTGTGATGTGAGAGCTCA 3875  
Qy 613 ----- 613  
Db 3874 CTGCTCCGCGCTGTCCGAGGCTCTGTGGGATTTCTGAGTTGTCTTACAGGGCCCTAG 3815  
Qy 613 ----- 613  
Db 3814 GAGCCCACTGTCCCCAGAACCTTGAGTATGAGTGGGTCTGGTCTCTCTCAGCTG 3755  
Qy 614 -----GlyGluProGlu 617  
3754 CCTGGGCTCGGGAGACTGAGTGTCACTGAGGCTCCGCGCTTGACAGGGAGCCCGAG 3695  
Db 618 PheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGlyIuLeuLeuLeu 637  
3694 TTCGGCTTACACTGTGGGATTCATGGAACGAGGTGTGGGCCGAGAGCTGTGCTGTG 3635  
Qy 638 LeuMetGlnTyrLeuCysArgGlyIuTyrArgAspGlyAsnProArgValArgSerLeuVal 657  
3634 CTATGCACTACCTGTGTGCGAGAGTACCGGATGGGAAACCAAGTGTGCGAGCTGGTG 3575  
Qy 658 GlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAla 677  
3574 CAGGACACAGCATCACTGTGTGCTCACTGAACCTTGATGTGCTACGAGGTGGCAGGCG 3515

QY	678	GIInet-----	672
Db	3514	CAGATGGTGGGTTGAAGGCTGAGCGTCCAGGGTCCAGGCACTGGGGGTTGGGGGT	3455
QY	680	-----GlySerGluPheGlyAsnTyrPAl	687
Db	3454	GTGGGTAGCCGATGCTACCTCGTGTGCTGCCACAGAGGGCTCAGAGTTTGGGAATGGGC	3395
QY	687	aLeuGlyLeuThrPheArgGluGlyPheAspLLeuPheAspPheProAspLeuAsnSe	707
Db	3394	GCTGGGACTGTGGACTGAGAGGGGCTTTGAACATCTTTGAAATATTTCCGGATCTCAACTC	3335
QY	707	rValLeuTyrPglYalGluGluArgLysTyrValProTyrArgValProAsnAsnLeu	727
Db	3334	TGTGCTCTGGGGAGCTGAGAGAAATGGTCCCCCTACCGGGTCCCCCAATAACTT	3275
QY	727	uProLLeuProGluArgTyrLeuSerProAspAlaThrVal-----	740
Db	3274	GCCATCCCTGAACCGTACCTTTCGCCAGATGCCACGGT-GAGGCTACAGCTGGCTGAA	3216
QY	740	-----	740
Db	3215	AGGCGAGAGGAGCAGCTGCACCTCGGGTCTGCTGTGCTTGGGCTTGGGGTGGGCT	3156
QY	740	-----	740
Db	3155	GACGGTGCTGAACCTCAGACGCTGAGGCTCTGGGGGTTGGGGGACAGGGATCGTGC	3096
QY	740	-----	740
Db	3095	GTACTGCTGTGAACCTTCATGAGAGGTATCGGGCTAGTGGGATATGCGCGAGCT	3036
QY	741	-----SerThrGluValArgAlaIleI	748
Db	3035	GCAGCGCTGGCTCAACGTGCTGGCCACTCCAGGTATCCAGAGAGTCCGGGCATAT	2976
QY	748	aAlaTyrPheGluLysAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLe	768
Db	2975	TGCCCTGATGGAGAAACCCCTTGCTGCTGGGAGCAATCTGAACGCGCGAGCGCT	2916
QY	768	uValSerTyrProTyrAspMetAlaArgThrProThrGlnGluGluLeuAlaAlaI	788
Db	2915	AGTATCTTACCCCTACGATGATGGCCCGCACGCTACCCAGAGCACTGTGGCCGACG	2856
QY	788	aMetAlaAlaAlaArgGlyGluAspGluAspGluValSerGluAlaGlnGluTyrProAs	808
Db	2855	CATGCACAGACGCGCGGGGAGAGATGAGAGACGAGGTCTCCAGGCGCCAGAGACTCCGA	2796
QY	808	PheAlaIlePheAspGlyTyrPheAlaIleSerPheAlaSerAlaHisLeuThrPheThrG	828
Db	2795	CCAGCCCATCTTCGCTGGCTTGCATCTCTTGCCTCCGACACTTCACCTTGACCGA	2736
QY	828	uProTyrArgGlyGlyCysGlnAlaGlnAspTyrThrGlyGlyMetGlyIleValAsnG	848
Db	2735	GCCCTACCGCGGAGGCTGCCAAGCCCAAGACTACACCGCGGCATGGGCATCTCAACG	2676
QY	848	YAlaLysTyrPheAsnProArgThrGlyThr-----	857
Db	2675	GGCCAAAGTGAACCCCGGACCGGAGTGAAGTCAAGCTGGAGGGGCTGTGGCGGGGCC	2616
QY	858	-----IleAsnAsp	861
Db	2615	TGGTCCGAGAGGGGCTGACTTTGGGCTCTGATCTGTCCCGGCACTATCAATGACTT	2556
QY	861	eSerTyrLeuHisThrAsnCyLeuGluLysSerPheTyrLeuGlyCyAspLysPhePr	881
Db	2555	CAGTTACCTGCATCAACCACTGCTGAGAGTCTCTTTCACCTGGGCTGTGACCAATGCC	2496
QY	881	oHisGluSerGluLeuProArgGluTyrPglLysAsnLysGluAlaLeuLeuThrPheMe	901
Db	2495	TCATAGAGGTGAGTGGCCCGGAGATGGAGAACAAAGAGGGGCTGTCACTTAT	2436

[illegible]







QY	84	-----	84
Db	146794	ATCAGGTTCTCAACAGCACTTGACGCTCCTGTTAGGGTCTGGAGATTCCATGGG	146735
QY	84	-----	84
Db	146734	AATCCTCACACCAAGTCCGTGCTCCTCTCCAGACTTGAAATGATGTGACCCACA	146675
QY	84	-----	84
Db	146674	GCTCCCTACCTGTCTTTCTGTCTGTGTGTATCCCTGAACCCCGAGACTCCTATC	146615
QY	84	-----	84
Db	146614	CTTCCAAATTCACAAACCCCTTACTCTCGAAGAGACACCTTCTCTTCTTGGGC	146555
QY	84	-----	84
Db	146554	TTCAATACTCAACCAAGTGTCCCTTTCTTTGAACTTTCTTGCCCGTAGAGACAG	146495
QY	84	-----	84
Db	146494	GGAAGGTCTTGAGGCCCATGTCCCTCTTTGTATGAGAGTTGGCAGGATGACAGATG	146435
QY	84	-----	84
Db	146434	CTCTCCAGGCTGTGATGGCTAGTCACTCTGCCCCCTTGCCAGAACAGATA	146375
QY	84	-----	84
Db	146374	GTGGAGAGTGGATAGTAAGAAACCCCTATTGAGGTTTGGCAGGTGGGGGATGAGGGC	146315
QY	84	-----	84
Db	146314	CTCCCCCTGGGAACCTGAACCTAGCTCACTTTAGAGAGTTGAGATTGGTGTC	146255
QY	84	-----	84
Db	146254	CAGCCCCAGACTTGACAGACAGAAATCTGGGTCCGATCCAGTTTGCCACTTGGCANA	146195
QY	84	-----	84
Db	146194	TGACTTAACCTCTCACTTGTCTGATCCGACCTGGGAACCTGACAGAGTCCCTGTGCCAG	146135
QY	84	-----	84
Db	146134	GTTCTGGGATCTAGAGAGGGGCTCATGGGGCACAGAGCTGGCTGTTCATTTGACA	146075
QY	85	-----	85
Db	146074	CGAGTCTGCATCTTGACAGAGTGTCTCGGAAAAAGACCAAGGAGAAAGGACAA	146015
QY	98	-----	98
Db	146014	GAAAGCAAAAGCCCCCAAGGTGCCAAAGAGTCTTTGGAGGGTCCCCAGAGGCCCA	145955
QY	118	-----	118
Db	145954	GAAAGGGAAGGAGAACCCACCAAGGCCACCAAGAGCCCAAGAGAAAGCCTTAAGGC	145895
QY	138	-----	138
Db	145894	CAACCAAGAAAGCCCAAGAGGACCAAGGACCAAGAGGACCAAGAGAGGACCAAC	145835
QY	158	-----	158
Db	145834	CAAGGCAACCAAGAGGACCCCGTCAAGAGAGAGGCCCCCATCTTGCTCCCAAGAAC	145775
QY	178	-----	178
Db	145774	CCTGGAGTGCCACTGCCCCCAGCCCTGGCCCTGGAGAGACTTACCCAGAGAGG	145715
QY	198	-----	198

Db	145714	AGGTTTGCGCGGCTCTCTCTGGGGTGAATGGGGCTGTGACTGCTGCTGGGGTGAAGGA	145655
QY	198	-----	198
Db	145654	GGGAGTGGAGGACAGGTTTCTGGGGCCCTGCTTCTATAGACCTTCACTCCCACTGGA	145599
QY	198	-----	198
Db	145594	TGGGAACCTCACTTGTGCTATTAATTTCACAAATTGATTGGGGCTCCCTCAGTCTGT	145535
QY	198	-----	198
Db	145534	AGCCTTTTGGGTTAGGGAGAGGGCTTGGCAGCCTTTTGGTGGGACCTGTGCTCCTAG	145475
QY	198	-----	198
Db	145474	GCCCTGCCCAAGATGTCCCTGGGCTTGTAGCCCATGAGATTCTCTGCTTCCCGC	145415
QY	198	-----	198
Db	145414	TGGGACAGCTTTTGTGTAGGGCTTCCAGACACAGTAGTTCCTCCAGAGTGGGCC	145355
QY	198	-----	198
Db	145354	AGCTCTGGCCCATGAGATGCGACAGAGTGTGAAGGCCAGAGAGCTCAGGCTCC	145295
QY	198	-----	198
Db	145294	TTGAGTAGCTCGGCTCAGAGGGGTGTCCAAGGCTTGTGTGGGCTTATGGGTGC	145235
QY	198	-----	198
Db	145234	TGGTGGCTGAGGCTCCCAAGTGTGACAGAGAGGCTTCCGCCCACTGCTTGTGAAC	145175
QY	199	-----GlyAlaProLeuSerAsnAsnTProIAsnProGluGluThrI	214
Db	145174	TCCTGTGTGACAGGGCG-CCCTCTCAATATCTGGCAGATTCAGAGAGAGACCCA	145116
QY	214	gValGluAlaGlnIuHLeGlnPro-----	222
Db	145115	TGTGAGGCACGGAGCACAGCCTGTGAGTGCCGTCATCCGCTGGCCTTGGGGCA	145056
QY	222	-----	222
Db	145055	GCTGCCCTGGCTGTGTGACTGAGGCTTCCCAAGTAGGCTGGTGGGTTGTCAAG	144996
QY	223	-----GluProGluGluGluThrGluGlnProThrLeuAspT	235
Db	144995	CAGTACCAAGCGCTTTCCTTCAGAGCGGAGAGAGAACCGAGCAACCACTGTGACT	144936
QY	235	YTrAsnAspGlnIleGluArgIuAspTYrGluAsp-----	246
Db	144935	ACAAATGACCAATCGAGAGGGAGCACTGTAGAGCTGTGATGAGGTCTTGCAGCCCA	144876
QY	246	-----	246
Db	144875	CCTGGGTGGACCCCTGGCTGGGGGATGTGCCAATGGGCCATCCAGCTTGGGCCC	144816
QY	247	-----PheGluYrIleArgArgGlnIuYsGlnProArgProp	259
Db	144815	ACTGTAGACCAAGCTCCCTCTCAGTTGAGTACATTGGCGCGCAGAGCAACCAAGGCCAC	144756
QY	259	roProSerArgArgArgArgProGluArgValITrProGlnIuProProGluGluIuValAP	279
Db	144755	CCCCAAGAGAAAGAGAGAGGCCCGAGCGGCTGTGCGCAGAGCCCCCTTGAAGAAAGGCC	144696
QY	279	roAlaProAlaProGluGluArgIle-----	287
Db	144695	CGGCCCAAGCCCCGAGAGAGAGATTTGTAGATGGGGGACAGAGAGAGGTGCATGG	144636
QY	288	-----GluProProValIuYsProI	294

D	b		144635	CCACGGCGCTCTGAGGCCCTCCTTAACCTCCCGGCCTCCCCAAGAAGCTCCTGTGAAGACTTC	144576
O	y	294	euleuProPoleuProPoaAspTyrglyIaspGlyTyrValleProAntyrrAspAsp-	313	
D	b		144575	TGCTGCCCCCGCTGGCCCTCTGACTATGTGTGATTACGTGATCCCAACTTCGATGACACA	144516
O	y	313	-----	313	
D	b		144515	GTTGACTACCAGCACCCCAGAGACTCTGAGGGAGACATAGAGCAGTGGGGGTCGGGGCTGGGGGT	144456
O	y	313	-----	313	
D	b		144455	GTTGTCAAGAGACCAAGCTGGGGCACTACCCCACTTGCACCCCACTGTGCCGTGT	144396
O	y	313	-----	313	
D	b		144395	ACCTGCTGTCCCTGCTGTCCCTGGGTGCCAACCCAGCACTGCCCTGTCTTCCTCTGCC	144336
O	y	313	-----	313	
D	b		144275	GGTGTCCCTAGAGACACACTCTGCCCCCTGTACCCCATGTGGTTCAGCCCTCCAGTCTCT	144216
O	y	313	-----	313	
D	b		144215	GTTGCTTAACCTGGCTTCCCGCTGGCTGTGGCCACTTGCCCCACTCTTTCAGGAGACCCG	144156
O	y	313	-----	313	
D	b		144155	AAGGCTTTTGCTCCTCCTGTGTCTCATGCCCCCTGGCTCCTGAGACCCTCAGGTTCCCTTT	144096
O	y	313	-----	313	
D	b		144095	CCTCCTGGGTGGAGCCCGCTGCATGCCCATTTCCCTGCCCCAGGTCCCATCATGTCCT	144036
O	y	313	-----	313	
D	b		144035	CCAATGTCTCCCATCTCAACCCCGCAGCCCGCAACCCAGGACAGGTGCAGTGTGCC	143976
O	y	313	-----	313	
D	b		143975	TCCAGGCTTTTCCCATGCTGCCCTGGGCTCGAGTCTTTCCCGAGGCCAGATGCTCTGGAA	143916
O	y	313	-----	313	
D	b		143915	GGCCGGGCTGTGACTTTCAGCAGAGGCTTGTCTCAGCTGCCCTGAGACTGGGGCTGCTCT	143856
O	y	313	-----	313	
D	b		143855	GACTCCTGCAMAGACCTCTCCAACTCAGCTGTCCCCCATTCGCCGTCTCTCCCTCT	143796
O	y	313	-----	313	
D	b		143795	GGCGGGTCTCTGCTCTGAGCTCCTGTGGACCCAGAGCTGAGGCCCCCGACGAGGCT	143736
O	y	314	-----MetAspTyrTyrPheglyProPropio	322	
D	b		143725	CAGGGCAGCTCAGCTGCTCTCCCTCCCATATGTGAGACTATTACTTTGGGGCTCTCCG	143676
O	y	323	ProGlnIysPProAspAlaGluLarArgGlnThrAspGluGluLysGluLysLeu-----	339	
D	b		143675	CCCCAGAAAGCCGATGTCTGAGCGCCAGACAGAGAAAGAGAGAGCTGAGTAGTGG	143616
O	y	339	-----	339	
D	b		143615	GACCAAAGACTTCCACACCAAGGCTGCCCTGAAGGCCACTGGGGCTGCCGTGATCCAC	143556
O	y	339	-----	339	
D	b		143555	CCCACTGCTCTCAAAAGCCAGAGCCAGGCTGAGTGGCCCTCTTAACCTTGACCTTCC	143496

[illegible]



Db 140256 AGGCGAGAGGAGAGAGCTGACACCTGGGGTCTCGTGTCTTGGGCTTGAGGGGTGGGGCT 140197  
QY 740 ----- 740  
Db 140196 GACGGTCTGTAACCTCAGACCGCTGAGCTTGGGGGTTGGGGGACAGGGGATCTGTGCGA 140137  
QY 740 ----- 740  
Db 140136 GTACTGTGTGAAGCTTCATGAGGGGTATCGGGCTAGGTTGGGATGATGCGCGGAGCT 140077  
QY 741 -----SerrThrgluValArgAla1le1 748  
Db 140076 GCAGCCCTGGCTCAGACGTGCTGGCACTCCAGGATATCCAGGAGGTCCGGGCCATCAT 140017  
QY 748 ealatrPwecGluLysAsnProPheValleuGlyAlaAsnLeuAsnGlyGlyGluArgle 768  
Db 140016 TTCCTGTGATGAGAGAACCCCTTCGTGCGAGGAGCAATCTGMAACGGGGCGAGGGCT 139957  
QY 768 uValSerTyrrProTyrrAspMetAlaArgThrProThrglnGlnLeuLeuAlaAla1 788  
Db 139956 AGTATCTACCCCTACGATATGGCCCGACGCTTACCGAGAGCAAGCTTGCGCGCAC 139897  
QY 788 aMetAlaAlaAlaArgGlyGluAspGluAspGluValSerGluAlaGlnGluThrProAs 808  
Db 139896 CATGGCAGCAGCCCGGGGGAGGATGAGAGCGAGGTCTCCGAGGCCCAAGAGACTTCAGA 139837  
QY 808 phiSalAla1lePheArgTrrPleuAla1leSerPheAlaSerAlaHisLeuThrLeuThrG1 828  
Db 139836 CCACGCACTCTCCGGTGGCTTGCCATCTCTCCGCTCCGACACCTTGACCTTGACCA 139777  
QY 828 uProTyrrArgGlyGlyCyseGlnAlaGlnAspTyrrThrglyGlyMetGly1leValAsnG1 848  
Db 139776 GCCCTACCCCGAGGCTGCCAGACCAGACCTACACCGCGGATGGGATGCTCAACG 139717  
QY 848 yAlaTyrrPAsnProArgThrglyThr----- 857  
Db 139716 GGGCAAGTGAACCCCGGACCGGAGTGAAGTCAAGCTGGAGGGGCTGGGGGGGCG 139657  
QY 858 -----1leAsnAspH 861  
Db 139656 TGGTCCGAGAGGGGCTGACTTTGGTCTGTATCTGTCCCGGCACTATCATATCACTT 139597  
QY 861 eSerTyrrLeuHisThrAsnCybLeuGluLeuSerPheTyrrLeuGlyCyseAspLysPhePr 881  
Db 139596 CAGTTACTCTGCATACCACTGCTGAGGCTCTCTCTTACTGAGGCTGTGACAGTTC 139537  
QY 881 ohIsGluSerGluLeuProArgGluTrrPgluAsnAsnLysGluAlaLeuLeuThrPhe 901  
Db 139536 TCATGAGAGTGAAGCTCCCGGAGTGGAGAACCAAGAGAGGCGCTGCTCACTTCAT 139477  
QY 901 tGluGln----- 903  
Db 139476 GAGGAGGTGGGTGGCTAGGCAATGCTGGGAGAGAGAGCTGCACAGGCTCTGTAT 139417  
QY 903 ----- 903  
Db 139416 GGGCGGAGGAGAGACGACGACCATTTGACCTTCTCGAGAGACACAGCCCTCACTGCG 139357  
QY 904 -----ValHisArgGlyIleLysGlyValValThrAspGlnGlnGlyIlePro1leA 921  
Db 139356 TTCCTTAGTGCACCGCGGATTTAAGGGGTGTGACGAGCGAAGGATCCCATG 139297  
QY 921 laAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAla----- 937  
Db 139296 CCAACGCCACATCTGTGTAGTGACATTATATACGCGCTGAAGACAGG-TACCTAGTGT 139238  
QY 937 ----- 937  
Db 139237 GCACACCTTTACCCCATCTTTCTGAGGAGAGACCCCGCAGAGAGGTGGGGCTTAGAGA 139178  
QY 937 ----- 937  
Db 139177 ACTCAGCAGAGCAGTAGAGTCTGGGAGCCTGGGGGCAAAATTCAAGAGAGGAGGGCGGT 139118

QY 937 ----- 937  
Db 139117 GCTGGGGCGGAACTCAGAGGGGAGGGCGGGCTGGGGCGAGACTGAGTGGAGGCT 139058  
QY 938 -----SerrGlyG 940  
Db 139057 GGGGGCTGGAGAGGGGCGCTCTGGGGCAGCCGGATCTGTTCCCTCCGACAGCATGTGG 138998  
QY 940 lYAspTyrrTyrrArgGlyLeuAsnProGlyGlyTyrrArgValThrAlaHisAlaGlnGlyT 960  
Db 138997 GTGATTACTGGCGAATCTTGAACCCGGGTGATACCGGTGACAGCCACGCGGGAGGCT 138938  
QY 960 yrrThrProSerAlaLysThrCyseAsnValAspTyrrAspGlyValThrGlnCyseAsn 980  
Db 138937 ACACCCCGAGGCGCAAGACCTGCAATGTGACTATGACATGGGGCCTCACTGATCACT 138878  
QY 980 he1leuAlaArgSerAsnTrrPylsArgGlyLeuGlu1leMetAlaMetAsnGlyAsn 1000  
Db 138877 TCATCTGTGCTGCTCCAACTGGAAGGCATCCGGAGATCATGGCCATGAACGGGAAC 138818  
QY 1000 rGPro1leProHis1leAspProSerArgProMetThrProGlnGlnArgleuGlnG 1020  
Db 138817 GGCCTATCCACACATAGACCATCGCGCCTATGACCCCCCAAGAGAGCGCTTGACG 138758  
QY 1020 lArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgleuAsn 1040  
Db 138757 AGCGAGCCTACACACACCGCTTGCGGCTTCGGGCAAGATGGGCTGGCGCTCAACG 138698  
QY 1040 lArThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrT 1060  
Db 138697 CCACCAACACCTTAGCGCCCACTGCTGCTCCACGCTGCGCCCTGCGCACCA 138638  
QY 1060 hTrLeuSerThrThrIleGluProTrrPglLysLeu1leProProThrThrAlaGlyTrrPgl 1080  
Db 138637 CCTGAGACCTACCTAGAGCCTTGGGGCTCTATGCCCAACACCGCTGCTGGAGG 138578  
QY 1080 lUsErGluThrGlnThrTyrrThrgluVal1leThrgluPheGlyThrgluValGluProG 1100  
Db 138577 AGTCGAGACTGAGACCTTACACAGAGGTGTGACAGATTTGGACCGAGGTGAGCCG 138518  
QY 1100 lUpheGlyThrLysValGluProGluPheGluThrglnLeuGluProGluPheGluThrg 1120  
Db 138517 AGTTGGGACCAAGGTGAGCCGAGTTTGAGACCAAGTTGAGCTGAGTTGAGACCC 138458  
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Homnidae; Homo.  
1 (sites)  
REFERENCE  
AUTHORS Ohno,I., Hashimoto,U., Shimizu,K., Takaoka,K., Ochi,T.,  
Mateubara,K. and Okubo,K.  
TITLE A cDNA cloning of human AEBP1 from primary cultured osteoblasts and  
its expression in a differentiating osteoblastic cell line  
JOURNAL Biochem. Biophys. Res. Commun. 228 (2), 411-414 (1996)  
PUBMED 8920928  
REFERENCE 2 (bases 1 to 2839)

AUTHORS  
JOURNAL

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Fax:81-6-877-1922)

FEATURES  
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 1 (bases 1 to 2759)  
 Flory, D.M., Kollar, J., Huynh, T.D. and Hering, T.M.  
 Transcription factor AEBP1 expression during chondrocyte  
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 Unpublished  
 2 (bases 1 to 2759)  
 Hering, T.M., Flory, D.M., Kollar, J. and Huynh, T.D.  
 Direct Submission  
 Submitted (20-JAN-1998) Medicine, Case Western Reserve University,  
 10900 Euclid Avenue, Cleveland, OH 44106-4946, USA  
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Db 2222 CTTCAATGCAACACAGAGC-----CCAGCCAGAGCCCACTCCCTCCACTCC 2275  
Qy 1056 -----AlaProAlaThrThrLeuSerThrThrlleGluP 1067  
Db 2276 AACACTGCTCCCACTGCGGACCTTCCCTTCCCAAGCCCAAGTTTCACTAGGGGGC 2335  
Qy 1067 oTPG1Yleu1leProProThrThra1ag1YTrpGluJuser----- 1081  
Db 2336 CTGGAGGTTTTCACAGAGACCAAGTCAATTGGGAGATGGAGAAAGAGAGAGAGAG 2395





C	1	21.2	9.0	49	3	US-09-849-069-9	Sequence 9, Appl.
C	2	20.8	8.8	43	2	US-08-324-001-19	Sequence 19, Appl.
C	3	20.8	8.8	43	2	US-08-324-001-20	Sequence 20, Appl.
C	4	19.6	8.3	50	3	US-10-111-827-584	Sequence 584, Appl.
C	5	19.6	8.3	50	5	US-10-111-831-584	Sequence 584, Appl.
C	6	19.4	8.2	45	3	US-08-480-640A-210	Sequence 210, Appl.
C	7	19.4	8.2	45	3	US-08-666-968C-210	Sequence 210, Appl.
C	8	19.4	8.2	45	3	US-08-488-337A-210	Sequence 210, Appl.
C	9	19.4	8.2	45	3	US-08-375-992A-210	Sequence 210, Appl.
C	10	19.4	8.2	45	3	US-08-472-679H-210	Sequence 210, Appl.
C	11	19.4	8.2	50	3	US-10-111-827-4246	Sequence 4246, Appl.
C	12	19.4	8.2	50	3	US-10-111-827-4412	Sequence 4412, Appl.
C	13	19.4	8.2	50	5	US-10-111-831-4246	Sequence 4246, Appl.
C	14	19.4	8.2	50	5	US-10-111-831-4412	Sequence 4412, Appl.
C	15	19.2	8.1	50	3	US-10-111-827-1437	Sequence 1437, Appl.
C	16	19.2	8.1	50	5	US-10-111-831-1437	Sequence 1437, Appl.
C	17	19	8.1	36	3	US-08-805-813-7	Sequence 7, Appl.
C	18	19	8.1	43	3	US-09-561-490E-49	Sequence 49, Appl.
C	19	19	8.1	50	3	US-10-111-827-1800	Sequence 1800, Appl.
C	20	19	8.1	50	5	US-10-111-831-1800	Sequence 1800, Appl.
C	21	18.6	7.9	50	3	US-10-111-827-2249	Sequence 2249, Appl.
C	22	18.6	7.9	50	5	US-10-111-831-2249	Sequence 2249, Appl.
C	23	18.4	7.8	47	3	US-09-422-978-765	Sequence 765, Appl.

C 24	18.4	7.8	50	3	US-09-371-489-4	Sequence 206f, Appl
C 25	18.4	7.8	50	3	US-10-131-827-2060	Sequence 206g, Ap
C 26	18.4	7.8	50	5	US-10-131-831-2060	Sequence 206o, Ap
C 27	18.2	7.7	44	2	US-08-471-791-39	Sequence 39, Appl
C 28	18.2	7.7	44	3	US-09-182-145-152	Sequence 152, Ap
C 29	18.2	7.7	44	7	PCT-US91-01746-39	Sequence 39, Appl
C 30	18.2	7.7	44	7	PCT-US91-01750-10	Sequence 10, Appl
C 31	18.2	7.7	47	3	US-09-422-978-2714	Sequence 2714, Ap
C 32	18	7.6	47	3	US-09-422-978-1100	Sequence 1100, Ap
C 33	18	7.6	47	3	US-09-422-978-2579	Sequence 2579, Ap
C 34	18	7.6	50	3	US-10-131-821-5658	Sequence 5658, Ap
C 35	18	7.6	50	5	US-10-131-831-5658	Sequence 5658, Ap
C 36	17.8	7.5	50	3	US-09-270-767-25514	Sequence 25514, A
C 37	17.8	7.5	50	3	US-10-131-821-2354	Sequence 2354, Ap
C 38	17.8	7.5	50	5	US-10-131-831-2354	Sequence 2354, Ap
C 39	17.6	7.5	40	3	US-09-721-544A-17	Sequence 17, Appl
C 40	17.6	7.5	42	3	US-09-551-737C-65	Sequence 65, Appl
C 41	17.6	7.5	42	3	US-09-551-737C-66	Sequence 66, Appl
C 42	17.6	7.5	43	3	US-08-331-625A-50	Sequence 50, Appl
C 43	17.6	7.5	43	3	US-09-494-151-50	Sequence 50, Appl
C 44	17.6	7.5	43	3	US-09-972-484-50	Sequence 50, Appl
C 45	17.6	7.5	43	7	PCT-US93-04384-21	Sequence 21, Appl

## ALIGNMENTS

```

RESULT 1
US-09-849-069-9/c
: Sequence 9, Application US/09849069
: Patent No. 6630306
: GENERAL INFORMATION:
: APPLICANT: Ronald R. Breaker
: TITLE OF INVENTION: Biotreactive Allosteric Polynucleotides
: FILE REFERENCE: OCG-754.CIP
: CURRENT APPLICATION NUMBER: US/09/849,069
: CURRENT FILING DATE: 2001-05-07
: PRIOR APPLICATION NUMBER: US 09/331,809
: PRIOR FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: MS-DOS
: SEQ ID NO 9
: LENGTH: 49
: TYPE: DNA
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: G8 DNA
US-09-849-069-9

```

Query Match 9.0%; Score 21.2; DB 3; Length 49;

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Matches    26;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
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QY      100  CCCCCTCATTTCTCCTGTCGCCACTTTCATG 133
          ||| ||| ||| ||| ||| ||| ||| |||
DB      35  CCGCGTCATCTCCAGCTCCCTTGGCTG 2

```

RESULT 2  
 US-08-324-001-19  
 ; Sequence 19, Application US/08324001  
 ; Patent No. 5624803  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: NOONBERG, SARAH B.  
 ; APPLICANT: HUNT, C. ANTHONY  
 ;  
 ; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND  
 ; METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING  
 ;  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM

;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO

STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/324,001  
FILING DATE: 13-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 22000-20544.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSN FOERSSFO  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-324-001-19

Query Match 8.8%; Score 20.8; DB 2; Length 43;  
Best Local Similarity 78.1%; Pred. No. 3.2e+03;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168  
DB 10 CTCCTCTCCACCTCTCTCTCTCTCTGATT 41

## RESULT 3

US-08-324-001-20/c  
Sequence 20, Application US/08324001  
Patent No. 5624803

GENERAL INFORMATION:  
APPLICANT: NOONBERG, SARAH B.  
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR AND  
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/324,001  
FILING DATE: 13-OCT-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 22000-20544.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSN FOERSSFO  
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-324-001-20

Query Match 8.8%; Score 20.8; DB 2; Length 43;  
Best Local Similarity 78.1%; Pred. No. 3.2e+03;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168  
DB 34 CTCCTCTCCACCTCTCTCTCTCTCTGATT 3

## RESULT 4

US-10-131-827-584  
Sequence 584, Application US/10131827  
Patent No. 6905827

GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 584  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-827-584

Query Match 8.3%; Score 19.6; DB 3; Length 50;  
Best Local Similarity 66.7%; Pred. No. 8.1e+03;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGCTGTTGTTTAAAGAGCTGAGCCCTCTGATT 112  
DB 6 GTGACCTGTTTGTAAATATGTTCCCATGTCATC 47

## RESULT 5

US-10-131-831-584  
Sequence 584, Application US/10131831  
Patent No. 7026121

GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
TITLE OF INVENTION: TRANSPLANT REJECTION  
FILE REFERENCE: 506612000121  
CURRENT APPLICATION NUMBER: US/10/131,831  
CURRENT FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9190  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 584  
LENGTH: 50

TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-831-584

Query Match  
Best Local Similarity 66.7%; Score 19.6; DB 5; Length 50;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGCTGTTGTAAGAGCTGAGCCCTCTCATTC 112  
DB 6 GTGAGACCTGTTGTTTAAATATCTGTCCTCATGCATC 47

RESULT 6  
US-08-480-640A-210/c  
Sequence 210, Application US/08480640A  
Patent No. 6033904

GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,640A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 210:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-480-640A-210

Query Match  
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTGTTCTGTCGCAAACT 235  
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 7  
US-08-686-968C-210/c  
Sequence 210, Application US/08686968C  
Patent No. 6221361  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
FILE REFERENCE: 39119-H/JML

CURRENT APPLICATION NUMBER: US/08/686,968C  
CURRENT FILING DATE: 1996-07-25  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 210

LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Homology  
US-08-686-968C-210

Query Match  
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTGTTCTGTCGCAAACT 235  
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 8  
US-08-488-237A-210/c  
Sequence 210, Application US/08488237A  
Patent No. 6251403

GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,237A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 210:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-488-237A-210

Query Match  
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTGTTCTGTCGCAAACT 235  
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 9  
US-08-375-992A-210/C  
; Sequence 210, Application US/08375992A  
; Patent No. 6328975  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 220  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/375,992A  
; FILING DATE: Herewith  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 210:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; US-08-375-992A-210

Query Match  
Best Local Similarity 8.2%; Score 19.4; DB 3; Length 45;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 199 ATGCTAACGCCATGCTTCTTGTCTGTCGCAAACT 235  
Db 41 ATGATTACGCCAAGCTTCTAGTACAGTATTTCAGACT 5

RESULT 10  
US-08-472-679H-210/C  
; Sequence 210, Application US/08472679H  
; Patent No. 6497882  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 267  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pamela G. Salkeid  
; STREET: 2000 Galloping Hill Road  
; CITY: Kenilworth  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07033  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,679H  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Salkeid, Pamela G.  
REGISTRATION NUMBER: 38,607  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 298-2135  
TELEFAX: (908) 298-5388  
INFORMATION FOR SEQ ID NO: 210:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEtical: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 210:  
US-08-472-679H-210

Query Match  
Best Local Similarity 8.2%; Score 19.4; DB 3; Length 45;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 199 ATGCTAACGCCATGCTTCTTGTCTGTCGCAAACT 235  
Db 41 ATGATTACGCCAAGCTTCTAGTACAGTATTTCAGACT 5

RESULT 11  
US-10-131-827-4246  
; Sequence 4246, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4246  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-131-827-4246

Query Match  
Best Local Similarity 8.2%; Score 19.4; DB 3; Length 50;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 104 CTCATCTCTCTGCTCCACTCTTGCACT 132  
Db 22 CCTCATCTCTGCTCACTCTCTTCAT 50

RESULT 12  
US-10-131-827-4412  
; Sequence 4412, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert

```

; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4412
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-4412

Query Match      8.2% Score 19.4; DB 3; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCCACTCTTGATGAGACA 138
Db      13 TTATCTGCTTCCACTATAGCATGATCA 41

RESULT 13
US-10-131-831-4246
; Sequence 4246, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4246
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-831-4246

Query Match      8.2% Score 19.4; DB 5; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      104 CTCTCATTCCTGCTCCCACTCTTGAT 132
Db      22 CCTCATCTTCTGCTCCTCATCTTCCAT 50

RESULT 14
US-10-131-831-4412
; Sequence 4412, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
```

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; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4412
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-831-4412

Query Match      8.2% Score 19.4; DB 5; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCCACTCTTGATGAGACA 138
Db      13 TTATCTGCTTCCACTATAGCATGATCA 41

RESULT 15
US-10-131-827-1437/C
; Sequence 1437, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1437
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-1437

Query Match      8.1% Score 19.2; DB 3; Length 50;
Best Local Similarity 67.5%; Pred. No. 1.1e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY      66 TTCACGTGAGAGCTGTGTTGAAGAGCGCCCT 105
Db      46 TTCTCTCAGACTGTGTGTAAGAAAGCCCTTCTCT 7

Search completed: October 1, 2006, 01:24:47
Job time : 112.569 secs
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1 FILE REFERENCE: 5066120000121
2 CURRENT APPLICATION NUMBER: US/10/131,831
3 PRIOR FILING DATE: 2002-08-05
4 PRIOR APPLICATION NUMBER: US 10/006,290
5 PRIOR FILING DATE: 2001-10-22
6 PRIOR APPLICATION NUMBER: US 60/296,764
7 PRIOR FILING DATE: 2001-06-08
8 NUMBER OF SEQ ID NOS: 9190
9 SOFTWARE: PatentIn version 3.1
10 SEQ ID NO 7899
11     LENGTH: 50
12     TYPE: DNA
13     ORGANISM: Homo sapiens
14     US-10-131-831-7899

```

Query Match	8.6%;	Score 20.8;	DB 5;	length 50;
Best Local Similarity	70.0%;	Pred. No. 1.7e+03;		
Matches	28;	Conservative	0;	Mismatches 12;
				Indels 0;
				Gaps 0

**OY** 54 AGCTGCTGCCTCACCCTGCTTTTCCAAACCCCACCCTGTAA 93  
| | | | | | | | | | | | | | | | | | | |  
**Db** 1 AGCTGCTGCTTCTCTTCAGTTGCAAAATGCAAACTGTTA 40

```

RESULT 3
PCT-US94-14106-20/c
; Sequence 20, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION:  Process for Generating Specific Antibodies

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Query Match	8.1%	Score 19.6	DB 7	Length 42
Best Local Similarity	66.7%	Pred. No. 4.2e+03		
Matches 28; Conservative	0	Mismatches 14	Indels 0	Gaps 0

```
Oy      177 TTAGCCCAACCGTGTCTGTTAGGGTGTCCTAGGCTGTATCAG 218
          ||| ||||| | | | | | | | | | | | | | | | |
Db      42 TTGAGCCCAAGCGGCCACTAGTATATCTGGGCGAACAG 1
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1  RESULT 4
2  US-08-503-730-37
3  ; Sequence 37 Application US/08503730
4  ; Patent No. 5780269
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Inouye, Sumiko
7  ; APPLICANT: Inouye, Masayori
8  ; TITLE OF INVENTION: NEW HYBRID MOLECULES
9  ; NUMBER OF SEQUENCES: 45
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Welser & Associates
12 ; STREET: 230 South Fifteenth Street Suite 5000
13 ; CITY: Philadelphia
14 ; STATE: PA
15 ; COUNTRY: USA
16 ;

```

[illegible]

Query Match	8.1%	Score 19.6	DB 2	Length 50
Best Local Similarity	66.7%	Pred. No. 4	5e+3	
Matches 28	Conservative 0	Mismatches 14	Indels 0	Gaps 0

```

Oy      41  GCTCCACCTCCCCAGCTGCTGCCTCACCTGCTTTTCCAACC 82
          | | | | | | | | | | | | | | | | | | |
Db      2  GGTAACAACCTCCACCTGCGTCACTGCGTTGGCAACC 43

```

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RESULT 5
US-10-131-827-1159/c
; Sequence 1159, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wollgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1159
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1159

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Query Match	8.1%	Score	19.6	DB	3	Length	50
Best Local Similarity	66.7%	Pred. No.	4.5e+03				
Matches	28	Conservative	0	Mismatches	14	Indels	0
						Gaps	0

ay 35 CTGGAGCTCCACCTCCCCAGCTGCTCCTCACCCTGTTTC 76  
Db 50 CTGTGCGCTTCCCCCTTTCAGTTACAGCCCCAGCCTCTTCTC 9

## RESULT 6



NT, 1967 = 1

US-10-131-831-1159/c  
; Sequence 1159, Application US/10131831  
; Patent No. 7026121  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
; TITLE OF INVENTION: TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000121  
; CURRENT APPLICATION NUMBER: US/10/131,831  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9190  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1159  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-831-1159

Query Match 8.1%; Score 19.6; DB 5; Length 50;  
Best Local Similarity 66.7%; Pred. No. 4.5e+03;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 35 CTGGAGCTCCACCTCCAGCTGCTCCTCCTCCTTTC 76  
Db 50 CTGGCGCTTCCCTTCCAGTTACAGCCCGAGCTTCTC 9

RESULT 7  
US-08-644-664B-35/c  
; Sequence 35, Application US/08644664B  
; Patent No. 5776746  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Gene Amplification Methods  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medien & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/644,664B  
; FILING DATE: 01-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET INFORMATION:  
; TELECOMMUNICATION INFORMATION: GENTOPE-00912  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-644-664B-35

Query Match 7.9%; Score 19.2; DB 2; Length 39;  
Best Local Similarity 75.0%; Pred. No. 5.6e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 211 TGTATCAGTACCACTAAACTGATTCAC 242  
Db 37 TGAACAGATGACAACTTAACCTTGATCCAC 6

RESULT 8  
US-08-761-277A-35/c  
; Sequence 35, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medien & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER: 424  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENTOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-761-277A-35

Query Match 7.9%; Score 19.2; DB 2; Length 39;  
Best Local Similarity 75.0%; Pred. No. 5.6e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 211 TGTATCAGTACCACTAAACTGATTCAC 242  
Db 37 TGAACAGATGACAACTTAACCTTGATCCAC 6

RESULT 9  
US-08-391-000-25  
; Sequence 25, Application US/08391000  
; Patent No. 5723752  
; GENERAL INFORMATION:  
; APPLICANT: Houtz, Robert L.  
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF  
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE  
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE  
; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Burns, Doane, Swecker & Mathis  
;; STREET: P.O. Box 1404  
;; CITY: Alexandria  
;; STATE: Virginia  
;; COUNTRY: United States  
;; ZIP: 22133-1404  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/391,000  
;; FILING DATE: 21-FEB-1995  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meuth, Donna M.  
;; REGISTRATION NUMBER: 36,607  
;; REFERENCE/DOCKET NUMBER: 028750-123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 836-6620  
;; TELEFAX: (703) 836-2021  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 42 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-391-000-25

Query Match 7.9%; Score 19.2; DB 2; Length 42;  
Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70  
Db 8 GAACCTGCTGCTGCTGCTGCTGCTTACCTG 39

RESULT 10  
US-08-741-931-25  
; Sequence 25, Application US/08741931  
; Patent No. 5866394  
; GENERAL INFORMATION:  
; APPLICANT: HOUTZ, Robert L.  
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF  
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE  
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22133-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/741,931  
; FILING DATE: 31-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/391,000  
; FILING DATE: 21-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607

;; REFERENCE/DOCKET NUMBER: 028750-123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 836-6620  
;; TELEFAX: (703) 836-2021  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 42 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-741-931-25

Query Match 7.9%; Score 19.2; DB 2; Length 42;  
Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70  
Db 8 GAACCTGCTGCTGCTGCTGCTGCTTACCTG 39

RESULT 11  
US-09-475-947A-43  
; Sequence 43, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTS00667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: human  
; US-09-475-947A-43

Query Match 7.9%; Score 19; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 CCACCTCCCGAGCTGCTGC 62  
Db 13 CCACCTCCCGAGCTGCTGC 31

RESULT 12  
US-10-131-827-6394/C  
; Sequence 6394, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 6394  
; LENGTH: 50

TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-827-6394

Query Match  
Best Local Similarity 71.4%; Score 19; DB 3; Length 50;  
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54  
DB 46 ATCTGTGTTCCCGACGAGGTGCTGCACCTCCCA 12

## RESULT 13

US-10-131-827-6784  
Sequence 6784, Application US/10131827  
Patent No. 6905827  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6784  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-827-6784

Query Match  
Best Local Similarity 71.4%; Score 19; DB 3; Length 50;  
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54  
DB 5 ATCTGTGTTCCCGACGAGGTGCTGCACCTCCCA 39

## RESULT 14

US-10-131-831-6394/C  
Sequence 6394, Application US/10131831  
Patent No. 7026121  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
FILE REFERENCE: 506612000121  
CURRENT APPLICATION NUMBER: US/10/131,831  
CURRENT FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9190  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6394  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-831-6394

Query Match  
Best Local Similarity 71.4%; Score 19; DB 5; Length 50;  
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54  
DB 46 ATCTGTGTTCCCGACGAGGTGCTGCACCTCCCA 12

## RESULT 15

US-10-131-831-6784  
Sequence 6784, Application US/10131831  
Patent No. 7026121  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
FILE REFERENCE: 506612000121  
CURRENT APPLICATION NUMBER: US/10/131,831  
CURRENT FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9190  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6784  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-831-6784

Query Match  
Best Local Similarity 71.4%; Score 19; DB 5; Length 50;  
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54  
DB 5 ATCTGTGTTCCCGACGAGGTGCTGCACCTCCCA 39

Search completed: October 1, 2006, 01:24:47  
Job time: 116.431 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: September 30, 2006, 23:53:03 ; Search time 488 Seconds

(Without alignments)  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued\_Patents\_NA.\*

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8: /EMC\_Celerra\_SIDS3/prodata/2/ina/PP-COMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/ina/RE-COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6272	100.0	3935	US-09-060-482-1	Sequence 1, App1
2	6264	99.9	4082	US-09-949-016-2722	Sequence 2722, Ap
3	5054	80.6	3728	US-08-111-939-1	Sequence 1, App1
4	4787	76.3	14205	US-09-949-016-14464	Sequence 14464, A
5	2171.5	34.6	3772	US-09-991-181-61	Sequence 61, App1
6	2171.5	34.6	3772	US-09-990-444-61	Sequence 61, App1
7	2171.5	34.6	3772	US-09-997-333-61	Sequence 61, App1
8	2171.5	34.6	3772	US-09-992-598-61	Sequence 61, App1

9	2171.5	34.6	3772	US-09-989-735-61	Sequence 61, App1
10	2171.5	34.6	3772	US-09-989-726-61	Sequence 61, App1
11	2171.5	34.6	3772	US-09-997-514-61	Sequence 61, App1
12	2171.5	34.6	3772	US-09-989-728-61	Sequence 61, App1
13	2171.5	34.6	3772	US-09-997-349-61	Sequence 61, App1
14	2171.5	34.6	3772	US-09-997-653-61	Sequence 61, App1
15	2171.5	34.6	3772	US-09-989-923A-61	Sequence 61, App1
16	2106.5	33.6	3470	US-09-976-594-345	Sequence 345, App
17	1748.5	27.9	2382	US-09-641-741-1	Sequence 1, App1
18	1748.5	27.9	2719	US-08-706-216-1	Sequence 1, App1
19	1748.5	27.9	2585	US-09-650-284B-1	Sequence 270, App
20	1733.5	27.6	2585	US-09-774-528-270	Sequence 270, App
21	1733.5	27.6	2585	US-10-120-988-270	Sequence 270, App
22	1653	26.4	2624	US-09-370-838-19	Sequence 19, App
23	1653	26.4	2624	US-09-854-133-19	Sequence 19, App
24	1310	20.9	1811	US-09-280-116-94	Sequence 94, App1
25	1104.5	17.6	1316	US-09-148-545-17	Sequence 17, App1
26	1104.5	17.6	1316	US-09-621-011-17	Sequence 17, App1
27	1031	16.4	1285	US-09-148-545-84	Sequence 84, App1
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29	988	15.8	557	US-09-702-705-918	Sequence 918, App
30	988	15.8	557	US-09-736-457-918	Sequence 918, App
31	988	15.8	557	US-09-671-325-918	Sequence 918, App
32	988	15.8	557	US-09-671-325-918	Sequence 918, App
33	988	15.8	557	US-09-658-824-918	Sequence 918, App
34	988	15.8	557	US-10-017-754-918	Sequence 918, App
35	988	15.8	557	US-09-651-563-918	Sequence 918, App
36	936	14.9	1702	US-09-949-016-3160	Sequence 3160, Ap
37	897.5	14.3	2433	US-09-949-016-5336	Sequence 5336, Ap
38	897.5	14.3	2433	US-09-233-889-1	Sequence 1, App1
39	897.5	14.3	2443	US-08-452-262-1	Sequence 1, App1
40	897.5	14.3	2443	US-08-734-550-1	Sequence 1, App1
41	897.5	14.3	2443	US-09-917-254-16	Sequence 16, App1
42	897.5	14.3	2443	PCT-US96-07528-1	Sequence 1, App1
43	895.5	14.3	2097	US-09-949-016-5524	Sequence 5524, Ap
44	895.5	14.3	2100	US-09-949-016-530	Sequence 530, App
45	885	14.1	5766	US-09-949-016-3679	Sequence 3679, Ap

#### ALIGNMENTS

RESULT 1  
US-09-060-482-1  
; Sequence 1, Application US/09060482  
; Patent No. 6468766  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Mu-En  
; APPLICANT: Layne, Matthew D.  
; APPLICANT: Yet, Shaw-Fang  
; TITLE OF INVENTION: AORTIC CARDIOPROTEPTIDASE-LIKE POLYPEPTIDE  
; FILE REFERENCE: 05433/036001  
; CURRENT APPLICATION NUMBER: US/09/060,482  
; CURRENT FILING DATE: 1998-04-15  
; EARLIER APPLICATION NUMBER: US 08/818,009  
; EARLIER FILING DATE: 1997-03-14  
; EARLIER APPLICATION NUMBER: US 60/013,439  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 3935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (140)...(3613)  
US-09-060-482-1  
Alignment Scores:  
Pred. No.: 0  
Score: 6272.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Length: 3935  
Matches: 1158  
Conservative: 0  
Mismatch: 0

Query Match:	100.0%	Indels:	0
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QY	21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40	
DB	200 CCTGGAGGGCGCCCGCAGACGGGTGTCGACCGACGACGAGATCGAGGATTCCTCGAGGGC	259	
QY	41 PheLeuSerGluLeuGluProGluPProArgGluAspAspValGluAlaProProProPro	60	
DB	260 TTCCTGTCAAGAGCTAAGACCTGAGCCCGGAGAGAGACGTGAGGCGCCGCTCTCC	319	
QY	61 GluProThrProArgValArgLysAlaGlnAlaGlyGlyAspProGlyLysArgProGly	80	
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QY	81 ThrAla1aGluValProProGluGlyThrLysAspLysGlyLysLysGlyLysLysAsp	100	
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QY	121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys	140	
DB	500 AAGAGAAAGCCCAAGCCCAAGCCCAAGAAAGCCCAAGAGAGAGCCACTAAGGCCCAAG	559	
QY	141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla	160	
DB	560 AAGCCCAAGAGAGGACCAAGCCCAAGCCCAAGAAAGCCCAAGAGAGGACCAAGGCGC	619	
QY	161 ThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGluThrLeuGlu	180	
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QY	181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyAla	200	
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QY	441 ThrGlnTrpIleGluValAspThrArgTrpThrArgPheThrGlyValIleThrGln	460	
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DB	1760 TCTGTGGCCCTGTCTACAGCTACACGACAGAAATGAGTGTGGCCACCATGACCTG	1819	
QY	561 AspPheArgHisHisSerTyrgLysAspMetArgGlnLeuMetLysValAlaAsnGluGln	580	
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QY	581 CyProThrIleThrArgThrTyrgSerLeuGlyLysSerSerArgGlyLeuLysIleTyrg	600	
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QY	601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheAspGly	620	
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Qy 861 PheSerTyrLeuMetIleThrAenCyseGluLeuSerPheTyrLeuGlyCyseAenPhe 880
Db 2720 TTCAGTAACTGTGATACCACTGCTGAGCTCTCTTCACTGAGCTGTGACAGTTC 2779
Qy 881 ProHISGluSerGluLeuProArgGluTyrGluAenAenAenGluAlaLeuLeuThrPhe 900
Db 2780 CTTCAAGAGTGAAGTACCTCCCGGAGTGGAGAGAACAGAGGCGCTGCTCACTTC 2839
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Db 2840 ATGAGACAGAGTGCACCGCGCATTTAAGGGGTGTGTGACGAGCAGCAAGCATCCCAT 2899
Qy 921 AlaAenAlaThrIleSerValSerGlyIleAenHISGlyValIleThrAlaSerGlyGly 940
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Db 3380 TCGAGACTGAGACTACACAGAGGTGTGACAGAGATTGGAGCCGAGGTGAGCCGAG 3439
Qy 1101 PheGlyThrThrValGluProGluPheGluThrGluLeuGluProGluPheGluThrGlu 1120
Db 3440 TTGGGACCAAGGTGAGCGCGGATTGAGACCCAGTTGAGAGCTTGTGAGACCCAG 3499
Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
Db 3500 CTGGAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTGCG 3559
Qy 1141 GluAlaPheProPheThrThrValGluThrTyrThrValAenPheGlyAenPhe 1158
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RESULT 2
US-09-949-016-2722
; Sequence 2722, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2722
; LENGTH: 4082
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2722

Alignment Scores:
Pred. No.: 0 Length: 4082
Score: 6264.00 Matches: 1156
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 99.8% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 3 Gaps: 0

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Db 367 CCGGAGGGCGCGCGGAGAGCGGTGCTGACGACGACGACGATGAGAGATTCCTCGAGGGG 426
Qy 41 PheLeuSerGluLeuGluProGluProArgGluAenAspValGluAlaProProProPro 60
Db 427 TTCCTGTCAAGCTAGAACTGAGCGCCCGGAGAGAGAGAGTGAAGGCCCGCGCTCC 486
Qy 61 GluProThrProArgValArgValArgValArgValArgValArgValArgValArgVal 80
Db 487 GAGCCACCCCGCGGCTCCGAAAGCCCAAGCGGGGCGCAAGCTGAGGAGGAGGAGGAGG 546
Qy 81 ThrAlaIleGluValProProGluTyrThrIleAspIleGlyIleValIleGlyIleVal 100
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QY 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140  
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QY 141 LysProLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla 160  
DB 727 AAGCCCAAGAGAACCCACCAAGGCCACCAAGAACCCCAAGAGAACCCCAAGGCC 786  
QY 161 ThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGluThrLeuGlu 180  
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QY 181 TrpProLeuProProProProSerProGlyProGluLysLeuProGluGlyGlyAla 200  
DB 847 TGGCCACTGCCCAACCCCGCAGCCCTGGCCCGAGAGACTACCCAGAGAGAGGGCG 906  
QY 201 ProLeuSerAsnAsnTrpGluAsnProGlyGluGluThrHisValGluAlaGluGluHis 220  
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QY 221 GlnProGluProGluGluGluThrGluGluGlnProThrLeuAspTyrAsnAspGlnLeu 240  
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QY 241 ArgGluAspTyrGluAspPheGluTyrLeuArgGluLysGluProArgProProPro 260  
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DB 1087 ACAGAGAGAGAGAGGCCCAAGCGGCTCTGCGCAGAGCCCTGAGAGAGAGGCCCGGCG 1146  
QY 281 ProAlaProGluGluGluArgLysGluProValLysProValLysProLeuLeuProProPro 300  
DB 1147 CCAAGCCCCGAGAGAGAGATGAGCTCTCTGTGAACCTCTGTCGCCCGCTGCCCT 1206  
QY 301 AspTyrGlyAspGlyTyrValLysProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320  
DB 1207 GACTATGGTGAATGATACGTGATCCCAACTACGATGACATGACATTAATTTGGGCGCT 1266  
QY 321 ProProProGluLysProAspAlaGluArgGluThrAspGluGluLysGluGluLeuLys 340  
DB 1267 CCTCCGCCCAAGAGGCCATGCTGAGCCCAAGCCAGACGAGAGAGAGAGAGGAGCTGAAG 1326  
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QY 461 GlyArgAspSerSerLeuHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480

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QY 521 ArgLeuTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540  
DB 1867 CGCATCTACCACTCAGCTGGAATGGCAGCTGTGTCATGCCGCTGAGAGTGTGGGATGC 1926  
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 ; Sequence 1, Application US/08111939  
 ; Patent No. 5460951  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kawai, Shinji  
 ; APPLICANT: Takehite, Sunao

; APPLICANT: Okazaki, Makoto  
 ; APPLICANT: Amann, Egon  
 ; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like  
 ; TITLE OF INVENTION: Protein and Process for its Production  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/111,939  
 ; FILING DATE: 26-AUG-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 324033/92  
 ; FILING DATE: 03-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 230029/92  
 ; FILING DATE: 28-AUG-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Foreman, David S.  
 ; REGISTRATION NUMBER: 33,694  
 ; REFERENCE/DOCKET NUMBER: 02481.1321-00000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-408-4000  
 ; TELEFAX: 202-408-4000  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3728 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mus musculus  
 ; STRAIN: osteoblastic cell line MC3T3E1  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 69..3452  
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 ; Score: 5054.00  
 ; Percent Similarity: 87.1%  
 ; Best Local Similarity: 82.3%  
 ; Query Match: 80.6%  
 ; DB: 2  
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RESULT 4
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; Sequence 14464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14464
; LENGTH: 14205
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14464

Alignment Scores:
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Best Local Similarity: 35.8% Mismatches: 4
Query Match: 76.3% Indels: 201
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RESULT 5  
US-09-991-181-61  
Sequence 61, Application US/09991181  
Patent No. 6913919  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C53  
CURRENT APPLICATION NUMBER: US/09/991,181  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17





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## RESULT 7

US-09-997-333-61  
 ; Sequence 61, Application US/09997333  
 ; Patent No. 6953836  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/065311  
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 33 PRIOR APPLICATION NUMBER: 60/091992  
 34 PRIOR FILING DATE: 1998-07-07  
 35 PRIOR APPLICATION NUMBER: 60/092182  
 36 PRIOR FILING DATE: 1998-07-09

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Db 2272 AGATTCACATGGAAGAAAGAAATCCCAACGCCATTATCTCCGTAAGAGCATTAACATGA 2331  
QY 933 yValIleThrAlaSerGluYGluYAspTYrTPArgIleLeuAsnProGluYGluTYrArgYla 953  
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QY 953 lThrAlaHisAlaGluGluTYrThrProSerAlaTYrThrCYsAsnValAspTYrAspI1 973  
Db 2392 CACACAAAGCCGAAGTTTCACTGCATCCACCAAGAACTATAGCTTGGCTATGACAT 2451  
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Db 2452 GGGGCGCACAGAGTGTGACTTCACTTACCACTTACCAAAACCAATGGCCAGATCCGAGAGAT 2511  
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Db 2512 CATGAGAAATTTGGGAAGCAGCCGTC----- 2539  
QY 1013 oGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMe 1033  
Db 2540 -----AGCTTCCACAGCCAGCGGCTGAGAGCTGGCGGGCGGAGAGACGACAGCG 2589  
QY 1033 rArgLeuArgArgLeuAsnAlaThrThrThrLeuGluYProHisThrValProProThr 1052  
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## RESULT 8

US-09-992-598-61

Sequence 61, Application US/09992598

Patent No. 6956108

GENERAL INFORMATION:

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APPLICANT: Gurney, Austin L.

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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC20

CURRENT APPLICATION NUMBER: US/09/992, 598

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

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APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC60
CURRENT APPLICATION NUMBER: US/09/989,726
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42	PRIOR APPLICATION NUMBER: 60/089908	
43	PRIOR FILING DATE: 1998-06-18	
44	PRIOR APPLICATION NUMBER: 60/089947	
45	PRIOR FILING DATE: 1998-06-19	
46	PRIOR APPLICATION NUMBER: 60/089948	
47	PRIOR FILING DATE: 1998-06-19	
48	PRIOR APPLICATION NUMBER: 60/089952	
49	PRIOR FILING DATE: 1998-06-19	
50	PRIOR APPLICATION NUMBER: 60/090246	
51	PRIOR FILING DATE: 1998-06-22	
52	PRIOR APPLICATION NUMBER: 60/090252	
53	PRIOR FILING DATE: 1998-06-22	
54	PRIOR APPLICATION NUMBER: 60/090254	
55	PRIOR FILING DATE: 1998-06-22	
56	PRIOR APPLICATION NUMBER: 60/090349	
57	PRIOR FILING DATE: 1998-06-23	
58	PRIOR APPLICATION NUMBER: 60/090355	
59	PRIOR FILING DATE: 1998-06-23	
60	PRIOR APPLICATION NUMBER: 60/090429	
61	PRIOR FILING DATE: 1998-06-24	
62	PRIOR APPLICATION NUMBER: 60/090431	
63	PRIOR FILING DATE: 1998-06-24	
64	PRIOR APPLICATION NUMBER: 60/090435	
65	PRIOR FILING DATE: 1998-06-24	
66	PRIOR APPLICATION NUMBER: 60/090444	
67	PRIOR FILING DATE: 1998-06-24	
68	PRIOR APPLICATION NUMBER: 60/090444	
69	PRIOR FILING DATE: 1998-06-24	
70	PRIOR APPLICATION NUMBER: 60/090444	

1	PRIOR APPLICATION NUMBER: 60/090443
2	PRIOR FILING DATE: 1998-06-24
3	PRIOR APPLICATION NUMBER: 60/090427
4	PRIOR FILING DATE: 1998-06-24
5	PRIOR APPLICATION NUMBER: 60/090535
6	PRIOR FILING DATE: 1998-06-24
7	PRIOR APPLICATION NUMBER: 60/090540
8	PRIOR FILING DATE: 1998-06-24
9	PRIOR APPLICATION NUMBER: 60/090542
10	PRIOR FILING DATE: 1998-06-24
11	PRIOR APPLICATION NUMBER: 60/090557
12	PRIOR FILING DATE: 1998-06-24
13	PRIOR APPLICATION NUMBER: 60/090678
14	PRIOR FILING DATE: 1998-06-25
15	PRIOR APPLICATION NUMBER: 60/090678
16	PRIOR FILING DATE: 1998-06-25
17	PRIOR APPLICATION NUMBER: 60/090690
18	PRIOR FILING DATE: 1998-06-25
19	PRIOR APPLICATION NUMBER: 60/090694
20	PRIOR FILING DATE: 1998-06-25
21	PRIOR APPLICATION NUMBER: 60/090695
22	PRIOR FILING DATE: 1998-06-25
23	PRIOR APPLICATION NUMBER: 60/090696
24	PRIOR FILING DATE: 1998-06-25
25	PRIOR APPLICATION NUMBER: 60/090862
26	PRIOR FILING DATE: 1998-06-26
27	PRIOR APPLICATION NUMBER: 60/090863
28	PRIOR FILING DATE: 1998-06-26
29	PRIOR APPLICATION NUMBER: 60/091360
30	PRIOR FILING DATE: 1998-07-01
31	PRIOR APPLICATION NUMBER: 60/091478
32	PRIOR FILING DATE: 1998-07-02
33	PRIOR APPLICATION NUMBER: 60/091544
34	PRIOR FILING DATE: 1998-07-01
35	PRIOR APPLICATION NUMBER: 60/091519
36	PRIOR FILING DATE: 1998-07-02
37	PRIOR APPLICATION NUMBER: 60/091626
38	PRIOR FILING DATE: 1998-07-02
39	PRIOR APPLICATION NUMBER: 60/091633
40	PRIOR FILING DATE: 1998-07-02
41	PRIOR APPLICATION NUMBER: 60/091978
42	PRIOR FILING DATE: 1998-07-07
43	PRIOR APPLICATION NUMBER: 60/091982
44	PRIOR FILING DATE: 1998-07-07
45	PRIOR APPLICATION NUMBER: 60/092182
46	PRIOR FILING DATE: 1998-07-09

### Alignment Scores:

Pred. No.:	3772
Score:	2171.50
Percent Similarity:	58.3%
Best Local Similarity:	45.7%
Query Match:	34.6%
DB:	5
	Gaps:
	24

US-10-642-946-3 (1-1158) x US-09-989-726-61 (1-3772)

[illegible]

QY	159	lysaIaIthrluLybPrProserGlybYsArGPrProIleuAlaProserGIunTr	178
Db	199	-----CCTCCCGCGCCAAAGCGCGCGCTGTGTCGTGGCCCTGG-----	237
QY	179	LeuGIunTrProLeuPro-----ProProSerProGly	190
Db	238	-----CCCTTGCGCCCGCCAGCCTTCGCGCCCGAGCCCGCGCGCCCGGT	288
QY	191	ProGIunGlu-LeuPro--GInGIunGlyAlaPrOLEuserAmaantTrpGlnAsnPr	209
Db	289	GACCGGTGACCTGCGCCCTGGCGCGCGGGCGGAGAGCATGTC-----CGCCC	336
QY	209	oGlyGIunGIunTrHIsval-----	215
Db	337	GGGGACCGGTATCCCAAGCGCTGGCCCTGGTGCCTCTGGAGTGAACCTTGCGGGGTCCG	396
QY	216	-----G1	216
Db	397	AGCCAGGGCGAGCCCTCGAGGACCTGATTTATTCGGGAGAGATGTCGAGCCGGAG	456
QY	216	uAlaGIunGluHIsGInPrroGIunGIunGIunTrpGIunGluInProThrlLeuAspTrAs	236
Db	457	GCCCTACTAGCGCGCGCGCGAGCGAGCTCGAGACCTTCTCTCGCGCGCTGCTCGGG	516
QY	236	naSPeGInIeGIunArGIunAspTrGIsIunAspPheGIunTrIleArGIunGluAsGInPr	256
Db	517	G-----CCGGGGAGAGTGGAG-----CGCGCGCCGAGAGGACC	552
QY	256	oArGPrProProserArGIunArGIunArGIunGluAlaTrpProGIunProProGIunGI	276
Db	553	CAGG---CCGCCAAGAGGGCCACCAAGCCCAAGAAAGCT-----CCCAAGAGGA	600
QY	276	uLybAlaPrOAlaPrOAlaPrOGIunGIunArGIleGIunProValIyAspPheLeuEnPr	296
Db	601	GAAATCG-----GCTCCGGAG-----	616
QY	296	oProLeuPrProAspTrGlyAspGlyTrValIleProAsnTrAspAspMetAspTr	316
Db	616	-----	616
QY	316	rTrYrPheGIunProProGIunLybPrOAspAlaGIunArGIunThrlAspGIunGluTr	336
Db	617	-----CGCCTCCACCA-----GCTAA	633
QY	336	gGIunGluLeuLybAspProLybGIunAspSerSerProLybGIunGluThrlAspLyTr	356
Db	634	ACACAGACACAAAAAGTTATGAGAACCAAGACCTCTGAGAGAGCTGCCAACAT-----	688
QY	356	pAlaValGIunLybGlyLybAspHIslybGIunProArGIbGlybGIunGluLeuGIunGI	376
Db	689	-----GATCACAGTGTCCGTGGCCCCGTGAAGATGCAGAG--	727
QY	376	uTrpTrPrProThrlGluLybValIyAspPrProIleGIunMetGluSerHIsArGIleGI	396
Db	728	-----AGTGGCCACCTTGGCTGGAACCTTAATAATCAC	765
QY	396	uAspPheGInIleArGIAlaSerSerMetLeuArGHisGlyLeuGIAlaGlnArGIyAr	416
Db	766	AACTTCCAGCTCCATGCTCCACCGGTGAACCCCTTGGCTGGGGGCACATGAGAGGAG	825
QY	416	gLeuAsnMetGIunThrlGlyAlaThrlGluAspAspTrTrYrAspGIAlaATrPCyAlaGI	436
Db	826	ACTCAACATCCAGCGCGCATTAATGAATATTTTATGACGAGCGGTGGCCGGG	885
QY	436	uAspAspAlaArGIunTrpIleGIunAlaAspTrHArGIunArGIunThrlArGpHethrGI	456
Db	886	AAGAATGACCTCCACAGCTGATTAAGATGATGTCGGCGCCTGACCACTGATTCCTGG	945
QY	456	yAlIleThrlGInGIunArGIAspSerSerIleHIsAspAspPheValThrlThrlPheHeth	476
Db	946	TGTCACTACTCAAGGAGGAACTCCCTGGCTGAGTGAAGTGGATGATCATCTATTAAGT	1000
QY	476	IglYpHeSerAsnAspSerGIunThrlrPValMetTrYThAspGITrYrGIunGluMetTh	496

Db 1006 CATGTGATGACATACAGCCACACCTGGGTGACCTGTTAAAGATCGATCTGGAGACATCAT 1065  
 Qy rPhehIEGLYAsnValAspLyAspThrProValLeuSerGluIueProGluProValVa 516  
 Db 1066 ATTTGAGGGAAACAGTGAAGAGGAGATCCCTGTCTTCATAGAGCTACCCGTCCCATAGT 1125  
 Qy 516 IAlAArgPheLeaArgLeIeYrProLeuThrTP-----AsnGlySerLeuCyMetCar 534  
 Db 1126 GGGCCGCTACACTCCGCAATAACCTCAGCTCCGTGGTTGATTAAGGAGCACTCTGCATGAG 1185  
 Qy 534 gLeuGIuValLeuGIYCySerValAlaProValTYrSerTYrTYr--AlaGlnaenGI 553  
 Db 1186 AATGAGATCTCGTGGCTGCCCATCGGCAGATTCCTAATTAATTAATATATACCGCGGAAGCA 1245  
 Qy 553 uValValAlaThrAspAspLeuAspPheAlaGhiHisSerTYrLyAspMetArGlnle 573  
 Db 1246 GATGACACACCATGATACCTGATTTTAAAGCACCAATTAATAAGAAATAGCCCGCAT 1305  
 Qy 573 uMetLeValValAsnGIuCySPProThrIleThArGThrTYrSerLeuGIYLySe 593  
 Db 1306 GATGAAGTGTGATGAATGAATGTGTCCCAATATACACGAATTTACAACATTGGAAAAAG 1365  
 Qy 593 rSerArgLYLeuLYsIleTYrAlaMetGluIleSerAspAsnProGIYGLuHISGluLe 613  
 Db 1366 CCACACGGGGCTGTGAAGCTGATGCTGGAGATCTCGATCAACCTTGGGAGCATGTAGAT 1425  
 Qy 613 uGIYGIuProGIuPheArgTYrThrAlaGIYIleHISGIYAsnGIuValLeuGIYArGI 633  
 Db 1426 CGGTGAGCCGAGTTCCACThCATCGCGGGGGCCCAAGCAATAGAGTGTCTGGCCGGGA 1485  
 Qy 633 uLeuLeuLeuLeuLeuMetGlnTYrLeuCYArGIuTYrArGIAspGIYAsnProArGIa 653  
 Db 1486 GCTGCTGCTGCTGCTGGTGACAGTTCCGTGTACAGAGATACTTGCCCGCGAATGCGGCAT 1545  
 Qy 653 lArGIserLeuValGlnAspThrArGIleHISleuValProSerLeuAsnProAspGIYTY 673  
 Db 1546 CGTCCACCTGGTGGAGAGACGGCGGATTCAGTCTCCCTCCCTCAACCCCGAGTGGCTA 1605  
 Qy 673 rGIuValAlaAlaGlnMetGIYserGIuPheGIYAsnTrPAleuGIYleuTrpThrGI 693  
 Db 1606 CGAGAAGCCCTACGAAAGGGGGCTCGAGACGTGGAGCGCTGGGCCCTGGAGCCGCA 1665  
 Qy 693 uGIuGIYPheAspIlePheGIuAspPheProAspLeuAsnSerValleuTrpGIYAlaGI 713  
 Db 1666 CGATGGAAATTACATCAACAACAATTCTCGATTAAACAAGCTGCTCTGGAGGAGACA 1725  
 Qy 713 uGluArGIuTYrValProTYrArGIValProAsnAsnAsnLeuProIleProGIYArGIY 733  
 Db 1726 GGATTCAGACGAATGTCCCGAGAAAGTTCCCACTACTATATTCGATCCTCGTAGTGTT 1785  
 Qy 733 rLeuSerProAspAlaThrValISerThrGIuValAlaGIAlaIleAlaTrpMetGIYLY 753  
 Db 1786 TCTGTCCGAAATAATCCACGAGTGGCTGCCGAGACACGAGCAGTCAATGCTGGATGGAAA 1845  
 Qy 753 sAsnProPheValleuGIYAlaenLeuAsnGIYGIYGIuAspLeuValISerTYrProTY 773  
 Db 1846 AATCCCTTTTGTGTGGCGGCAACTGTCAGAGGCGGAGCTGTGTGTGGCTATCCCTA 1905  
 Qy 773 rAspMetAlaArgThrProThrGIuGIuGIuGIuLeuLeuAlaAlaIleMetAlaAlaAr 793  
 Db 1906 CGACCTGTGGTGGTCCCTCGAAGACGAG----- 1936  
 Qy 793 gGIYGIuAspGIuAspGIuValISerGIuAlaGlnGIuThrProAspHisAlaIlePheAr 813  
 Db 1937 -----GAACACACCCCAACCCCGATGACCAAGTGTTCG 1971  
 Qy 813 gTrpLeuAlaIleSerPheAlaSerAlaHisLeuThleuThrGIuProTYrArGIYGI 833  
 Db 1972 CTGGCTGGCCACTACTCTATGCTTCACACACCGGCTCATAGCAACCGCGGAGAGAGGT 2011  
 Qy 833 YCyGlnAlaGlnAspTYrThrThrGIYGIYMetGIYIleValAsnGIYAlaLYsTrPAsnBr 853



Db 2032 GTGCCACACGAGAGACTTCCAGAAAGAGAGGACCTGTAATGGGGCTCTGGACAC 2091  
Qy 853 oagthgclgylthrlaenaprpheSerlytleuhithaencysleugluSerph 873  
Db 2092 CGTGGCTGGAAGTGTGAACGATTTTCACCTTCAATACAAACGCTTCGAACTGTCCAT 2151  
Qy 873 eTyleugllyCyhaerlyvPheProHlsglusergluLeuProaHgluTPgluaAna 893  
Db 2152 CTAGTGGGCTGTGATTAATTAATCCCATGAGAGGACCTGCCAGAGAGTGGGAAATAA 2211  
Qy 893 nlysglualeuLeuThrPheMetGluGlnValHlaArgGlylleysgllyVal1th 913  
Db 2212 CCGGGAATCTGTATGCTGTTCATGAGAGGTTTCATCGTGGCATTAAGCTTGGTGA 2271  
Qy 913 rAerGluGlnGlylleProHlealaAna1athrlleSerValserGlylleaHlsgl 933  
Db 2272 AGATTCAATGAAAGAAAGAAATCCCAAGCCCATTTATCTCGTGAAGAGCATTAACATGA 2331  
Qy 933 yVallyeThralaserGlylylePheProHleuThrParglileuAnaProgllylyrArgVa 953  
Db 2332 CATCCGAACAGCCCAACATGGGATTAAGTACGCGCTCTGAACCTTGAAGATGTGTGT 2391  
Qy 953 lthraHlaHlaGluGlylyrThrProSerAlalyeThrCyhaAnaValaerlyrAerP1 973  
Db 2392 CACAGCAAAAGCCGAAAGTTTCACTGATCCACCAAGAACTGTATGTTGGTATGACAT 2451  
Qy 973 eGlyAlaThrlGlnCyhaenPheHleuAlaArgSerAsnTrplyaHgl1leArgGlu1 993  
Db 2452 GGGGGCCCAAGAGGTGACTTCACTTACCAAAACCAATGCGCAGATCCGAGAT 2511  
Qy 993 eMeAlaMeAlaenGlyAnaHrProHleProHlelaaPProSerHrProMetHrP 1013  
Db 2512 CATGGAGAACTTTGGGAGAGCCCGTC----- 2539  
Qy 1013 oGlnGlnArgArgleuglnGlnArgleuglnHlaArgleuArgleuArglaGlnme 1033  
Db 2540 -----AGCTGCGACCGACGCGGCTGAAGCTCGGGGGGGAAGAGACGACGCG 2589  
Qy 1033 tAArgleuArgArgleuAna1athrlthrlleuglyProHleThrValProProthr 1052  
Db 2590 TGGGTGACCTCTCTGGGCTTGAAGACTCGTGGAGCCCATGAATTAACCAACC 2647

RESULT 11  
US-09-97-514-61  
Sequence 61, Application US/0997514  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C46  
CURRENT APPLICATION NUMBER: US/09/97,514  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
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PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
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PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
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PRIOR APPLICATION NUMBER: 60/088217  
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PRIOR FILING DATE: 1998-06-09  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11



Db	457	GCCTACTACGGCGCGCCGAGCCGACGCTCGAGACCTTCTCTCCGCGCTGCTCGG	516
Oy	236	naerglnlleglwaixglnaaprtglnaaprhnegluyrlleaargxglnlyaglnpr	256
Db	517	G-----CCCGGGGAGAGTGGAG-----CGCGCCGCCGAGAGCC	552
Oy	256	oargproproproseratargatgargprogluaargvaltrprogluproproglu1	276
Db	553	CAGG---CCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCT-----CCCAAGAGGA	600
Oy	276	nllyalaaproalaaproalaiprogluaargllegluproprovallyaproleuleur	296
Db	601	GAAAGTCG-----GCTCCGAG-----	616
Oy	296	oproleuproproaprtglnaaprluytrvalleproamntyraapraarmetaprtg	316
Db	616	-----	616
Oy	316	rtgtrhegluproproprogluylaproalaagluarglnthraproglu1ly	336
Db	617	-----CCGCTCCACCA-----GCTAA	633
Oy	336	eglululeuyllylprolyllyllyllyllyllyllyllyllyllyllyllyllyl	356
Db	634	ACACAGCAACMAAAAGTTATGAAACCAAGAGCTCTGAGAAAGCTGCCACAGAT---	688
Oy	356	palavalglyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl	376
Db	689	-----GATCACAGTCTCCGTGTGCGCCGCTGAAAGATGTCAGAG--	727
Oy	376	utrtprthrtrothrglyllyllyllyllyllyllyllyllyllyllyllyllyllyl	396
Db	728	-----AGTTGCCACCTGTGCTCGAAACCTTAAATATC	765
Oy	396	uaprahnglnlleaarglaasersemetleudarghilegluleuylalaglnarglyl	416
Db	766	AGACTTCCAGCTCCATGCTCCACGCTGAAGGCTATGCTCGGGGCACTCGAGGAG	825
Oy	416	gleuammetglnthrglylalthglnuaprahprtytrgaaprglylaltprocyalagl	436
Db	826	ACTCAACTCCAGCGGGGAGTTAATGAATAATATTTTATGACGAGACGCTGTGCGGG	885
Oy	436	uaprahprlaargthrglntrp1leglualaaprtgtrgaargthrtargphehtg1	456
Db	886	AAGAAATGACCTCCAGAGTGAATGAAGTGAAGTGTGCGCCCTGACCAAGTTCACTG	945
Oy	456	yvallethrglnglyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl	476
Db	946	TGTCATCACTCAAGGAGAGAACCTCCCTGCTGCTGATGACTGGGTGACATCTTAAGGT	1005
Oy	476	lglylphseeraprahprserglnthtrpvalmeturythraanglyllyllyllyllyl	496
Db	1006	CATGTGAGCAATGACAGCACACGTGGGTCACTGTAAAGATGATCTGAGACATGAT	1065
Oy	496	rphetisgllyaenvalaaplylaaprtgtrprovalleuserglnleuprogluprovalya	516
Db	1066	ATTGAGGGAAACATGAGAGGAAGATCCCTTTCTCAATGAGCTACCCGTCCCATGCT	1122
Oy	516	lalaargpheleargllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl	534
Db	1126	GAGCCGCTACATCCCATTAACCTCCAGCTCGGTGTGATATGAGGAGCATGTGCATAG	1189
Oy	534	gleuuglyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl	553
Db	1186	AATGAGAGATCCGTGGCTGCCCATCCAGATCTTAATATTTATTTATCAACCGCGGAGCA	1244
Oy	553	uvalalalathraprahprleuaprahprhahiserlyllyllyllyllyllyllyllyllyl	573
Db	1246	GATGACCAACCACTGATGACTGGATTTTAAGACCAACATTTTAAGAAATGCGCAGTT	1305
Oy	573	lmetlylvalalaauglulucyaprothrllethraargthrtysertleuuglyllylse	593

Db	1306	GATGAAAGTTGTGAATGAATGATGTCCTCCAAATATACCAAGAAATTTACAACTTGGAAAAAG	1365
Qy	593	rserarglglyleuylserlyrtaametglutileseraspasnproglynhisglule	613
Db	1366	CCACGAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATACACCTTGGAGCATGAAGT	1425
Qy	613	uglyglubproglunphearglyrthrtaaglylilehisgluvasngluvalleuglyargl	633
Db	1426	CGGTAGAGCCGAGTTCCACTACATCGGGGGGGCCACGGCAATAGAGTGTGGCCGGGA	1485
Qy	633	uileuleuleuleuleumetglntryrleucysarggluttryrargaspeliasnproargva	653
Db	1486	GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1545
Qy	653	largserleuvalglnaethrarrargilehisleuvalproserleuasnproaspglyty	673
Db	1546	CGTCCACCTGTGTGAGAGACGCGGATTCACGTCTCTCCCTCTCAACCCCGATGGCTA	1605
Qy	673	rgluvalalaalaglnmetglsersglnupheglivasntrpalaaleuglyleutprthgl	693
Db	1606	CGAAGAGGCTACAGAAAGGGGGCTCGAGAGCTGGAGGCTGGCCCTGGGACGCTGACCA	1665
Qy	693	uglulglypheaspiilephegluasapheproaspheuasnservalleutprglialgl	713
Db	1666	CGATGGAAATTTACATCAACAACATTTCTCGATTAAACACGCTGTCTGGAGGACAGA	1725
Qy	713	ugluabqlystrpvalprotyrargvalproasnaspheleuoproileprogluargty	733
Db	1726	GGATTCAGACAGATGCCCCAGAAAGTTCCCAATACATATTTGCAATCCCTGTGTGCTT	1785
Qy	733	rleuserproaspalaethrvaliserthrthrgluvalargalaleilealatrmetgltly	753
Db	1786	TCTGTGGAAATATCCACGCTGGCTGGCCAGAACCAAGACAGTCAATACCTGGATGGAAA	1845
Qy	753	asasnprophevalleuglyalaaenleuasnglylglyglubrgleuvalsertryproty	773
Db	1846	AATCCCTTTGTGTGTGGCGGCAACCTGCAGGGGCGAGCTGTGTGTGTGTGTGTGTGT	1905
Qy	773	raspmeralargthrprothrnglnuglnleuleuhalalalamechalaalalaar	793
Db	1906	CGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1936
Qy	793	gglglylunbspglunbspglunalserglualaglngluthrproaspiisalailephear	813
Db	1937	-----GAACACACCCCAACCCCGATGACACACGTTCCG	1971
Qy	813	gtrpleuhalaleserphealaseralanhisleuthrleuthrgludprotyrarglygl	833
Db	1972	CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2031
Qy	833	ycysglnalaglnaspyrthrnglyglmetglilevalasnglvalalaysrtpasnpr	853
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Qy	913	raspgluglnclyleproillealaaenalathrilleservalserglylileasnhisgl	933
Db	2272	AGATTCAACATGGAAGAAAGATCCCAACGCCCATTTATCTCGTGAAGAGCATTAACATGA	2331
Qy	933	valalysrthralsaserglylvaspyrtryrprargileleuasnproglygluttryrargva	953
Db	2332	CATCCGAAGCCCAACATGAGGGATTTCTGTGGCGCTCTGTAAACCTGTGAAGATGTGTGT	2391

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 Db 2540 -----AGCTTCCAGCCAGCGGCTGAGAGCTCGGGGCGGAGAGAGAGAGCGG 2589  
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RESULT 12  
 US-09-989-728-61  
 ; Sequence 61, Application US/09989728  
 ; Patent No. 7029873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gertlisen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tuma, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C72  
 ; CURRENT APPLICATION NUMBER: US/09/989,728  
 ; PRIOR FILING DATE: 2001-11-20  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
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Qy 1013 oGluGluArgArgLeuGluGluArgArgLeuGluHisArgLeuArgLeuValAlaGluMet 1033  
Db 2540 -----ACCTGACAGCGAGGCGGCTGAAGCTGGGGGGGAGAGAGAGAGAGAG 2589  
Qy 1033 rArgLeuArgArgLeuAsnAlaThrThrThrLeuGluProHisHisThrValProProThr 1052  
Db 2590 TGGGTGACCTCTGGGCTTGAAGATCTGTGTGGAACCATGCAAAATTAACCAACC 2647

RESULT 13  
US-09-997-349-61  
Sequence 61, Application US/09997349  
Patent No. 7034106  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C37  
CURRENT APPLICATION NUMBER: US/09/997,349  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
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US-09-997-653-61
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/ Patent No. 7034122
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gettitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James

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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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QY 993 eMetAlaMetAsnGlyAsnArgProIleProHisLeAspProSerArgProMetThrPr 1013  
Db 2512 CATGAGAAAGTTTGGAGACAGCCGCTC----- 2539  
QY 1013 oGlnGlnArgArgLeuGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMe 1033  
Db 2540 -----AGCTGCGACGACGCGGCTGTAAGCTGCGGGGCGGAGAGACGACAGCG 2589  
QY 1033 rArgLeuArgArgLeuAsnAlaThrThrThrLeuGlyProHisThrValProProThr 1052  
Db 2590 TGGGTGACCTCTGGGCTTGAAGACTGCTGGAGCCATGCAAAATTTAAACCAAC 2647  
  
RESULT 15  
US-09-989-293A-61  
Sequence 61, Application US/09989293A  
Patent No. 7034136  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austlin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P166  
FILE REFERENCE: P2730P166  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

1	PRIOR APPLICATION NUMBER: 60/066770
2	PRIOR FILING DATE: 1997-11-24
3	PRIOR APPLICATION NUMBER: 60/075945
4	PRIOR FILING DATE: 1998-02-25
5	PRIOR APPLICATION NUMBER: 60/078910
6	PRIOR FILING DATE: 1998-03-20
7	PRIOR APPLICATION NUMBER: 60/083322
8	PRIOR FILING DATE: 1998-04-28
9	PRIOR APPLICATION NUMBER: 60/084600
10	PRIOR FILING DATE: 1998-05-07
11	PRIOR APPLICATION NUMBER: 60/087106
12	PRIOR FILING DATE: 1998-05-28
13	PRIOR APPLICATION NUMBER: 60/087607
14	PRIOR FILING DATE: 1998-06-02
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17	PRIOR APPLICATION NUMBER: 60/087759
18	PRIOR FILING DATE: 1998-06-02
19	PRIOR APPLICATION NUMBER: 60/087827
20	PRIOR FILING DATE: 1998-06-03
21	PRIOR APPLICATION NUMBER: 60/088021
22	PRIOR FILING DATE: 1998-06-04
23	PRIOR APPLICATION NUMBER: 60/088025
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088026
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088028
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088029
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32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088033
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088326
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39	PRIOR APPLICATION NUMBER: 60/088202
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55	PRIOR APPLICATION NUMBER: 60/088824
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57	PRIOR APPLICATION NUMBER: 60/088826
58	PRIOR FILING DATE: 1998-06-10
59	PRIOR APPLICATION NUMBER: 60/088858
60	PRIOR FILING DATE: 1998-06-11
61	PRIOR APPLICATION NUMBER: 60/088861
62	PRIOR FILING DATE: 1998-06-11
63	PRIOR APPLICATION NUMBER: 60/088876
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65	PRIOR APPLICATION NUMBER: 60/089105
66	PRIOR FILING DATE: 1998-06-12
67	PRIOR APPLICATION NUMBER: 60/089440
68	PRIOR FILING DATE: 1998-06-16
69	PRIOR APPLICATION NUMBER: 60/089512
70	PRIOR FILING DATE: 1998-06-16
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72	PRIOR FILING DATE: 1998-06-16
73	PRIOR APPLICATION NUMBER: 60/089532

[illegible][illegible]

1 PRIOR APPLICATION NUMBER: 60/091544-01  
2 PRIOR FILING DATE: 1998-07-01  
3 PRIOR APPLICATION NUMBER: 60/091519  
4 PRIOR FILING DATE: 1998-07-02  
5 PRIOR APPLICATION NUMBER: 60/091626  
6 PRIOR FILING DATE: 1998-07-02  
7 PRIOR APPLICATION NUMBER: 60/091633-01  
8 PRIOR FILING DATE: 1998-07-02  
9 PRIOR APPLICATION NUMBER: 60/091978-01  
10 PRIOR FILING DATE: 1998-07-02  
11 PRIOR APPLICATION NUMBER: 60/091978-01  
12 PRIOR FILING DATE: 1998-07-02  
13 PRIOR APPLICATION NUMBER: 60/091982-01  
14 PRIOR FILING DATE: 1998-07-07  
15 PRIOR APPLICATION NUMBER: 60/092162-01  
16 PRIOR FILING DATE: 1998-07-09

### Alignment Scores:

Pred. No.:	3 01e-135	length:	3772
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Percent Similarity:	58.3%	Conservative:	129
Best Local Similarity:	45.7%	Mismatches:	227
Query Match:	34.6%	Indels:	199
DB:	5	Gaps:	24

US-10-642-946-3 (1-1158) X US-09-989-293A-61 (1-3772)

OY		60	GlyThrAlaIaGlnValProProGluLysThrllysAspArgSerlYlsylsGIYLVLys	99
Dd		44	GGACCGGCCTCGAGGGGTCCGCC-----GAAAGGGAGGAAGAAG	85
OY		100	AspLysGlYProllysValProlysGluSerLeuGluGlyserProAtpProPolYlys	119
Dd		86	-----GAAAGGGGGGCGGCCCTG----	108
OY		120	GlyLysGluLysProProLysAlaThrlYsLysProlYsgluysProPolYs---Ala	138
Dd		109	-----CGCCCCCGCGCCTTCGCGGCC--TGTCCGCCCAGCCAGC	153
OY		139	ThrlYsLysProlYsgluGluProProLYsaLaThrlYsLysProlYsgluysProPro	158
Dd		154	CAAGCCAGCCCCCGCGCGCGGTACAACGGGAGCAGCGCGCG-----	198
OY		159	LysAlaThrlYsLysProProSerGlyLysArgProProIlleualaProSerGluThr	178
Dd		199	-----CCTCCCGGCCCAAAGCGCGCGCTGTGTGACCCTTGCG--	237
OY		179	LeuGluTrpProLeuPro-----ProProSerProGly	190
Dd		238	-----CCCTTGCCCGCGCGCACGTTCTGGCCCGCAGCCCGCCGCGCCCGGT	288
OY		191	ProGluGlu-LeuPro--GIngluglYglaIaProlEusefAmnaSnTrpGluAnPr	209
Dd		289	GACCGTAGCCCTGCTCCGCGGCGCGGGGAGGAGCATGTCC-----CGCCC	336
OY		209	oGluGluGluThrHisVal-----	215
Dd		337	GGAGAACCTACCCCAAGCGGTGSCCTGGTCTCTCGACATGACTGCGCGGGGTCCG	396
OY		216	-----G1	216
Dd		397	AGCCCAAGGCGCAGCCCTCGAGACCTGATTATTAAGCGGAGAGATCTGAGCCGGGA	456
OY		216	uAlagIngluHIselnProGluuProGluGluGluThrlngluInProthrLeuAspTryas	236
Dd		457	GCCCTACTACGCGCGCGGAGGCCAGAGCTCGAGACCTTCTTCGCGCGCTCGCTCGGG	516
OY		236	nAspGlnlleGluArgGluAspTrycgluasArpheGluTrylEarArgGlnIynSclnPr	256
Dd		517	G-----CCGGGGAGAGAgTGGAG-----CGGCGCCCGCAGAGACC	555
OY		256	aArgProProProSerfArgArgArgArGPProGluuArgValITrpProGluuProProGluG1	276
Dd		553	CAGG---CCGCCCCMAAGGGCCCAACAGCCCAAGAAAGCT-----CCCAAGAGGA	600



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: SOFTWARE: FASTSEQ for Windows Version 3.0.
: SEQ ID NO 1
: LENGTH: 3935
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

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Qy 681 SerGluheglYanTTPAlaLeuGlyLeuTTPThrgLugLyeuGlyPheAspIlePheGlu 700  
Db 2180 TCAGAGTTTGGGAAGCTGGGCGCTGGGACTGGAGCTGAGAGGAGGAGTGGGCTCCCTAC 2239  
Qy 701 AspPheProAspLeuAnSerValLeuTTPGlyValaGluGlyValaGlyLysTPValProDyr 720  
Db 2240 GATTTCCTGGATCTCAACTCTGTCTCTGGGAGCTGAGAGGAGAAATGGGCTCCCTAC 2299  
Qy 721 ArgValProAsnAnAnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740  
Db 2300 CGGGTCCCAACAATTAATTGGCCATCCCTGGAACGCTTACCTTGGCCAGATGCCAGGTA 2359  
Qy 741 SerThrgLyuValaGlyAlaIleIleAlaTTPMeGluLysAnProPheValLeuGlyAla 760  
Db 2360 TCCAGAGAGTCCGGGCGCATCATCTGCTGATGAGAGAAACCCCTTCGTCGTGGAGCA 2419  
Qy 761 AsnLeuAnngLysGlyLysArgLeuValSerTyrProTyrAspMetAlaArgTPProThr 780  
Db 2420 AATCTGAAGCGCGGCGAGCGGCTGATCTTACCCCTACGATATGGCCCGCAGCCTTACC 2479  
Qy 781 GlnGluGlnLeuLeuValaAlaAlaMetAlaAlaAlaArgGlyLysAspGluAspGluVal 800  
Db 2480 CAGGAGCAGCTGCTGGCGCAGCCATGGCAGCAGCCCGGGGGAGAGTGAAGAGAGCTC 2539  
Qy 801 SerGluAlaGlnGluThrProAspPheAlaIlePheArgTPLeuAlaIleSerPheAla 820  
Db 2540 TCCGAGGCCAGGAGAGCTCCAGACACAGCCCTCTCCGCTGGCTTGCATCTCTTGGCC 2599  
Qy 821 SerAlaIleSerThrLeuThrGluProTyrArgGlyLysGlyAlaGlnAspTyrThr 840  
Db 2600 TCCGACACCTTCACTTGACCGAGCCCTACCGCGGAGGCTGCGCAAGCGCAGATACAC 2659  
Qy 841 GlyGlyMetGlyLysValaGlnGlyAlaLysTTPAsnProArgTPThrgLysIleAsnAsp 860  
Db 2660 GGGGGCATTGGGCATCTGCAACGGGGGCAAGTGAAGAACCCCGGAGCGGAGCTATCAAGAC 2719  
Qy 861 PheSerTyrLeuHisThrAnCyLeuGluLeuSerPheTyrLeuGlyCyAspLysPhe 880  
Db 2720 TTCAGTACCTGCTACCACTGCTGAGCTCTCTTCACTGAGCTGCTGACCAAGTTC 2779  
Qy 881 ProHisGluSerGluLeuProArgGluTTPGluAsnAnLysGluAlaLeuLeuThrPhe 900  
Db 2780 CCTCATGAGAGTGAAGTGGCCCGGAGTGGAGAAACAAGAGGGCTGCTACCTTC 2839  
Qy 901 MetGluGlnValHisArgGlyLysLeuGlyValValaThrAspGluGlnGlyIleProIle 920  
Db 2840 ATGGAGCAGGTGCACCGGCGATTAAAGGGGTGTGACGACAGCAAGGCATCCCAT 2899  
Qy 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleYThrAlaSerGlyGly 940  
Db 2900 GCCAAGCCGACCACTCTGTGAGTGGCATTAATCAAGCGCTGAAGACAGCAGGTGGT 2959  
Qy 941 AspTyrTTPArgGlyLeuLeuAnProGlyLysTyrArgValThrAlaHisAlaGluGlyTyr 960  
Db 2960 GATTACTGGGAATCTTGAACCGGGGTGAGTACCGCTGACAGCCACGGGAGGGGTAC 3019  
Qy 961 ThrProSerAlaLysThrCyAsnValAspTyrAspIleGlyAlaThrGlnCyAsnPhe 980  
Db 3020 ACCCGAGCGCCCAAGACTGCATTAATGTGACTATGACTCCGGGCGCATCTGCTCAATTC 3079  
Qy 981 IleLeuAlaArgSerAnTTPLysArgIleArgGluIleMetAlaMetAnGlyAsnArg 1000  
Db 3080 ATCTGCTGCTGCTCCAACTGGAAGCGCATCCGGGAGATCATGGCCATGAACGGGAAACCG 3139  
Qy 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLeuGlnGln 1020  
Db 3140 CCTATCCCAACATGAGCCCATTCGCGCTTATGACCCCCCAACAGGCAAGCCCTGACGAG 3199  
Qy 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgLeuAsnAla 1040  
Db 3200 CGAGCGCTTACAAACCGGCTGGCGCTTGGGCAAGATGGCGGCTGGCGCCTTCAAGCC 3259

Qy 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaPProAlaThrThr 1060  
Db 3260 ACCACCACTTAAAGCCCGCCACACTGTGCTCCCAAGCTGGCCCTGCGCCACACAC 3319  
Qy 1061 LeuSerThrThrIleGluProTTPGlyLeuIleProProThrThrAlaGlyTTPGluGlu 1080  
Db 3320 CTGAGCACTACATAGAGCCCTGGGCTCATACCCGCAACACCGCTGCTGGAGAGAG 3379  
Qy 1081 SerGluThrGluThrTyrThrgLyuValaThrGluPheGlyThrgLyuValaGluProGlu 1100  
Db 3380 TCCGAGACTAGACTTACACAGAGGTGTGACAGAGTTTGGAGCCGAGGTGGAGCCGAG 3439  
Qy 1101 PheGlyThrgLysValGluProGluPheGluThrgLyuGluProGluPheGluThrgLyn 1120  
Db 3440 TTTGGGACCAAGGTGAGCGCCGAGTTTGAACCCAGTTGAGCCTGATTCGAGACCCAG 3499  
Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
Db 3500 CTGGAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCCTTGGC 3559  
Qy 1141 GlnAlaPheProPheThrThrValaGluThrTyrThrValaAnPheGlyAspPhe 1158  
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RESULT 3  
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; Sequence 288, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Melzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159, 563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133, 937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 288  
; LENGTH: 3935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-288

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Score: 6272.00 Matches: 1158  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
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US-10-642-946-3 (1-1158) x US-10-159-563-288 (1-3935)

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Qy 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40  
Db 200 CTTGAGGGGGCGCCGAGAGCGGTGTGACGAGCAGAGATCGAGAGTTCTCGAGGGG 259  
Qy 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProPro 60  
Db 260 TTCCTGTCAAGCTTAACCTGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319  
Qy 61 GluProThrProArgValaArgLysAlaGlnAlaGlyLysProGlyLysArgProGly 80

Db 320 GAGCCACCCCGGGTCCGAAAAGCCAGCGGGGGGCAAGCGAAGGCGGCCAGGG 379  
Qy 81 ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp 100  
Db 380 AGGGCCGAGAAAGTGCCTCCGGAAAAGACAAAGACAAAGGGAGAAAGCAAGAAC 439  
Qy 101 LysGluProLysValProLysGluSerLeuGluGluSerProArgProProLysLysGly 120  
Db 440 AAAAGCCCCAAGGTGCCAAAGAGTCTTGAGAGGGATCCCCAGGCGGCCCAAGAAAGGG 499  
Qy 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140  
Db 500 AAGGAAAGACCAACCAAGGCCACCAAGAAAGCCCAAGAGAGGCACTTAAGGCCACCAAG 559  
Qy 141 LysProLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla 160  
Db 560 AAGCCCAAGAGAGGACCCCAAGGCGCACCAAGAACCCCAAGAAAGACCCCAAGGGCC 619  
Qy 161 ThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGluThrLeuGlu 180  
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Db 680 TGGCCACTGCCCCACCCCGAGCCCTGGGCCCGAGAGACTACCCAGAGAGGAGGGCG 739  
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Qy 221 GluProGluProGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 240  
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Qy 241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGluLysGluProArgProPro 260  
Db 860 AAGGAGACTATAGAGACTTGAGTACATTCGCGCAGAGCAACCCAGGCCACCCCA 919  
Qy 261 SerArgArgArgArgProGluLysValTrpProGluProProGluLysLysAlaProAla 280  
Db 920 AGAGAGAGAGAGAGGCGCGAGCGGTCTGGCCAGAGCCCTGAGAGAGAGGCGCGGCC 979  
Qy 281 ProAlaProGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 300  
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Qy 301 AspTyrGlyAspGluTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320  
Db 1040 GACTATGATGATGATTACGTGATCCCACTAGCATGACATGAGACTATTACTTTGGGCT 1099  
Qy 321 ProProProGluLysProAspAlaGluLysGluLysLysLysLysLysLysLysLys 340  
Db 1100 CTTCCGCCCAAGAGCCGATGCTGAGCGCAGACGAGCAAGAGAGAGAGGAGCTGAAG 1159  
Qy 341 LysProLysLysGluAspSerSerProLysGluGluLysLysLysLysLysLysLys 360  
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Qy 381 GluLysValLysLysProProLysLysLysLysLysLysLysLysLysLysLysLys 400  
Db 1280 GAAAGAGTCAAGTGTCCCATTTGGATGAGTCAACCGTATTAAGAGCAACGAGATC 1339  
Qy 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGluLysLysLysLysLysLysLys 420  
Db 1340 CGAGCTCTCTCCATGCTGCCCAAGCGCTGGGGGCAAGCGCGCGGCTCAACATGAG 1399  
Qy 421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg 440  
Db 1400 ACCGGTGCACCTAGAGAGCACTACTATGATGTCGTGTGTCGAGAGGAGTGCAGAG 1459

Qy 441 ThrGluTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGlu 460  
Db 1460 ACCCATGATATGAGAGTGAACCAAGAGAGTACCCGGTCTCAGCGGTCTACCCAG 1519  
Qy 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480  
Db 1520 GGCAGAGACTCAGATCATGAGATTTTGTGACCACTTCTGTGGGCTTCAGCAAT 1579  
Qy 481 AspSerGluThrTrpValMetTyrThrAsnGlyTyrGluLysLysLysLysLysLys 500  
Db 1580 GACACCGAGACATGGGTGATGACCAACCGCTATGAGAAATACCTTCATAGGGAAC 1639  
Qy 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaArgPheIle 520  
Db 1640 GTGACAGAGACACACCCGTGTGATGAGTCCCAAGAGCCGGTGTGGCTTTCATC 1699  
Qy 521 ArgIleTyrProLeuThrTrpAsnGlySerLeuCyMetArgLeuGluValLeuGlyCys 540  
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Qy 541 SerValAlaProValTyrSerTyrTyrAlaGluAsnGluValAlaThrAspAspLeu 560  
Db 1760 TCTGTGGCCCTGTCTTACAGCTTACGACAGATGAGGTGGCCACGATGACCTG 1819  
Qy 561 AspPheArgHisHisSerTyrLysAspMetArgGluLeuMetLysValAlaAsnGlu 580  
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Qy 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgLysLeuLysIleTyr 600  
Db 1880 TGCCCCACATCACCCGCACTTACAGCTGGGCAAGAGCTCAGAGGCTTCAAGATCTAT 1939  
Qy 601 AlaMetGluLysSerAspAsnProGluLysLysLysLysLysLysLysLysLysLys 620  
Db 1940 GCCATGAGATCTCAGAACCCCTGGGAGAGATGAATCGGGGAGCCCAAGTTCGCTAC 1999  
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Db 2000 ACTGCTGGATCATTGAGCAAGAGTGTGGCCAGAGCTTGTGCTGCTCATGAG 2059  
Qy 641 TyrLeuCyArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
Db 2060 TACCTGTGCGAGAGTACCGGATGGAAACCACTGTGCGCAGCTGGTGCAGAGACAC 2119  
Qy 661 ArgIleHisLysValProSerLeuAsnProAspGlyTyrGluValAlaAlaGluMetGly 680  
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Qy 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700  
Db 2180 TCAAGATTGGGAATCGGGCGCTGGGACTGTGAGTGAAGAGAGGCTTTGACATCTTGA 2239  
Qy 701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyr 720  
Db 2240 GATTTCCGGATCTCAACTGTGCTGGGAGCTGAGAGAGAAAGAGTCTCCCTAC 2299  
Qy 721 ArgValProAsnAsnAsnLeuProLysProGluLysLysLysLysLysLysLysLys 740  
Db 2300 CGGGTCCCAAAATTAATTCCTGCACTCCAGAGCTTCTTCGCAATGCCACAGTA 2359  
Qy 741 SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla 760  
Db 2360 TCCACGAGAGTCCGGGCACTTTCCTGAGTGAAGAAACCTTCTGCTGGAGAGCA 2419  
Qy 761 AsnLeuAsnGlyGlyLysLysLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
Db 2420 AATCTGAACGGCGGAGGGCTTACTATCTACCTCAGATATGGCCGCGACGCTTACC 2479  
Qy 781 GlnGluGluLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal 800  
Db 2480 CAGAGCAAGCTGTGCGCAGACCAATGAGAGCCCGGGGAGAGATAGAGACGAGTGC 2539

QY 801 SerGluValGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 820  
DB 2540 TCCGAGGCCAGAGAGACTCCAGACCAAGCCACTTCGGGGCTTGCCACTCTCCGCC 2599  
QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840  
DB 2600 TCCGACACACTCACTTGACCGAGCCCTTACCGGGAGAGCTGCCAAGCCAGCACTACACC 2659  
QY 841 GlyGlyMetGlyIleValaIleGlyAlaValTyrTrpAsnProArgThrGlyThrIleAsnAsp 860  
DB 2660 GGGGGCATGGGCATCGTCACAGGGGCCAAGTGAACCCCGGAGCTTACATGATGAC 2719  
QY 861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880  
DB 2720 TTGAGTTACTGCACTACCACTGCTGAGACTCTCTCTTCACTGGAGCTGACAGAGTTC 2779  
QY 881 ProHisGluSerGluLeuProArgGluTyrGluValaAsnAspIleGluAlaLeuLeuThrPhe 900  
DB 2780 CCTCATGAGAGTGAAGTGGCCCGGAGTGGAGAACACAGAGAGGGCTGCTCACCTTC 2839  
QY 901 MetGluGlnValHisArgGlyIleValGlyValaThrAspGluGlnGlyIleProIle 920  
DB 2840 ATGAGAGAGGTGACCCGCGCATTAAGGGGTGTGACGAGACAGCAAGCATCCCATTC 2899  
QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValaLysThrAlaSerGlyGly 940  
DB 2900 GCCAAGCCACCACTCTGTGAGTGCATTAACTACCGGCTGAAAGACAGCAGTGGTGGT 2959  
QY 941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960  
DB 2960 GATTACTGGGGAATCTTGAAACCGGGGTGATACCGCTGACACCCAGCGGAGGGCTAC 3019  
QY 961 ThrProSerAlaLysThrCysAsnValaAspTyrAspIleGlyAlaThrGlnCysAsnAsp 980  
DB 3020 ACCCCAGGCGCCAAAGACTGTGCACTATGATGACATCGGGGCCACTCGTCAACTTC 3079  
QY 981 IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000  
DB 3080 ATCTGAGCTGCTCCAACTGGAAAGCGCATCGGAGATCATGGCCATGAAACGGGAACCG 3139  
QY 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020  
DB 3140 CCAATCCACACATAGACCATCGCGCCCTATGACCCCCCAACAGAGAGCCCTGACAGCAG 3199  
QY 1021 ArgArgLeuGlnHisArgLeuAlaGlyLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040  
DB 3200 CGACGCTTACAAACAGCGCTGCGGCTTCGGGCAACAGTGCAGCTGGCGCCCTCAACGCG 3259  
QY 1041 ThrThrThrLeuGlyProHisThrValaProProThrLeuProProAlaProAlaThrThr 1060  
DB 3260 ACCACCACTTAGGCCCCCACTGTGCTCCCAAGCTGCCCCCTGCTGCACACACC 3319  
QY 1061 LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGlu 1080  
DB 3320 CTGAGCATTACATAGAGCCCTGGGGCTCATACCGCAACACCCCTGCTGGAGAGAG 3379  
QY 1081 SerGluThrGluThrTyrThrGluValaThrGluPheGlyThrGluValaGluProGlu 1100  
DB 3380 TCCGAGACTGAGACTTACACAGAGGTGTGACAGAGTTTGGAGCCAGGTGGAGCCGAG 3439  
QY 1101 PheGluThrLysValaGluProGluPheGluThrGluGluGluProGluPheGluThrGln 1120  
DB 3440 TTGGGACCAAGGTGGAGCCGAGTTTGAGACCCAGTTGAGGCTGAGTTGAGACCCAG 3499  
QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
DB 3500 CTGGAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3559  
QY 1141 GluAlaPheProPheThrThrValaGluThrTyrThrValaAsnPheGlyAspPhe 1158  
DB 3560 CAGGCAATCCCTTCAACACAGTAGAGACTTACACAGTGAACCTTGGGGGACTTC 3613  
RESULT 4

US-10-775-920-194  
; Sequence 194, Application US/10775920  
; Publication No.: US2004017574A1  
; GENERAL INFORMATION:  
; APPLICANT: Merzen Ltd  
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES  
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED  
; TITLE OF INVENTION: IN CERTAIN CANCERS  
; FILE REFERENCE: Merzen - 0010B  
; CURRENT APPLICATION NUMBER: US/10/775, 920  
; PRIOR FILING DATE: 2004-02-10  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 385  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 194  
; LENGTH: 3935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-920-194  
Alignment Scores:  
Pred. No.: 0 Length: 3935  
Score: 6272.00 Matches: 1158  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0  
US-10-642-946-3 (1-1158) x US-10-775-920-194 (1-3935)  
QY 1 MetAlaAlaValaArgGlyAlaProIleLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20  
DB 140 ATGGCGCGCGTGGCGGGCGCGCCCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199  
QY 21 ProGlyAlaArgProGlnThrValaLeuThrAspAspGluIleGluGluPheLeuGluGly 40  
DB 200 CCGAGAGGGCGCGCGAGCGGGTGTGACCGACGAGAGATGAGAGATTCCTCGAGGGC 259  
QY 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValaGluAlaProProProPro 60  
DB 260 TTCCTGTGAGAGTGAACCTTAGCGCCCGGAGAGAGAGTGTGAGAGCCCGCGCTCC 319  
QY 61 GluProThrProArgValaArgGlyAlaGlnAlaGlyGlyLysProGlyLysArgProGly 80  
DB 320 GAGCCCAACCCCGGGTCCGAAAGCCAGGGGGGGGCAAGCCAGGAGAGGGCCAGGG 379  
QY 81 ThrAlaAlaGluValaProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp 100  
DB 380 ACGGCCGCAAGAGTGCCTCCGAAAGAACCAAGAACCAAGAACCAAGAACCAAGAAC 439  
QY 101 LysGlyProLysValaProLysGluSerLeuGluGlySerProArgProProLysGly 120  
DB 440 AAAGGCCCAAGAGTGCCTCCGAAAGAGTCTTGAAGGGGTCCCAAGGCCCGCAAGAGGG 499  
QY 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140  
DB 500 AAGGAGAACCAACCCAGGCGCAACCAAGAACCCCAAGAACCAACCAAGAACCAAG 559  
QY 141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla 160  
DB 560 AAGCCCAAGAGAGAGCACCAAGGCCACCAAGAACCCCAAGAACCAAGAACCAAGAGGC 619  
QY 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180  
DB 620 ACCAAGAACCCCGCTCAGAGAGAGAGGCCCCCATTTGCTGCTCCCTCAGAAACCTGGAG 679  
QY 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyGlyAla 200  
DB 680 TGGCCACTGCCCCCAACCCCGAGCCCTGCGCCCGAGAGACTACCCAGAGAGAGAGGGGG 739  
QY 201 ProLeuSerAsnAsnTrpGluAsnProGluGlyGluThrHisValaGluAlaGlnGluHis 220



[illegible]

QY	581	CysProThrIlethraGthrTYrSerLeuGlyLysSerzArgGlyLeuValIleTyr	600
Db	1880	TGCCCCACCAATCACCCCCACCTTACAGGCTGGGCAAGAGCTCACAGAGCCCTCAAGATCTAT	1939
QY	601	AlaMetGluIleSerAspAsnProGlyGlyNHISgluLeuGlyGluProGluPheArgTYr	620
Db	1940	GCCATGGAGATCTCAGACCAACCCTGGGGAGCATGACCTGGGGAGCCGAGTCCGCTAC	1999
QY	621	ThraIagIyIleHISglYasngIuValleuGlyAArgGluLeuLeuLeuLeuLeuMetGln	640
Db	2000	ACTCTGGGATCCATGCGCAACGAGGCTCTGGGCGGAGAGCTGTGCTGCTCATCTCAG	2059
QY	641	TyrLeuCyAsArgGluTYrArgAsngIyAsnProArgValArgSerLeuValGlnAsnThr	660
Db	2060	TACCTGTGCGAGAGTACCGGATGGGAGCCAGTGTGGACCTGTGTGCAGACACA	2119
QY	661	ArgIleHISleuValProSerLeuAsnProAspGlyTYrGluValAlaIagIleMetGly	680
Db	2120	CGCATCCACCTGTGGCTCCTCACTGAACCTGATGCTACAGGGTGGCAGCGCAGATGGCC	2179
QY	681	SerGluPheGlyAsnTPRAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCAAGATTGGGAAGCTGGCGCTGGAGCTGGAGCTAGAGAGGCTTTGACATTTGAA	2239
QY	701	AspPheProAspLeuAsnSerValLeuTrpGlyValIagIuGluArgLysTPRValProTyr	720
Db	2240	GATTTCGGGATCTCAACTCTGTGCTCTGGGGAGCTGAGGAGAGAAATGGGTCCCTTAC	2299
QY	721	ArgValProAsnAsnAsnLeuProIleProGluArgTYrLeuSerProAspAlaThrVal	740
Db	2300	CGGGTCCCAACAAATACCTGGCCATCTGCATCCGTAAAGCTACCTTTGCCAGATGCCAGGTA	2359
QY	741	SerThrGluValArgAlaIleIleAlaTrpMetGluTyAsnProPheValIleuGlyAla	760
Db	2360	TCCACGAGAGTCCGGGCCATCATTTGCTCGATGAGAAAGAACCCCTTCGTCTGGAGCA	2419
QY	761	AsnLeuAsngIyGlyGluArgLeuValSerTYrProTYrAspMetAlaArgThrProThr	780
Db	2420	AATCGAAACGGCGGCGAGCGGCTGTGTCTCAACCCCTACGATATGAGCCGCGACCCCTAAC	2479
QY	781	GlnGluGluLeuLeuAlaAlaIleMetAlaAlaIaArgGlyAsnAspGluAsnGluVal	800
Db	2480	CAGAGACAGCTGTGGCCGACCGCATGGCAGACACCAGGGGGAGATGAGAGAGAGTCTC	2539
QY	801	SerGluIagInGluTrnProAspHISAlaIlePheArgTrpLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGCGCAGAGACTCCAGACACAGCCATCTTCGGTGGCTTGGCATCTCTCTGCC	2599
QY	821	SerAlaHISleuThrLeuThrGluProTYrArgGlyGlyCyArgGlnIagInAspTYrThr	840
Db	2600	TCCGACACCTCACCTTGAACGAGCCCTACCGGAGAGCTGCCAAGCCACAGACTTACACC	2659
QY	841	GlyGlyMetGlyIleValAsnGlyAlaIaIySTPRAsnProArgTrnGlyTYrHISAsnAsp	860
Db	2660	GCGGCGATGGGCATCTGTCAACGGGGCCAAIGTGAACCCCGGACCGGGACATCAATGAC	2719
QY	861	PheSerTYrLeuNHISThrAsnCyLeuGluLeuSerPheTYrLeuGlyCyAspLysPhe	880
Db	2720	TTCAAGTTACCTGCATACCAACTGGCTGTGAGCTCTCTTCACTCTGGGCTGTGACAAGTTC	2779
QY	881	ProHISgluSerGluLeuProArgGluTrnGluAsnAsnLysGluAlaLeuLeuThrPhe	900
Db	2780	CCTACATGAGATGACTGCCCCCGAGTGGAGAAACAACAGAGGGCGCTCTCACTTC	2839
QY	901	MetGluGlnValHISArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIle	920
Db	2840	ATGGAGCAGTGGCAACCGCGCATTAAGGGGTGTGTACGCGACGACGAAGGCATCCCATY	2899
QY	921	AlaAsnAlaTrnIleSerValSerGlyIleAsnHISglYValLysTrnAlaSerGlyGly	940
Db	2900	GCCAACGGCACCATCTCTGTAGTGGCATTAATACCGCGTGAAGACACCGCCAGTGGTGT	2959



Qy 941 AsptYrTpArGtIleAenProGluYlUyRyArValThRaHlAglUglYlTyR 960  
Db 2960 GATTACTGGGAACTTGAACCGGGTGAAGTACCGGCGTGAACGCGGAGGGCTAC 3019  
Qy 961 TheProSeRaIaYsThrCyAsnVaIAspTyRAspIleGlyalATHrGlnCyAsnPh 980  
Db 3020 ACCCGAGCGGCAAGACTGGAATGTTGACTATGACATCGGGGCACTCATGTGCACTTC 3079  
Qy 981 ILeuAAlAaRgSerAsnTrpLyAsrGleArGluIleMeAlaMeAaenGlyAsnArG 1000  
Db 3080 ATCTGTGCTGCTCCCACTGGAAACGATCCGGAGATCATGCGCATGAACCGGAAACCGG 3139  
Qy 1001 ProIleProHsIleAaProSeRaRgProMeThrProGlnGlnAgaYglUglUln 1020  
Db 3140 CCTATCCCACTAGAACCCATCGCGCTTATGACCCCAACAGCAACGCTGCAACAG 3199  
Qy 1021 ArgArGleuGlnHsArGleuArGleuArGlnMeArGleuArGleuArGleuArGleu 1040  
Db 3200 CGAGCGCTACACACCGCGCTGCGGCTTCCGGCAAGATCGCGGCGCGCTCAACGCC 3259  
Qy 1041 ThrThrThrLeuGlyProHsArThraIProProThrLeuProProAlaProAlaThrThr 1060  
Db 3260 ACCACCAACCTAGGCCCCCACTGCTCCCAACGCTGCGCGCTGCGCCACCAAC 3319  
Qy 1061 LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThraIaGlyTrpGluGlu 1080  
Db 3320 CTGAGCACTACCAATAGAGCCCTGGGGCTCATACCGCAACACCGCTGCTGGAGAG 3379  
Qy 1081 SerGluThrGluThrTyRThrGluValIaThrGluPhagIYThrGluValIaGluProGlu 1100  
Db 3380 TCGAGACTAGACCTTACACAGAGTGTGACAGAGTTGGGACCGAGGTGAGCCGAG 3439  
Qy 1101 PhagIYThrLyValIaGluProGluPhagIuThrGlnLeuGluProGluPhagIuThrGln 1120  
Db 3440 TTTGGGACCAAGGTGAGCCCGAGTTGAGCCAGTTCGAGCTGAGTTCGAGACCCAG 3499  
Qy 1121 LeuGluProGluPhagIuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
Db 3500 CTGGAACTCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3559  
Qy 1141 GlnAlaPhProPherThrThraIaGluThrTyRThraIaPhPhagIYAspPh 1158  
Db 3560 CAGGCACTCCCTTCACACAGTAGAAGCTTACATGAACTTTGGGAGCTTC 3613

RESULT 5  
US-10-775-920-195  
Sequence 195, Application US/10775920  
Publication No. US20040175744A1  
GENERAL INFORMATION:  
APPLICANT: Merzen Ltd  
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES  
TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED  
FILE REFERENCE: Merzen - 00108  
CURRENT APPLICATION NUMBER: US/10/775, 920  
CURRENT FILING DATE: 2004-02-10  
PRIOR APPLICATION NUMBER: US 60/447, 900  
NUMBER OF SEQ ID NOS: 385  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 195  
LENGTH: 3935  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-775-920-195

Alignment Scores:  
Pred. No.: 0 Length: 3935  
Score: 6272.00 Matches: 1158  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 9 Gaps: 0

US-10-642-946-3 (1-1158) x US-10-775-920-195 (1-3935)  
Qy 1 MeAlaAlaValaArgGlyAlaProLeuLeuSerCySeLeuLeuAlaLeuLeuAlaLeuCyS 20  
Db 140 ATGGCGGCGGTGGCGGGGGGCGCCCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199  
Qy 21 ProGlyGlyArGProGlnThrValIleuThraAspAspGluIleGluGluPhelLeuGluGly 40  
Db 200 CTTGAGGGGGCGCGGAGAGAGGTGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259  
Qy 41 PhelLeuSerGluLeuGluProGluProArGAspGluAlaProProProProProProPro 60  
Db 260 TTCTGTGACAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 319  
Qy 61 GluProThraProArGValaArgValaArgAlaGlyGlyLyAsProGlyLyAsArProGly 80  
Db 320 GAGCCCAACCGCGGGGTCCGAAAGCCAGGCGGGGGGCAAGCCAGGAGAGAGAGAGAGAGAGAG 379  
Qy 81 ThrAlaAlaGluValaProProGluIuLySerThraAspLyGlyLyLyLyGlyLyLyLyAsp 100  
Db 380 ACCGCGCAGAAAGTGCCTCCGAGAAAGCAAAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 439  
Qy 101 LySeGlyProLySerValaProLySerLeuGluGlySerProArProProProLySerGly 120  
Db 440 AAGGCGCCCAAGGTGCCCAAGAGTCTTGAAGAGGTCCCAAGCGCCCGCCCAAGAGAGAG 499  
Qy 121 LySeGluLyAsProProLySaIaThrLyLyAsProLySeGluLyAsProProLySaIaThrLy 140  
Db 500 AAGGAGAGAGCAACCAAGGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559  
Qy 141 LyAsProLySeGluGluProProLySaIaThrLyLyAsProLySeGluLyAsProProLySaIa 160  
Db 560 AAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 619  
Qy 161 ThrLyLyAsProProSeSerGlyLyAsArGProProIleLeuAlaProSeSerGluThrLeuGlu 180  
Db 620 ACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 679  
Qy 181 TrpProLeuProProProProProProProProGlyProGluGluLeuProGlnGluGlyAla 200  
Db 680 TGGCACTGCGCCCAACCGCCCGAGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 739  
Qy 201 ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThraIaGluGlnProProProProPro 220  
Db 740 CCCCTCTCAATTAACGTGAGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799  
Qy 221 GlnProGluProGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 240  
Db 800 CAGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859  
Qy 241 ArgGluAspTyRGlYAspPhagIuTyRleArGArGlnLySeGlnProArProProProPro 260  
Db 860 AGGAGAGACTATAGAGACTTGTAGTACATTCGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 919  
Qy 261 SerArGArGArGArGProGluArGValITrpProGluProProGluGluLySaIaProAla 280  
Db 920 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979  
Qy 281 ProAlaProGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 300  
Db 980 CAGCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1039  
Qy 301 AspTyRGlYAspGlyTyRValIleProAsnTyRAspAspMeAspTyRThrPhagIYPro 320  
Db 1040 GACTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099  
Qy 321 ProProProGluGluLyAsProAspAlaGluArGlnThraAspGluGluGluGluGluGluGlu 340  
Db 1100 CTTCCGCGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159  
Qy 341 LyAsProLySeGluLyAsProSerProLySeGluGluThraAspLyTrpAlaValIaGluLy 360

Db	1160	AAACCCAAAAGAGAGACGACGCCCCCAAGAGAGACCGAACATGGTGGCGCTGGAAGAG	1219
OY	361	GIlyVAspARhIbLyGluPrOArgrLygIuGluLeuGluGluGluGluTrpThrProThr	380
Db	1220	GGCAAGAGACCAAAAGAGCCCCCGAAAGGGCGGAGGTGGAGAGAGATGGACCGCTACG	1279
OY	381	GIuLyvValLyCySPProProIleGIuMetGluSerHiSaYgIIeGIuAspAsnGlnIle	400
Db	1280	GAGAAAGTCAAAGTGTCCCCCCATTTGGATGTGATCCACCGTATTTGAGAACACAGATC	1339
OY	401	ArGaIAsSerSerMetLeuArHiagIyLeuGluYIaGlnAysGlyYArXLeuAsnMetGln	420
Db	1340	CGAGCTCTCTCATCTGTGGCCACGCGCTGGGGGACACGGCGGCGGCTCAACATGGAC	1399
OY	421	ThrgIyAlaThrGluAspAsPTrTyTrzaSPglYalatrCybaIaGluAspAspAlaAr	440
Db	1400	ACCGGTGGCACTGAGAGAGAGACTACATATATGTGTGTGTGTGTGCGGAGAGAGATGCCAG	1459
OY	441	ThrGIInTrPIleGluValAspThrArgrArGThrThrArGPhetHrglyValIleThGln	460
Db	1460	ACCCAGTGAATGAGAGTGGACACCGAGAGAGACTACCCGGTTCACAGCGGTATACCCAG	1519
OY	461	GIyArGAspSerSerIleHiSaSPAspPheValThrThrPhePheValGlyPheSerAsn	480
Db	1520	GGCAAGAGACTCCAGCATCCATGACATATTTGGACACACTTCTTGtGTGGCTTCACGCAAT	1579
OY	481	AsPserGIInThrTrpValMetTyTrzAsnGlyYrGluGluMetThPheHiagIyAsn	500
Db	1580	GACACCCAGACATGGGTGATGTACACCAACGGCTATGAGAAATGACTTTCAATGGAAAC	1639
OY	501	ValAspLyAspPTrProValIleuSerGluLeuProGluProValValAlaArGPhetIle	520
Db	1640	GTGGACAAAGACACACCGGTGCTGTAGTACCTCCAGAGCGGTGTGTGCTGCTTCATC	1699
OY	521	ArgIleTyTrProLeuThrTrpAsnGlySerLeuCyMeArGLeuGluValIleGlyCySe	540
Db	1700	CGCATCTACCCACTACCTGGAAATGGACGCTGTGCATGCGCTGTGAGAGTCTGGGTGC	1759
OY	541	SerValAlaProValTySerTyTrYrAlaGlnAsnGluValValAlaThAspAspLeu	560
Db	1760	TCTGTGGCCCCCTGTCTTACAGCTACACGACAGAAATGAGTGTGTGGCACCGAGTACCTG	1819
OY	561	AspPheArGHiBHiSerTyLyAspPheArGlnuMetLyValValAsnGluGln	580
Db	1820	GATTTCCGGACACACAGCTAACAGAGACATGCGCCAGCTCATGAAGTGTGTAAAGAGAG	1879
OY	581	CySPProThrIleThArGrThrTyTrSerIleuGlyLySPSerArGgIyLeuLyBileTy	600
Db	1880	TGCCCCACCATTCACCGCATTAACGCTTGGGCAAGACTCAACGAGGCTTCACAGATCTAT	1939
OY	601	AlaMetGluIleSerAspAsnProGlyGlnHiagIyLeuGlyGluProGluPheArGrTy	620
Db	1940	GCCATGGAGATTTCAAGACAACTCTGGGAGCATGAATCTGGGGGAGCCCGAATTCCGCTAC	1999
OY	621	ThralaGlyIleHiagIyAsnGluValIleuGlyArGluLeuLeuLeuLeuMetGln	640
Db	2000	ACTGTGGGATCATGAGCAACGAGGTGCTGGGCGAGAGACTGTCTCTGCTCATGACAG	2059
OY	641	TyTrLeuCyBaYgGluTyTrArGrAspGlyAsnProArGValAlaGSerLeuValGlnAspTh	660
Db	2060	TACCTGTGTCCGAGATTACCGCATGAGGAACCACTGTGTGCGAGCTGTGTACAGACACA	2119
OY	661	ArgIleHiBleuValProSerIleuAsnProAspGlyTyTrGluValAlaAlaGlnMetCy	680
Db	2120	CGCATTCACCTGTGTGCTCATCTGAACCTGTATGGCTACGAGGTGGACCGCAAGATGGGC	2179
OY	681	SerGIuPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCAGAGTTTGGGAACTGGGCGCTGGGACGTGTGACTGAGAGAGGCTTTGACATCTTTGAA	2239
OY	701	AspPhePProAspLeuAsnSerValLeuTrpGlyAlaGluGluArGlyTrpValProTy	720
Db	2240	GATTTCCCGGATCTCAACTGTGTGTCTGTGGGAGCTGAGAGAGGAATGGGTCCCTTAC	2299

QY	721	ArgValaProaAnbAnbAnleuProIleProGluArgTyrLeuSerProaPa1aThrVal	740
Db	2300	CGGGTCCCAACATAATCTGGCCCATCCCGAAACGGATCACTTTCGCCAGATGCCACGGTA	2359
QY	741	SerThrGluValaArgAlaIleIleAlaTyrMetGluuYrAsnProPheValaLeuGlyAla	760
Db	2360	TCCACGGAGGTCCGGGCGATCATTTGCTCGATGGAGAGAACCCCTTCGTGCTGGAGCA	2419
QY	761	AsnLeuAnGlyGlyGluArgLeuValaSerTyrProTyrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAACGGCGCGCGAGCTGTAGTATCCTACCCCTACATATGAGCCCGCCAGCTTACC	2479
QY	781	GlnGlnGluMetLeuAlaAlaIleMetAlaAlaAlaArgGlyGluAspGluAspGluVala	800
Db	2480	CAGAGGAGCTGCTGGCGGAGCCATGGACAGCACCCGGGGGGAGATGAGACAGAGTC	2539
QY	801	SerGluAlaGlnGluThrProaSpHsaAlaIlePheArgTyrPheuAlaIleSerPheAla	820
Db	2540	TCCGAGGCCACGAGAGATCTCCAGACACAGCCATCTCCGGTGGCTTGCCATCTCCTTGCC	2599
QY	821	SerAlaHsaIleuThrLeuThrGluProTyrArgGlyGlyCyseGlnAlaGlnAspTyrThr	840
Db	2600	TCCGCACACCTCACCTTGCACCGACCCCTTACCGCGAGGCTGCCAACGCCAGAGTACAC	2659
QY	841	GlyGlyMetGlyIleValaAsnGlyAlaIleTyrAsnProArgThrGlyThrIleAsnAsp	860
Db	2660	GGCGGCGATGGGCATCGTCAACGGGGCCCAAGTGGAAACCCCGGAGCCGGGACATCAATGAC	2719
QY	861	PheSerTyrLeuHsaIleThrAsnCyseGlnGluLeuSerPheTyrLeuGlyCyseAspLysPhe	880
Db	2720	TTTCAGTTACCTCGATACCACTGCTCGAGCTCTCTTCACTCGGGCTGTGACAACTTC	2779
QY	881	ProHsaGlnSerGluLeuProArgGlnTyrGlnGluAsnLysGlnAlaLeuLeuThrPhe	900
Db	2780	CCTCATGAGATGAGCTGTCCCGCGAATGGAGAACACAAAGAGGGCTGTCACTTC	2839
QY	901	MetGlnGlnValaHsaArgGlyIleLeuGlyValaValaThrAspGlnGlnGlyIleProIle	920
Db	2840	ATGAGACAGGTGCACCGCGCATTTAAGGGGTGTGTACGAGACGCAAGGCATCCCATTC	2899
QY	921	AlaAsnAlaThrIleSerValaSerGlyIleAsnHsaGlyValaLysThrAlaSerGlyGly	940
Db	2900	GCCAACGCGACATCTCTGTGAGTGGCATTTATACAGCGCTGAAGACAGCCAGTGGTGT	2959
QY	941	AspTyrTyrArgIleLeuAsnProGlyGlyIleTyrArgValaThrAlaHsaIleGluGlyTyr	960
Db	2960	GATTACTGTGGAACTTTGAACCCGGGAGTGAACCGGCTGACAGCCACCGGGAAGGGTAC	3019
QY	961	ThrProSerAlaLysThrCyseAsnValaAspTyrAspIleGlyAlaThrGlnCyseAsnPhe	980
Db	3020	ACCCCGAGCGCAAGACCTGCAAAATGTGACTATACATCGGGGCACTCACTGCAACTTC	3079
QY	981	IleLeuAlaArgSerAsnTyrPheAsyGlyIleArgGluIleMetAlaMetAsnGlyAsnArg	1000
Db	3080	ATCTTGCTGCTCAACTGGAGCGAGTCCGGAGAGTCAATGCGCATGAACGGGAACCG	3139
QY	1001	ProIleProHsaIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln	1020
Db	3140	CCATATCCCAACATAGAACCATCCGCGCTTATGACCCCCCAACAGCAGCGCTTCACACAG	3199
QY	1021	ArgArgLeuGlnHsaArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla	1040
Db	3200	CGAGCGCTACAAACACCGCTGGGCTTCGGGCAAGATGGCGGTGGCGGCTTAAAGCC	3259
QY	1041	ThrThrThrLeuGlyProHsaIleThrValaProProThrLeuProProAlaProAlaThrThr	1060
Db	3260	ACACACACCTCAGGCCCCCAACATGTCCTCCACGCTGGCCCCCTGCGCCACACACC	3319
QY	1061	LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGlnGlu	1080
Db	3320	CTGAGCACTACATAGAGCCCTTGGGGCTCATACCGGCAACACACCGCTGTGCTGGAGAG	3379



Db 1460 ACCGATGGATAGAGGTGACACACAGAGGACTACCGGGTTTCACAGCGCTACACCCAG 1519  
 QY 461 G1YhAgAspSerSer11eh1sAspAspPheVal1Thr1ThrPhePheVal1Gly1PheSerAan 480  
 Db 1520 GGGAGAGATCCACGACATGACATGACATTTTGTGACACACCTTCTCGTGGCTTCACAGCAAT 1579  
 QY 481 AAspSerG1ThTh1ThPAlmet1YTh1Thraang1YTh1Glu1GluMet1ThrPheH1sG1YaaN 500  
 Db 1580 GACAGCCAGACATGGGTGATGATACACCAAGGCTTATAGAGAAATGACCTTTCATGGAGAAC 1639  
 QY 501 ValAspLyAspTh1ThProVal1LeuSerG1uLeuProGluProVal1Aa1ArgPhe1le 520  
 Db 1640 GTGGACAAAGGACACACCGGTGATGAGTCCAGAGCGGTGGTGGCTGTTTCATC 1699  
 QY 521 Arg1Le1YTh1ThProLeuTh1ThPheang1YSer1LeuCyMetA1ArgLeuGluVal1LeuG1YCy 540  
 Db 1700 CGCATCTACCCACTCACCTGGATGAGTGCAGCTGTGTGATGCGCTGGAGGTGCTGGGGGTGC 1759  
 QY 541 SerVal1A1ProVal1Y1Ser1YTh1Y1A1G1A1nG1uVal1Val1A1Th1ThraAspA1Leu 560  
 Db 1760 TCTGTGCCCCCTTCTTACAGCTTCTACGACACAAATGAGGTGTGGCCACCGATGACCTG 1819  
 QY 561 AspPheArgH1eh1sSer1YTh1Y1AspMetA1Arg1LeuMet1YsVal1Val1AsnG1uGlu 580  
 Db 1820 GATTTCCGGACCAACAGCTACAGAGACATGCGCCAGCTCATGAAAGGTGTGAACGAGAG 1879  
 QY 581 CyAspProTh1Th1ThTh1ThTh1Th1Y1Ser1LeuG1Y1Y1Ser1SerA1Arg1Y1LeuY1s1le1Y 600  
 Db 1880 TGGCCACACATCACCGGACTTACAGCTGGGGCAAGAGCTCACAGAGCCCTCAAGATCTAT 1939  
 QY 601 AlAmetG1u1eSerAspAanProG1YG1uH1sG1u1eG1Y1G1uProG1uPheArg1Y 620  
 Db 1940 GCCATGAGATCTCAACAAACCTGGGGAGCATGAACCTGGGGAGGCCCAAGTTCCGCTAC 1999  
 QY 621 Th1A1G1Y1Th1eh1sG1Y1AsnG1uVal1LeuG1Y1ArgG1uLeuLeuLeuLeuMetG1n 640  
 Db 2000 ACTGCTGGAGATCCATGGCAACGAGGTGTGGCCGAGAGCTGTGCTGCTCATGACAG 2059  
 QY 641 ThyLeuCyA1ArgG1u1Y1Th1ArgA1Arg1Y1AanProA1Arg1Y1ArgSer1eVal1G1nAanP1Th 660  
 Db 2060 TACCTGTGCGAGAGTACCGCGATGGGAAACCAAGTGTGGCGAGCTGTGTGCGAGCAACA 2119  
 QY 661 Arg11eh1s1eVal1ProSer1eAanProA1Arg1Y1Y1G1uVal1Aa1A1nG1MetG1Y 680  
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 Db 2180 TCAGAGTTTGGGAAC1GGGGCTGGGACTGTGAGCTGAGGAGGGCTTTGACATCTTGAA 2239  
 QY 701 AspPheProAsp1eAanSerVal1Leu1Th1Th1Y1A1G1uG1uArg1Y1Ser1Th1P1Val1Pro1Y 720  
 Db 2240 GATTTCCCGATCTCAACTGTGCTGTGGAGCTGAGAGAGGAAATGGGCTCCCTAC 2299  
 QY 721 ArgVal1ProAanAanLeuPro1leProG1uArg1Y1Th1LeuSerProA1A1Th1Val 740  
 Db 2300 CGGGTCCCAAA1Th1A1CTTGCCCATCCCTGAACGCTACTTTCGCGCAATGCCAGCTH 2359  
 QY 741 Ser1Th1G1uVal1Arg1A1e1le1A1ATPMe1G1u1Y1AanProPheVal1LeuG1Y1A 760  
 Db 2360 TCACAGAGAGTCCGGGCTCATGCTGTGATGAGAGAAACCCCTTCGCTGGAGAGCA 2419  
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 Db 2420 AACTTAAGCGCGCGAGCGGTAGTATCTTACCCCTACGATATGCGCGCAGCTTACC 2479  
 QY 781 G1nG1uG1nLeu1eAan1Aa1Aa1AmetA1Aa1Aa1ArgG1Y1G1uAspG1uA1ArgG1uA1 800  
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 QY 921 A1Aa1nA1A1Th1Th1eSerVal1SerG1Y1leAanH1sG1Y1Val1Y1Th1A1A1SerG1Y1 940  
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 Db 2960 GATTTACCGCAATCTTGAACCGGGTGAATACCGCGTGAACGCCACCGAGAGGCTAC 3019  
 QY 961 Th1ProSerA1A1Y1Th1CyA1AanVal1Asp1Y1A1Arg1Y1A1Th1Th1G1nCyA1AanPhe 980  
 Db 3020 ACCCGAGGCGCAAGACCTGCATGTGATGATATACATCGGGGCCACTCAGTGAACCTTC 3079  
 QY 981 1le1eAan1A1ArgSerA1Aan1Th1Y1A1Arg1le1A1ArgG1u1le1eMetA1MetA1nG1Y1AanA1G 1000  
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 QY 1001 Pro1leProA1H1sA1AspProSerA1ArgP1rometTh1ProG1nG1uA1ArgA1ArgLeuG1nG1n 1020  
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 QY 1021 ArgA1ArgLeuG1nH1sA1Arg1eVal1Arg1eVal1Arg1eVal1Arg1eVal1Arg1eVal1A 1040  
 Db 3200 CGAGCGCTAACAAACACCGCTGGCGCTTCGGGACAGATGGCGCTCGGGGCTCAACCGCC 3259  
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 QY 1081 SerG1uTh1G1uTh1Y1Th1G1uVal1Val1Th1G1uPheG1Y1Th1G1uVal1G1uProG1u 1100  
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 QY 1141 G1nA1A1PheProPheTh1Th1Th1Val1G1uTh1Y1Th1Th1AanPheG1Y1AspPhe 1158  
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RESULT 7  
 US-10-956-157-561  
 ; Sequence 561, Application US/10956157  
 ; Publication No. US20050118625A1

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/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounsee, William
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: 031896-043000 (AM 101081)
/ CURRENT APPLICATION NUMBER: US/10/956,157
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 561
/ LENGTH: 3935
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-956-157-561

Alignment Scores:
Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-642-946-3 (1-1158) x US-10-956-157-561 (1-3935)

QY 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuAlaLeuCys 20
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QY 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGlnIleGlnGluPheLeuGlnGly 40
DB 200 CCGAGGGGGCGGCGGAGAGCGTGTGACGACGACGAGATCCAGAGATTCCTCGAGAGG 259
QY 41 PheLeuSerGluLeuGlnProGluProArgGluAspAspValGluAlaProProProPro 60
DB 260 TTCCTGTACAGAGTAGAAGCTGAGCCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
QY 61 GluProThrProArgValArgGlyAlaGlnAlaGlyGlyLeuProGlyLeuAspProGly 80
DB 320 GAGGCCACCGCGGGGTCCGAAAGGCCGAGCGGGGGGCAAGCCAGAGAGAGAGAGAGAG 379
QY 81 ThrAlaAlaGluValProProGluLeuThrLeuAspLeuGlyLeuLeuGlyLeuLeuAsp 100
DB 380 AGCGCGCGCAGAGAGTGGCTCCGAGAAAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 439
QY 101 LysGlyProLysValProLysGluSerLeuGlnGlySerProArgProProLysGly 120
DB 440 AAAGGCCCAAGGTGCGCAAGAGAGTCTTGGAGGGGTCCCGAGCGCGCCCAAGAGAGG 499
QY 121 LysGluLeuProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140
DB 500 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559
QY 141 LysProLysGluGlnProProLysAlaThrLysLysProLysGluLysProProLysAla 160
DB 560 AAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 619
QY 161 ThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGluThrLeuGln 180
DB 620 ACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 679
QY 181 TrpProLeuProProProSerProSerProGlyProGlnGluLeuProGlnGlnGlyAla 200
DB 680 TGGCCACTGCGCCACCGCCAGCGCTGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 739
QY 201 ProLeuSerAspAspThrGlnAspProGlyGluGluThrHisValGluGlnGlnGln 220
DB 740 CCCCTCTCAAAATACGCGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799
QY 221 GlnProGluProGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 800 CAGCGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859
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QY 241 ArgGluAspTyrGluAspPheGlnTyrIleArgArgGlnLysGlnProArgProProPro 260
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QY 261 SerArgArgArgArgProGluArgValTrpProGluProProGluGlnLysAlaProAla 280
DB 920 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
QY 281 ProAlaProGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 300
DB 980 CAGCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1039
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DB 1040 GACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY 321 ProProProGluLysProAspAlaGluArgGlnThrAspGluGlnLysGlnGlnGlnGln 340
DB 1100 CTTCCCGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
QY 341 LysProLysLysGluAspSerSerSerProLysGlnGlnGlnGlnGlnGlnGlnGlnGln 360
DB 1160 AAACCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
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DB 1220 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279
QY 381 GluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAspAspGlnIle 400
DB 1280 GAGAAAGTCAAGTGTCCCTCCATTTGGAGTGAAGTCAACCTGTTAGAGAGAGAGAGAGAG 1339
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 420
DB 1340 CAGAGCTCTCCATGCTGCGCCAGCGGCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
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DB 1400 ACCGGTGCACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
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DB 1460 ACCAGTGAATGAGGTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
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DB 1520 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1579
QY 481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGlnGlnGlnGlnGlnGlnGlnGln 500
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QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520
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QY 541 SerValAlaProValLysSerTyrTyrAlaGlnAsnGlnValAlaAlaThrAspAspLeu 560
DB 1760 TGTGTGGCCCGCTGTCTACAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1819
QY 561 AspPheArgHisIleSerTyrLysAspMetCysGlnLeuMetLysValValAsnGlnGln 580
DB 1820 GATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1879
QY 581 CysProThrIleThrArgThrThrTyrSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 600
DB 1880 TCCCCACACATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1939
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QY	601	11aMetGlu1IleSerAspAsnProGlu1xGlu1uHISGluLeuGlu1yGlu1uProGlu1uPheArg1Ty	620
Db	1940	GCCATGAGAGATCTCAGACACCCTGGGGAGCATGAATCGGGGAGAGCCGAGTTCGGGTAC	1999
QY	621	ThralaGly1IleHISGluYAsnGlu1uValLeuGlu1yArgGluLeuLeuLeuMecGlu1	640
Db	2000	ACTGTGGGATTCGANTGGCAAGAGGTGCTGGGGCGAGAGCTGTGGCTGCTCATGAG	2059
QY	641	TyrLeuCybArgGluTyArgAspGluYAsnProArgValArgSerLeuValGlnAspThr	660
Db	2060	TACCTGTCCCGAGAGTACCAGCGATGGGAACCAACGCTGTGCCAGCTGTGTGCAGAGACACA	2119
QY	661	ArgIleHISLeuValProSerLeuAsnProAspGluTyArg1uValAlaIleGluMecGly	680
Db	2120	CGCATTCACCTGGTCCCTCACTGACCTATGAGCTTATGAGTGTGCGAGGTGGCCAGATGTGGC	2179
QY	681	SerGluPheGluYAsnTrpAlaLeuGlu1yLeuTyTrpTrpGluGluGluYPheAspIlePheGlu	700
Db	2180	TCAGAGTTTGGGAACCTGGGCGCTGGGACTGTGAGACTGAGAGAGGCTTTGACATCTTTGAA	2239
QY	701	AspPheProAspLeuAsnSerValLeuTrpGluYalagluGluArgTyLeuTyArg1uProTy	720
Db	2240	GATTTCCGGAGTCTCAACTCTGTGCTCTGGGGAGCTGAGAGAGGAATGTGGTCCCTAC	2299
QY	721	ArgValProAsnAsnAsnLeuProIleProGluArgTyLeuSerProAspAlaSerPAl	740
Db	2300	CGGGTCCCGAACAAATPACTGTGCCATCCCTGAACGCTACTTTCCCGAGATGCCAGGTA	2359
QY	741	SerThrGluValArgAlaIleIleIleATrPMeGluYAsnProPheValLeuGluYAla	760
Db	2360	TCCACGAGAGTCCGGGCCATCTTCCCTGGATGAGGAAGAACCTTGTGTCTGGAGCA	2419
QY	761	AsnLeuAsnGluYglYgluArgLeuValSerTyProTyArgPheValArgThrProThr	780
Db	2420	AATCGAACGGCGGAGGAGGGCTGATATCTTACCCCTGACATATGGCCGACAGCCTTAC	2479
QY	781	GlnGluGlnLeuLeuAlaAlaIleMetAlaAlaIleArgGlyGluAspGluAspGluVal	800
Db	2480	CAGGAGCAGCTGCTGGCCGACACCATGGAGCAGCCGGGGGAGAGATGAGAGCAAGGCTC	2539
QY	801	SerGluValagluGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGCCCAAGAGACTTCACACCAAGCCGATCTTCGGGTGCTGCATCTCTTCCGC	2599
QY	821	SerAlaHISLeuThrLeuThrGluProTyArgGlyGlyCybGlnAlaGluAspTyThr	840
Db	2600	TCCGACACCTCACTGACCGAGCCCTTACCGGAGGCTGCCAAGCCAGACATPACACC	2659
QY	841	GlyGlyMetGlyIleValIleGluYAlaIleTyTrpAsnProArgThrGlyThrIleAsnAsp	860
Db	2660	GCGGCGCATGGGATGCTGTCACACCGGGGCAAGGTGAAACCCCGGACCGGAGCTATCATATAC	2719
QY	861	PheSerTyLeuLeuHISThrAsnCybLeuGluLeuSerPheTyLeuGluYCybAspAspPhe	880
Db	2720	TTCAgTtACCTGCAHCCAACTGCTGGAGCTCTCTTCTACTCTGGCTGTGACAAAGTTC	2779
QY	881	ProHISGluSerGluLeuProArgGluTyTrpGluAsnAsnTyGluAlaLeuLeuThrPhe	900
Db	2780	CCTCATGAGAGTGAAGCTGCCCGCGAGGTGGAGAACACAAAGAGAGCGCTGTCACTTC	2839
QY	901	MetGluGlnValHISArgGlyIleLeuGlyValValThrAspGluGlnGlyIleProIle	920
Db	2840	ATGGAGCAGGTCCACCGCGCATTTAAAGGGGTGTGTGACCGAGACCAAGGCATTCCTT	2899
QY	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHISGluValTyLeuThrAlaSerGlyGly	940
Db	2900	GCCACGCGCACCATCTCTGTGATGGCATTTATTCAGGGGTATAGACAGCCAGCTGTGGT	2959
QY	941	AspTyTyTrpArgIleLeuAsnProGlyGluTyArgValThrAlaHISAlaGluGlyTy	960
Db	2960	GATTTACTGGCAATCTTGAAACCGGGTGAATACCGGTGACAGCCCAAGCGGAGGGGCTAC	3015
QY	961	ThrProSerAlaTyThrCybAsnValAspTyArgPleGlyAlaThrGlnCybAsnPhe	980

Db	3020	ACCCGAGGCCAAGACCTCGCATGTTGACTATGACATCGGGGCCACTGCACTGCAACTTC	3079
Qy	991	leuvalaargserasnttlybargl learglu leuvalametalamenglyasnaarg	1000
Db	3080	ATCTGGCTCGCTCCAACTGGAAGCGCATCTCGGGAGATGATGCGCATGMAAGGGGAACCGG	3139
Qy	1001	ProIIeProHISIIeAspProSerArgPrometThrProGlnGlnIAspArgLeuGlnGln	1020
Db	3140	CCATATCCACACATGAAACCATGCGGCTCTATGACCCCCCAACAGCGACGCTGCAAGAG	3199
Qy	1021	ArgArgLeuGlnHISargLeuArgLeuArgalGlnMetArgLeuArgArgLeuAsnAla	1040
Db	3200	CGACCGCTACACACACCGGCTTCGGGGCACAGATGGGGCTGGCGGCTTCAACGCC	3259
Qy	1041	ThrThrThrLeuGlyProHISThrValProProThrLeuProProAlaProAlaThrThr	1060
Db	3260	ACCACCAACCTTGAGGCCCCCACTGCTCCCACTGCGCCCTGCGCCCTGCCACCAAC	3319
Qy	1061	LeuSerThrThrIleGluProTPGIleuIleProProThrThrAlaGlyTrpGluGlu	1080
Db	3320	CTGAGACACTACCAATGAGCCCTGGGGCTCTATACCGCAACACACGCTGGCTGGAGAG	3379
Qy	1081	SerGluThrGluThrTyThrGluValIleThrGluPheGlyThrGluValGluProGlu	1100
Db	3380	TCGGAGACTGAGACCTACACAGAGGTGTGACAGAGTTGGGACGAGGTGGAGCCGAG	3439
Qy	1101	PheGlyThrLyValGluProGluPheGluThrGlnLeuGluPProGluPheGluThrGln	1120
Db	3440	TTTGGGACCAAGGTGAGCCCGAGTTGAGACCCAGTTGGAGCTGGAGCTGGAGACCCAG	3499
Qy	1121	LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	1140
Db	3500	CTGGAACCCGAGTTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGATGCGACTGGC	3559
Qy	1141	GlnAlaPheProPheThrThrValGluThrTyThrValAsnPheGlyAspPhe	1158
Db	3560	CAGGCACTCCCTTCACACACGATGAGACCTACACAGTGAACCTTGGGGGACTTC	3613
RESULT 8			
US-10-947-249-162			
; Sequence 162, Application US/10947249			
; Publication No. US20050287541A1			
; GENERAL INFORMATION:			
; APPLICANT: AKIRA NAKAGAWARA			
; APPLICANT: MIKI OHIRA			
; APPLICANT: Shin ISHII			
; APPLICANT: Takeshi GOTO			
; APPLICANT: Hiroyuki KUBO			
; APPLICANT: Takahiro HIRATA			
; APPLICANT: Yasuko YOSHIDA			
; TITLE OF INVENTION: YACDA			
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma			
; FILE REFERENCE: 117007			
; CURRENT APPLICATION NUMBER: US/10/947, 249			
; CURRENT FILING DATE: 2004-09-23			
; PRIOR APPLICATION NUMBER: US 60/505,614			
; PRIOR APPLICATION NUMBER: 2003-09-25			
; NUMBER OF SEQ ID NOS: 200			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 162			
; LENGTH: 3935			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-947-249-162			
Alignment Scores:			
Pred. No.: 0			
Score: 6272.00			
Percent Similarity: 100.0%			
Beet Local Similarity: 100.0%			
Query Match: 100.0%			
Length: 3935			
Matches: 1158			
Conservative: 0			
Mismatches: 0			
Indels: 0			

[illegible]

Db	1160	AAACCCAAAAGAGAGACAGCCCCAAAGAGAGACCCGACCAAGTGGGCACTGGAGAAG	121
Qy	361	GLYVSAAPHSLVYSGLUPROARPLVSGVLGVLULEUGLUGLUGLITRPHPROTHR	380
Db	1220	GGCAAGGACCAACAAAGAGCCCCGAAAGGGCCGAGAGTTGGAGAGAGATGGAGCCCTACG	127
Qy	381	GIULYVALVYCYSPROPROILEGLYMETGUSEIRHISARGILEGLVAPSAANGINILE	400
Db	1280	GAGAAAGTCAAGTGTCCCCCATTTGGATGGAGTCAACCCGATTTGAGGACAAACCAATGC	133
Qy	401	ARGALASERSEMERLEUARGHISGLYLEUGLYALAGINARGELYARGLEUASNMETGIN	420
Db	1340	CGAGGCTCTCCATCTCCGACCGCCAGCTGGGGGACAGCCGGCCGCTCAACATGACG	139
Qy	421	THRGVLAETHRGVLAASPSPTVRYRASPGLVLAETPCYBALAGVAPSAAPLAARG	440
Db	1400	ACCGGTGCCACTGAGAGACGACTACTATATAGTGGTGGTGTGGCCGAGAGACGATCCAGG	145
Qy	441	THRGINTPLIEGLVLAASPTVRYRARGRGTTHTRARGPHEHNGLYVALILETHRGIN	460
Db	1460	ACCGAGTGGATGAGGTGGACACCAAGAGAGACTACCCGGTTCAACAGSGTGTATCAACGAG	151
Qy	461	GLYARGAPSERSEIRLEHISAPSPHEVALTHTRPHEPHEVALGLYPHESEIRSN	480
Db	1520	GGCAGAGACTCCAGCATCATGACGATTTTGTGACCACTTCTTGTTGGGCTTCAGCAAT	157
Qy	481	ASPSEIRINTHTRPVAMETTYTRHANSGLYRGLUGLUMETTHPHHISGLYASN	500
Db	1580	GACAGCCAGCATGGGTGATGTATACCAACGCGCTATGGAGAAATGACCTTTCATGGGAAAC	163
Qy	501	VALASPLVASPTHRPROVALLEUSERGLUENUPROGLUPROVALVALAARPHELLE	520
Db	1640	GTGACAGAGACACACCCGTGTAGTAGTCTCCAGAGCCGGTGTGGTCTCGTTTCATC	169
Qy	521	ARGILETYRPROLEUTHTRIPASNGLYSERLEUCYMETARGLEUGLVALLEUGLYCS	540
Db	1700	CGCATCTACCACTCACTCGGAATGGCAGCTGTGACAGCCCTGGAGAGTCTGGGGTGC	175
Qy	541	SERVALIAPROVALTYRSEITYTRYVALAGINANGLVALVALAATHRASAPLEUEN	560
Db	1760	TCTGTGGCCCTGTCTTACAGGTACTACGCAAGATGAGTGGTGGCCACGATGACCTGG	181
Qy	561	ASPPHEARGHISHISERTYFLYASPMETARGGINLEUMETLYSVALVALASNGLUGL	580
Db	1820	GATTTCCGGCACACAGTCTAAGAGACTGGGCCAGCTCATGAAGGTGTATACAGGAG	187
Qy	581	CYSPROTHRIETHNRARGTHRYSERLEUGLYYSSERSEIRARGLYLEULYSILETYR	600
Db	1880	TGCCCAACCATCACCCGCACTTACAGCTGTGGCAAGAGCTCACAGAGGCTCAAGATCTAT	193
Qy	601	ALAMETGULIESERASPMANPROGLYGLUHSGLULEUGLYGLUPROGLUPHEARGTRYR	620
Db	1940	GCCATGAGAGACTCAGACMAACCTGGGGAGATGAACTGGGGGAGCCCGAATTCGCTAC	199
Qy	621	THRLAGLYLEHISGLYASNGLYVALLEUGLYARGGLULEULEULEULEULEUMETGIN	640
Db	2000	ACTGCTGGAGTCCATGGCAACGAGGTGTGGGCCGAGAGCTGTGTGCTGTCTCATGGAG	205
Qy	641	TYRLEUCYARGGLUTYRARGSPGLYASNPORARGVALARGSERLEUVALGINASPTHR	660
Db	2060	TACCTGTGCGAGAGTACCCGAGTGGGAACCACTGTGGCGCAAGCTGTGTCAAGACACA	211
Qy	661	ARGILEHISLEUVALPROSERLEUASNPORASPGLYTRYGLUVALAIALAGINMETGLY	680
Db	2120	CGCATCCACCTGGTGGCCCTCATCAACCTGTATGGCTATACGAGGTGGGACGCCAATGGGC	217
Qy	681	SERGLUPHEGLYASNTTPALALEUGLYLEUNTTRPHNGLUGLYPHEASPIILEPHEGLU	700
Db	2180	TCAAGTTTGGAACTGGGCGCTGGAGCTGTGGACTAGAGAGGCTTTGACATCTTTGAA	223
Qy	701	ASPSPHEPROAPLEUASNPORVALLEUNTPLVALAGLUGLUGLUSTRIPVALPROTYR	720



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Db      2240 GATTTCGGGAGTCTGCTGCTGCTGGGAGGCTGAGAGAGAAATGGTCCCTAC 2299
Qy      721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
Db      2300 CGGGTCCCCCAACAAATAACTTGGCCATCCCTGAACCTACCTTCCCGCATGCCAGGTA 2359
Qy      741 SerThrGluValArgAlaIleIleAlaTPrMetGluValAsnProPheValLeuGlyAla 760
Db      2360 TCCAGGAGAGGTCCGGGACCTCATGCTGGATGAGAGAAACCCCTGCTGCTGGAGCA 2419
Qy      761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
Db      2420 AATCTGAACGGCGGAGGCGGTAGATCTTACCCCTTACGATATGGCCGCGACGCTTACC 2479
Qy      781 GlnGlnGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal 800
Db      2480 CAGGAGCAGCTGCTGGCGCGACCATGGCAGCAGCCGCGGAGAGATGAGACCAAGGTG 2539
Qy      801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTPrLeuAlaIleSerPheAla 820
Db      2540 TCCGAGGCCCCAGAGACTCCAGACCAAGCCATCTTCGGTGGCTTGGCCATCTTCCTGCC 2599
Qy      821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840
Db      2600 TCCGCACACCTCACCTTGACCGAGCCCTTACCGGAGGCTGCGCAAGCCAGACTTACACC 2659
Qy      841 GlyGlyMetGlyTyleValAsnGlyAlaValTyrTrpAsnProArgThrGlyThrIleAsnAsp 860
Db      2660 GCGCGCATGGGATCGTCAACCGGGCCAAAGTGAACCCCGGACCGGGACTATCATATGAC 2719
Qy      861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880
Db      2720 TTCACTTACCTTGATTCACACTGCTGAGCTCTCTTACTTGGGCTGTACAAAGTTTC 2779
Qy      881 ProHisGluSerGluLeuProArgGluTyrGluAsnAsnGlyAlaLeuLeuThrPhe 900
Db      2780 CCTCATGAGAGTGAAGTGTGCCCGCGAGTGGAGAAACAAGAGGCGCTGTCACTTCC 2839
Qy      901 MetGluGlnValHisArgGlyTyleGlyValValThrAspGluGlnGlyIleProIle 920
Db      2840 ATGGAGCAGGTGCACCGCGGCATTAAAGGGGTGTGTACGAGCAGAGCAAGCATCCCAT 2899
Qy      921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly 940
Db      2900 GCCAAGCCCACTCTCTGTGAGTGCATTATCAGCGGCTGAGACCAAGCCAGTGTGAT 2959
Qy      941 AspTyrTPrArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960
Db      2960 GATTACTGGGAACTTTGAACCGGGGTGAATACCGGTGACAGCCACCGGAGGGCTAC 3019
Qy      961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980
Db      3020 ACCCCGAGGCGCAAGACTGCAATGTTCATATGACATGCGGGGCCACTAGTGCACATTC 3079
Qy      981 IleLeuAlaArgSerAsnTPrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000
Db      3080 ATCTGGCTGCTGCCCACTGGAAGCCCATCCGGAATCATGCGCCATGAACGGGAACCCG 3139
Qy      1001 ProIleProHisIleAspProSerArgPromeThrProGlnGlnArgArgLeuGlnGln 1020
Db      3140 CCTATCCCAACATTAACCATGGCGCTTATGACCCCAACAGAGGAGCGCTGCAGCAG 3199
Qy      1021 ArgArgLeuGlnHisArgLeuArgLeuAlaGlnMetArgLeuArgArgLeuAla 1040
Db      3200 CGAGCGCTTACAAACAGCGCTGCGGCTTGGGCAACAATGGCTGGGCGCTCAACGCGC 3259
Qy      1041 ThrThrThrLeuGlyProHisIleThrValProProThrLeuProProAlaThrThr 1060
Db      3260 ACCACCAACCTTAGGCCCCCACTGTGCTCCCAAGCTGCGCCCTGCTGCACACACC 3319
Qy      1061 LeuSerThrThrIleGluProTPrGlyLeuIleProProThrThrAlaGlyTPrGluGln 1080
Db      3320 CTGAGCACTACCATAGAGCCCTGGGCGCTCATACCGCAACCAACCGCTGGCTGGAGGAG 3379

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Qy      1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
Db      3380 TCGAGACTGAGACTTACACAGAGTGTGTACAGATTGGGACCGAGCTGAGCCGAG 3439
Qy      1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
Db      3440 TTTGGGACCAAGGTGGAGCCGAGTGTGAGACCCAGTGTGAGGCTTGAGACCCAG 3499
Qy      1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
Db      3500 CTGGAACCCGAGTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAGATGAGCCACTG 3559
Qy      1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
Db      3560 CAGGCATTCCTTCACAAAGTGAAGACTTACACAGTGAACCTTGGGGACTTC 3613

RESULT 9
US-11-245-147-128
; Sequence 128, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAMADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; PRIOR FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: Patencin Ver. 3.2
; SEQ ID NO 128
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-128

Alignment Scores:
Pred. No.: 0
Score: 6272.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 16
Gaps: 0

US-10-642-946-3 (1-1158) x US-11-245-147-128 (1-3935)
Qy      1 MetAlaAlaValArgGlyAlaProLeuLeuSerGlyLeuLeuAlaLeuLeuAlaLeuCys 20
Db      140 ATGGGCGCGCGTGGCGGGCGCGCGCTGCTGACACTGCTCTGCGCTTGGCGCTGTGC 199
Qy      21 ProGlyGlyArgProGluThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40
Db      200 CCTGAGGGCGCGCCGCGACAGGTGTCTGACCGACGACGAGATGAGAGATTCTCTCGAGGGC 259
Qy      41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60
Db      260 TTCTGTGTGAGACTGAACCTGAGCCCGGAGGAGCAGAGTGAAGGCCCGCGCGCTTCC 319
Qy      61 GluProThrProArgValArgValAlaGlyValAlaGlyGlyLysProGlyLysArgProGly 80
Db      320 GAGCCACCCCGCGGTCCGAAAAGCCCAAGCGGGGGGCAAGCCAGGAAAGCGGCCAGGG 379

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[illegible]

Db	1460	ACCAAGTGAATAGAGGTGACACACAGAGAGACTACCCGGTTACAGAGCCCTACACCCAG	1519
OY	461	GLYTRGASPSERISLEHISASPAAPPhValThThrPhePheValGlyPheSerAsn	480
Db	1520	GGCAGAGACTCCAGCATTCATGACGATTTTGTACCACTTCTTGTGTGGACTTCAGCAANT	1579
OY	481	ASPserGlnThrTPValMetYTrThAsnGlyTYrGluGluMetThrPheHisGlyAsn	500
Db	1580	GACAGCCAGCATGGGTGATGTACCAACGCGCTGATGAGGAATATGACTTTTCATGGGAAC	1639
OY	501	ValAspIysAspThrProValIleuSerGluLeuProGluProValValAlaArgPheIle	520
Db	1640	GTCAGCAAGGACACACCCCGTGTGAGTGAAGCTCCAGAGCCGAGTGTGTCTGTTCATTC	1699
OY	521	ArgIleYrProIleuThrTPAsnGlySerIleuCyMetArgIleuGluValIleuGlyCys	540
Db	1700	CGCATCTACCACTACCTGAAATGGAGGCTGTGTGATCGCTGGAGGTGTGTGGAGTGC	1759
OY	541	SerValAlaProValTYrSerTYrTYrAlaGlnAsnGluValValAlaThrAspAspIleu	560
Db	1760	TCTGTGGGCCCTGTCTACACTCTACCTACGACAGAAATGAGTGTGTGGCCACCGATACCTG	1819
OY	561	AspPheArgHisHisSerTYrIlyAspMetArgGluLeuMetIlyValValAsnGluGlu	580
Db	1820	GATTTCCGGCACCCAGACTCAAGAGCAATCCGCCACATCATAGAGTGTGTGAAACAGAGAG	1879
OY	581	CysProThrIleThraGthrTYrYrSerIleuGlyIlySerSerArgGlyIleuIlyIleYr	600
Db	1880	TGCCCAACATCACCCGACTTACAGCTGTGGGCAAGAGCTCACAGAGGCTTCAAGATCTAT	1939
OY	601	AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGluGluProGluPheArgTYr	620
Db	1940	GCCATGAGAGTCTCAGACAACTCTGGGGAGCATGAACTGGGGAGACCCGAGTTCGGCTAC	1999
OY	621	ThraGlyIleHisGlyAsnGluValIleuGlyArgGluLeuLeuIleuIleuMetGln	640
Db	2000	ACTCTGGAGATCCATGAGCAACGAGGTGCTGGGCGCAGAGCTGTGTGCTGCTCATGACAG	2059
OY	641	TyrIleuGlyAspArgIlyTYrArgAspGlyAsnProArgValArgSerIleuValGlnAspThr	660
Db	2060	TACCTGTGCGGAGAGTACCCGAGTGGAAACCAACGCTGTGCGGAGCGCTGTGTGAGGACACA	2119
-OY	661	ArgIleHisIleuValProSerIleuAsnProAspGlyTYrGluValAlaAlaGlnMetGly	680
Db	2120	CGCATTCACCTGTGTGCCCTCACCTGAACCTGTAGTGGTACGAGTGGCAGCCAGATGGGCG	2179
OY	681	SerGluPheGlyAsnTPAlaIleuGlyIleuTPThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCAAGATTGGGAACCTGGCGGTGGAGACTGTGGACTGAGAGAGGGCTTTGACATCTTTGAA	2239
OY	701	AspPheProAspIleuAsnSerValIleuTPGlyValIleuGluIlyArgIlySerTPProYr	720
Db	2240	GATTTCCCGGATCTCAACTGTGCTCTGTGGAGCTGAGAGAGAAATGGGTCCCTCAC	2299
OY	721	ArgValProAsnAsnIleuProIleProGlyIlyIleuSerProAspAlaThrVal	740
Db	2300	CGGATCCCCAACAATACCTTGCCCATCTGTGAACGCTACCTTTCGCCAGATGCCAGGTA	2359
OY	741	SerThrigluValArgAlaIleIleAlaTPMetGluIlyAsnProPheValIleuGlyVala	760
Db	2360	TCCACGGAGGTCCGGGCGCATCTGTGCTGTGATGGAGAAAGAACCCCTGTGTGTGGAGACA	2419
OY	761	AsnIleuAsnGlyIlyGluIlyArgIleuValSerTYrProTYrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAAACGGCGGCGAGCGGCTAAGTATCTTACCCCTTCAATATGAGCCCGACGCTTACC	2479
OY	781	GlnGluGlnIleuIleuAlaAlaIleMetAlaAlaIleArgIlyGluAspGlyAspGluVala	800
Db	2480	CAGGAGAGACTGCTGGCCGACGACATGACAGACGCCCGGGGGAGAGATGAGAGCAGGCTC	2539
OY	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTPLeuAlaIleSerPheAla	820

Db 2540 TCCGAGGCCGACGAGACTCCAGACCAAGCCATCTTCCGGTGGCTTGGCATCTCTCCCTCGCC 2599  
Qy 821 SerAlaHisLeuThrIleuThrIleuProTyraArgIlyCyseGlnAlaGlnAspTyrThr 840  
Db 2600 TCCGACACACTCACCCTTGACCGAGCCCTACCCGCGAGGCTGGCCAAAGCCAGACATACAC 2659  
Qy 841 GtlyGlyMetGlyIleValAlaSerGlyAlaValSerTPAAsProArgThrGlyThrIleAsnAsp 860  
Db 2660 GCGGGGATGGGACCTGCTCAACGGGGCCAAAGTGGAACCCCGAGCGAGGACTATCAATGAC 2719  
Qy 861 PheSerTyrLeuHisIleThrAsnCyseLeuGluLeuSerPheTyrLeuGlyCyseAspLysPhe 880  
Db 2720 TTCACTTACCTGATATCAAACTGGCTGGAGCTCTCTTCTTACCTGGGCTGTGACAAATTTC 2779  
Qy 881 ProHisGluSerGluLeuProArgGluTTPGluAsnAsnLysGluAlaLeuLeuThrPhe 900  
Db 2780 CCTCAAGAGATGAGCTGCCCCGCGAGTGGAGAACAAACAAGAGCGCTGTCTCACCTTC 2839  
Qy 901 MetGluGlnValHisArgGlyIleLysGlyValIleThrAspGluGlnGlyIleProIle 920  
Db 2840 ATGGACAGAGTGCACCGCGCATTTAGGGGGTGGTACCGACGAGACAGCATCCCATTT 2899  
Qy 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrIleSerGlyGly 940  
Db 2900 GCCAAGCCACCATCTCTGAGTGGCATTAATCACGGCGTGAAACAGCCAGTGGTGGT 2959  
Qy 941 AspTyrTPAArgIleLeuAsnProGlyGlyTyrArgValIleThrAlaHisAlaGluGlyTyr 960  
Db 2960 GATTACTGGCGAATCTTGAACCGGGGTGAGTACCGGGTGACAGCCACCGGAGGGCTTAC 3019  
Qy 961 ThrProSerAlaIleThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980  
Db 3020 ACCCCGAGGCCCAAGACCTGCAATTTGACTATGATATGGGGCCACTGATGCAACTTC 3079  
Qy 981 IleLeuAlaArgSerAsnTPyIleArgGlyIleArgGlyIleMetAlaMetAsnGlyAsnArg 1000  
Db 3080 ATCTCTGCTCGCTCCAACTGGAAAGCCATCCGGGATGATCATGGCATGAACGGGAACCGG 3139  
Qy 1001 ProIleProHisIleAsnProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020  
Db 3140 CCTATCCACACATACATACCATTCGCCCTATATGACCCCAACAGAGAGCGCTCGACGAG 3199  
Qy 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040  
Db 3200 CGAGCGCTACACACCGGCTCGCGCTTCGGGCAACATGGCTGGGGCGCTCAACCGCC 3259  
Qy 1041 ThrThrThrLeuGlyProHisIleThrValIleProProThrLeuProProAlaProAlaThrThr 1060  
Db 3260 ACCACCACTAGGCCCCCACTGTGCTCCCAAGCTGGCCCTGCCCTGCCACACAC 3319  
Qy 1061 LeuSerThrThrIleGluProTTPGlyLeuIleProProThrThrAlaGlyTTPGlyGlu 1080  
Db 3320 CTGAGACATACATTAAGCCCTGGGGCTCTATACCCCAACCAACCCCTGGCTGGAGAG 3379  
Qy 1081 SerGluThrGluThrTyrThrGluValIleThrGluPheGlyThrGluValIleGluProGlu 1100  
Db 3380 TCGGACATGAGACCTTACACAGAGTGTGTACAGAGTTTGGGACCGAGGTGGAGCCCGAG 3439  
Qy 1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120  
Db 3440 TTGGGACCAAGGTGAGCCCGAGTTTGAGACCCAGTTGGAGCCTGAGTTCCGAGACCCAG 3499  
Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
Db 3500 CTGGAAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3559  
Qy 1141 GlnAlaPheProPheThrThrValIleGluThrTyrThrValAsnPheGlyAspPhe 1158  
Db 3560 CAGGCACTCCCTTCAACAAGTACAGACCTTACACAGTGAACCTTTGGGAGCTTC 3613

RESULT 10  
US-10-956-157-5213  
; Sequence 5213, Application US/10956157

; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: NOCILETIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; NUMBER OF SEQ ID NOS: 319605  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5213  
; LENGTH: 3914  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-5213  
Alignment Scores:  
Pred. No.: 0 Length: 3914  
Score: 6264.00 Matches: 1156  
Percent Similarity: 100.0% Conservative: 2  
Best Local Similarity: 99.88 Mismatches: 0  
Query Match: 99.9% Indels: 0  
DB: 10 Gaps: 0  
US-10-642-946-3 (1-1158) x US-10-956-157-5213 (1-3914)  
Qy 1 MetAlaAlaValAlaArgGlyAlaAlaProLeuLeuSerCyseLeuLeuAlaLeuLeuAlaLeuCys 20  
Db 140 ATGGGGGCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 199  
Qy 21 ProGlyGlyArgProGluThrValIleuThrAspAspGluIleGluGluPheLeuGluGly 40  
Db 200 CTTGAGAGGGGCGCCGACAGCGTCTGTACCGACGACGAGTGTGAGAGTCTTCAGAGGGC 259  
Qy 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProPro 60  
Db 260 TTCTGTAGAGACTGAAGCTGAGCCCGGGAGACGACGTGAGAGGCCCGCGGCTCC 319  
Qy 61 GluProThrProArgValAlaGlyValAlaGlnAlaGlyLysPheProGlyLysArgProGly 80  
Db 320 GAGCCACCGCCCGGGGTCCGAAAGCCAGCGGGGGGCAAGCCAGAGAGAGCGCCAGGG 379  
Qy 81 ThrAlaAlaGluValProProGluTyrThrLysAspLysGlyLysLysGlyLysLysAsp 100  
Db 380 ACCGCCGCAAGTCTCTCCGAAAGACCAAGACCAAGGAGAAAGCAAGGAAAGG 439  
Qy 101 LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly 120  
Db 440 AAAGGCCCAAGGTCCCAAGAGTCTTGGAGGGGTCCCAAGGCCGCCCAAGAGGGGG 499  
Qy 121 LysGluLysProProLysAlaThrLysLysPheLysGluLysPheProProLysAlaThrLys 140  
Db 500 AAGGAGAGCCACCAAGGCCCAAGAGGCCCAAGAGAACCACTAAGGCCACACAG 559  
Qy 141 LysProLysGluGluProProLysAlaThrLysLysPheLysGluLysPheProProLysAla 160  
Db 560 AAGCCCAAGAGAAAGCAAGCCCAAGGCCCAAGAGGCCCAAGAGAGAACCAAGGCC 619  
Qy 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180  
Db 620 ACCAAGAGCCCGCGTCAAGGAGAGAGGCCCAATCTGTGCTCCCTCAAAAACCCCTGGAG 679  
Qy 181 TTPProLeuProProProProSerProGlyPProGluGluLeuProGlnGluGlyAla 200  
Db 680 TGGCCATGCCCCCAGCCCTTGGCCCCCGAGAGACTTACCCCGAGAGAGAGAGAGAGAG 739  
Qy 201 ProLeuSerAsnAsnTPGluAsnProGlyGluGluThrHisValGluAlaGlnGlnHis 220  
Db 740 CCCCTCTCAATTAATCTGGAGAAATCCAGAGAGAGAACCAATGTGAGGCAAGGAGGAC 799  
Qy 221 GlnProGluProGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 240

Dh 800 CAGCTGAGCGGAGGAGAGACCGAGAACCCACACTGAGCTACATGACCAATGAC

Qy 241 ArgGluAspTyrGluAspPheGluTyrTlleArgArgGlnLysGlnProAspProPro 260

Dh 860 AGGAGAGACTATGAGGACTTGTAGTACATTCGGCGCAGAGCAAGCAACCGAGCCACCCCA 919

Qy 261 SerArgArgArgArgProGluArgValTTPProGluProProGluGluValAlaProAla 280

Dh 920 AGCAGAGAGAGAGAGCCCGAGCGGGCTTGGCCAGAGCCCTCTGAGAGAGAGCCCGGGC 979

Qy 281 ProAlaProGluGluArgTlleGluProProValLysProLeuLeuProProLeuProPro 300

Dh 980 CCAAGCCCCGAGAGAGATTGAGCTCTGTAGAGCTCTGCTGCCCGCGCTGCCCT 1039

Qy 301 AspTyrGluAspGlyTyrValTlleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320

Dh 1040 GACTATGGTATGGTTACGTGATCCCACTACATGACATGAGCTATTCCTTTGGGCT 1099

Qy 321 ProProProGluLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLys 340

Dh 1100 CTTCCGCCCAAGAGCCCGATGCTGAGCGCCAGACAGACGAGAGAGAGAGAGCTGAG 1159

Qy 341 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTTPAlaValGluLys 360

Dh 1160 AAACCCAAAAGAGAGAGACAGACGCCCAAGAGAGAGACCGACAGTGGCAGTGGAGAG 1219

Qy 361 GlyLysAspHisLysGluProArgLysGlyGluGluLysGluGluGluTTPThrProThr 380

Dh 1220 GGGAGAGACCAAAAGAGCCCGCAAGGGAGAGAGTGGAGAGAGTGGAGCGCTACG 1279

Qy 381 GluLysValLysCysProProTlleGlyMetGluSerHisArgTlleGluAspAsnGlnTlle 400

Dh 1280 GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTACACACCGTATGGAGCAACCAAGATC 1339

Qy 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyValGlnArgGlyArgLeuAsnMetGln 420

Dh 1340 CGAGCCTCTCATGCTGCGGCCACAGCGCTGGGGGCAAGCGCGCGCTCAACATGAC 1399

Qy 421 ThrGlyValAlaThrGluAspAspTyrTyrAspGlyAlaTTPCysAlaGluAspAspAlaArg 440

Dh 1400 ACCGGTCCACTAGAGAGAGCTACTATGATGTCGTGTGTGCGCGAGAGAGATGACAG 1459

Qy 441 ThrGluTTPTlleGluValAspThrArgArgThrThrArgPheThrGlyValTlleThrGln 460

Dh 1460 ACCAGTGGATAGAGGTGAGACCAAGAGAGACTACCGGTTCAAGGCGATCATCACAG 1519

Qy 461 GlyArgAspSerSerTlleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480

Dh 1520 GGGAGAGACTCCAGCATCCATGAGATTTTGTGACCACTTCTTCGTGGGCTTCAGCAAT 1579

Qy 481 AspSerGlnThrTTPValMetTyrThrAsnGlyTyrGluLysMetThrPheHisGlyAsn 500

Dh 1580 GACAGAGACAGATGGGTGATGATCACCAAGCGCTATAGAGAAATGACCTTTCATGGGAC 1639

Qy 501 ValAspLysAspThrProValLysSerGluLeuProGluProValValAlaAspPheTlle 520

Dh 1640 GTGGACAGAGACACACCGGTGTGAGTACCTCCCAAGCGGTGTGTGTCTTCATC 1699

Qy 521 ArgTlleTyrProLeuThrTTPAsnGlySerLeuCysMetArgLeuGluValLysGlyCys 540

Dh 1700 CGCATCTACCATCTACCTGGATGGAGCTGTGATGCTGCTGAGAGTGTGGGTGC 1759

Qy 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaAlaThrAspAspLeu 560

Dh 1760 TCTGTGGCCCTCTCTACACTACCTACGACAGATAGAGTGTGTGGCCACGATGACCTG 1819

Qy 561 AspPheArgHisHisSerTyrLysAspMetArgGlnLysMetLysValValAlaAsnGluGlu 580

Dh 1820 GATTTCCGGGACCAAGACTACAGAGACATGCGCAGCTCATGAAAGGTGTGAACGAGAG 1879

Qy 581 CysProThrTlleThrArgThrTyrTyrSerLeuGlyLysSerSerArgGlyLeuLysTlleTyr 600

Dh 1880 TGGCCGACCATCACCGGCACTTACAGCTGTGGGCAAGAGCTCAAGAGGCTCCAGATCTTAT 1939

Qy 601 AlaMetGluTlleSerAspAsnProGluGluHisGluLeuGlyGluProGluPheArgTyr 620

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Dh 2060 TACCTGTGCCGAGAGATACCGCGATGGGAAACCAAGTGTGGACCGCTGGGTGAGGACACA 2119

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Qy 681 SerGluPheGlyAsnTTPAlaLeuGlyLeuTTPThrGluGluGlyPheAspTllePheGlu 700

Dh 2180 TCAGAGTTTGGAACTGGGCGCTGGGACTGTGACCTGAGAGGGCTTTGACATCTTTGAA 2239

Qy 701 AspPheProAspLeuAsnSerValLeuTTPGlyAlaGluGluArgLysTTPValProTyr 720

Dh 2240 GATTTCCGGATCTCAACTGTGTCTGGGAGCTGAGAGAGAGAAATGGCTCCCTTAC 2299

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Dh 2360 TCCAGAGAGTCCGGGCTCATCTGCTGGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2419

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Dh 2420 AATCTGAGAGCGGCGAGCGGCTGATATCTTACCTTACGATATGGCCCGCAGCGCTAC 2479

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Dh 2480 CAGAGACAGTGTGTGCGCGAGCATGAGCAGAGCGCGGGGAGAGATGAGAGCGAGTCC 2539

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Qy 821 SerAlaHisLeuThrLeuThrArgLysProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840

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Dh 2660 GCGGCGATGGGCTCTCTCAACGCGGCAAGTGGAAACCCCGGACCGGACTATCAATGAC 2719

Qy 861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880

Dh 2720 TTGATTAACCTGATACCAATGCTGAGCTCTCTTCACTGAGGCTGTGACAAAGTTC 2779

Qy 881 ProHisGluSerGluLeuProArgGluTTPGluAsnAsnLysGluAlaLeuLeuThrPhe 900

Dh 2780 CTTCAAGAGATGAGTGTGCGCGCGAGTGGAGAGACAAAGAGGCGCTGCTCACTTCC 2839

Qy 901 MetGluGlnValHisArgGlyTlleLysGlyValValThrAspGluGlnGlyTlleProTlle 920

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Qy 921 AlaAsnAlaThrTlleSerValSerGlyTlleAsnHisGlyValLysThrAlaSerGlyGly 940

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Dh 2960 GATTACTGGGAACTTTGAACCGGGTGTGATCCGGTGAACGCCAGCGGAGGGCTTAC 3019

QY	1	Meta	alaValaValaArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys	20
QY	961	ThrProSerAlaValaValaThyCysAsnValaAspTyrTrpAlaIleGlyAlaThrGlnCysAsn	Phe	980
Db	3020	ACCCGAGCGCCCAAGACCTGCAATGTTGACTATGACATCGGGGCGCACTGACGAACTTC		3079
QY	981	IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg		1000
Db	3080	ATCTGGGCTCGCTCCACTGGAGGGCATCCGGAGAGATCATGGCCATGAAACGGAAACGG		3139
QY	1001	ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln		1020
Db	3140	CCTATCCCAACATAGAACCCATCGCGCCCTATGACCCCAAGCGACGCTCGACAG		3199
QY	1021	ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetAlaGluArgArgLeuAsnAla		1040
Db	3200	CGACCGCTTACAAACCGCGCTCGCGCTCGGGGACGATGCGCGCGCGCTCGCAACGCC		3259
QY	1041	ThrThrThrLeuGlnGlyProHisThrValaProProThrLeuProProAlaProAlaThrThr		1060
Db	3260	ACCACACCCCTTAGGCCCCCACTGCTGCTCCACAGCTGCCCCCTGCCCCCAACCC		3319
QY	1061	LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGln		1080
Db	3320	CTGAGCACTACCATATGAGCCCTCGGGGCTCTATACCGCAACACCGCGCTGGGAGGAG		3379
QY	1081	SerGluThrArgLysThrTyrThrGluValaValaThrGluPheGlyThrGluValaGluProGlu		1100
Db	3380	TCGGAGACTGAGACCTTACACAGAGGTGGTGAACAGATTGGGAGCCGAGGTGAGCCCGAG		3439
QY	1101	PheGlyThrLysValaGluProGluPheGluThrGlnLeuGluGluProGluPheGluThrGln		1120
Db	3440	TTTGGGACCAAGGTGAGCCGAGTTTGAACCCAGTTGAGACCTGAGACCTGATTTGAGACCGAG		3499
QY	1121	LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu		1140
Db	3500	CTGGAACCCGAGTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACATGCGC		3559
QY	1141	GlnAlaPheProPheThrThrValaGluThrTyrThrValaAsnPheGlyAspPhe		1158
Db	3560	CAGCATTCCTCCCTTCAACAGTAGAGACTTACACAGTGAACCTTTGGGAGACTTC		3613
RESULT 11				
US-10-775-920-198				
; Sequence 198, Application US/10775920				
; Publication No. US20040175744A1				
; GENERAL INFORMATION:				
; APPLICANT: Merzen Ltd				
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES				
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED				
; FILE REFERENCE: Merzen - 0010B				
; CURRENT APPLICATION NUMBER: US/10/775,920				
; CURRENT FILING DATE: 2004-02-10				
; PRIOR APPLICATION NUMBER: US 60/447,900				
; PRIOR FILING DATE: 2003-02-13				
; NUMBER OF SEQ ID NOS: 385				
; SOFTWARE: PatentIn version 3.2				
; SEQ ID NO 198				
; LENGTH: 4125				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-775-920-198				
Alignment Scores:				
Pred. No.: 0 Length: 4125				
Score: 6264.00 Matches: 1156				
Percent Similarity: 100.0% Conservative: 2				
Best Local Similarity: 99.8% Mismatches: 0				
Query Match: 99.9% Indels: 0				
DB: 9 Gaps: 0				
US-10-642-946-3 (1-1158) x US-10-775-920-198 (1-4125)				

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Db	366	CCTGAGGGGCGCCGCGACAGCGTGTCTGACCGACGACGAGATGAGAGATGTTCTCCGAGGGG	425
QY	41	PheIeuSerGluLeuGluProGluProAArgIuAaAapAvalGluuAaProProPro	60
Db	426	TTCTGTCTAGAGCTAGAACTGAGGCCGGGGAGGACGAGTGGAGGCCCCCGGCTGCC	485
QY	61	GluProThraProAArgValaArgLysaIaGluIaGlyLysProGlyLysAArgProGly	80
Db	486	GAGCCACCCCGCGGTCTCGAAAGCCAGGCGGGGGGCGAACCCAGGGAGAGCGGCCAGGG	545
QY	81	ThraIaIaGluValaProProGluuLysThraLysAapLysGlyLysaLysGlyLysLysAap	100
Db	546	ACGGCGCGAGAAAGTGCTCTCGGAAAAAGACCAAAAGCAAAAGGAGAAAGGCAAAAGAAC	605
QY	101	LysGlyProLysValaProLysGluSerLeuGluGlySerProAArgProProLysLysGly	120
Db	606	AAAGGCCCCCAAGTGCCCAAGAGAGTCTTTGGAGGGGTCCCCCGAGGCGGCCCAAGAGGGG	665
QY	121	LysGluLysProProLysValaThraLysLysProLysGluLysProProLysValaThraLys	140
Db	666	AAGGAGAAAGCCACCCAAAGGCCAACAGAAAGCCCAAGAGAAACCACTTAAGGCCACCAAG	725
QY	141	LysProLysGluGluProProLysValaThraLysLysProLysGluLysAProProLysVala	160
Db	726	AAAGCCAAAGAGAAAGCCACCCAGGCCACCAAGAAAGCCCAAGAGAGCCCAAGAGAGCC	785
QY	161	ThraLysLysProProSerGlyLysAArgProProIleLysAaProSerGluThraLeuGlu	180
Db	786	ACCAAGAAAGCCCCGTCAAGGAGAGGGCCCCCATCTTGCGTCCCTCACAAGAACCTCGAG	845
QY	181	ThraProLysProProProProSerProGluProGluGluLysProGluGluGlyVala	200
Db	846	TGGCCACTGCCCCCAGCCCCCAGCCTTGCGCCCGAGAGACTACCCAGAGAGGGAGGGGG	905
QY	201	ProLysSerAaAaSerTrpGluAaAaProGlyGluGluThraIaGluIaGluIuHIs	220
Db	906	CCCCCTCAAAATTAAGTGGCAGAAATCCAGAGAGAGAGACCAATGTGGAGGACGGGAGCAC	965
QY	221	GluProGluProGluGluGluThraGluGluProThraLysAapLysAaAaAaGlu	240
Db	966	CAGCCTGAGCCGAGAGAGAGACCGAGCAACCACTGAGACTACATGACCAAGATCGAG	1020
QY	241	ArgGluAapLysArgLysAaAaPheGluuLysIleAaAaGluLysGluProAArgProProPro	260
Db	1026	AGGGAGGACTATGAGAGACTTTGATGACATTCGGCGCCAGAAACCAACCCAGGCCACCCCA	1080
QY	261	SerAArgAArgAArgProGluuAArgValaTrpProGluProProGluGluLysaIaProAa	280
Db	1086	AGCAAGAAAGAGAGGCCCGGAGCGGCTTGCGCCAGAGCCCCCTGAGAGAAAGCCCCGGCC	1140
QY	281	ProAaIaProGluGluuArgIleGluProProValaLysProLeuLysProProLysProPro	300
Db	1146	CCAGCCCCGAGAGAGAGATTTGAGCCTCTGTGAAGACCTCTGCTGCCCCCGCTGCCCT	1200
QY	301	AapLysArgLysAapGlyLysValaIleProAaSerTrpAaAaPheMetAapLysLysTrpPheGlyPro	320
Db	1206	GACTATGTGTATGTGTACGTATCCCAACTACGATGACATGACATTAATTAATTTGGGCTT	1260
QY	321	ProProProGluLysProAaAaIaGluuArgGluThraAaAaGluGluLysGluLysLys	340
Db	1266	CCTCGCCCGCCAGAGACCCGATCTAGCGCCCAAGACGAGCAAGAGAGAGAGAGAGCTGMA	1320
QY	341	LysProLysLysGluAaAaAaSerSerProLysGluGluThraAaAaLysTrpAaIaGluLys	360
Db	1326	AAACCCAAAAGAGAGAGACGAGCCCAAGAGAGAGAGACCGAACAGTGGGCAAGTGGAGAG	1380
QY	361	GlyLysAaAaPheLysGluProAArgLysGlyGluGluLeuGluGluGluLysTrpThraProThra	380

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Db 1446 GAGAAATCAAGTGTCCCCCATTTGGATGAGTCAACCCGATTTGAGGACCAACAGATC 1505  
Qy 401 ARGALASERSEMERLEUARGHLEGLYLEUGLYVALAGINARVGLYALASPANMERGLIN 420  
Db 1506 GMACTCTCTTCATGCTGCGCACGGCTGGGGGACAGCGGGCCGCTCAACATTCAG 1565  
Qy 421 THRGLVALATHRGUASPAPTYRTYRASPGLYALATRPCYALAGLUASPAPALARG 440  
Db 1566 ACCGGTCCACTGAGAGAGACTATATGATGTGTGCTGTGTGTGCGAGAGAGAGCCAGG 1625  
Qy 441 THRGINTRPILIEGLUVALASPETHARGARGTHRTHRARGPHETHRGLYVALIIETHRGLN 460  
Db 1626 ACCCAGTGGATGAGTGGGACACACAGAGAGACTACCCGGTTCCAGAGCGCATCACCCAG 1685  
Qy 461 GLYARGHAPSERSEIRIIEHAPAPAPHEVALIETHRPHRPHRPHRPHRPHRPHRPHRPHR 480  
Db 1686 GGGAGAGACTTCAGCATTCAGATTCAGATTTGTGACCACTTCTTCTGTGGGCTTCAGCAAT 1745  
Qy 481 ASPSERGINTHRTYRVALMETTYRTHRASNGLYTYRGLUGIUMECTHRPHEHISGLYASN 500  
Db 1746 GACAGCCAGCATGGGTGATGTATACCAACGGCTATGAGAAATGACCTTTCAATGGGAC 1805  
Qy 501 VALASPLYASAPTHRPROVALLEUSERGLULEUPROGLUPROVALVALAIAARGPHEIIE 520  
Db 1806 GTGACACAGAGACACACCGTGTGATGAGCTCCCAAGCCGGTGGTGGCTCGTTTCATC 1865  
Qy 521 ARGIIIEYRPROLEUHTRTPAENGLYSERLEUCYMERARGLEUGIUVALLLEUGLYCYG 540  
Db 1866 GCGATCTACCACTCACCTTGGAATGSCAGCTGTGACGCTGCGGAGAGTGTGGGGTGC 1925  
Qy 541 SERVALAJAPROVALTYRSEITYTYRVALAGINASNGLUVALAJATHRASPAPLEU 560  
Db 1926 TCTGTGGCCCTGTCTACAGCTACTACGCAACAGATAGGTGTGGCCACGATGACTG 1985  
Qy 561 ASPPHEARGHIEHISSEITYTYLYASPMETARGGLULEUMELYVALVALASNGLUGLU 580  
Db 1986 GATTTCCGGCACCACTCAACAGAGCATGCGCACGCTCATGAAGGTGTGAACAGAGAG 2045  
Qy 581 CYSPROTHRIIEHARGHTYRYSERLEUGLYYSESERSEARGGLYLEULYSIIETRY 600  
Db 2046 TGGCCCAACATCACCCGACCTTACAGCTCGGGCAAGAGCTCACAGAGCTCAAGATTCAT 2105  
Qy 601 ALAMERCULIIESEERAPANPROGLYGLUHIIEGLULEUGLYGLUPROGLUPHEARGTYR 620  
Db 2106 GCCATGGAGATCTCAGCAACCTCGGGGAGCATGMACTGGGGAGAGCCGAGTTCCGCTAC 2165  
Qy 621 THRVALAGLYIIEHISGLYASNGIUVALLLEUGLYARGGLULEULEULEULEUMERGILN 640  
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Qy 641 TYRLEUCYHARGGLUYTYRARGAARGGLYASNPPOARGVALARGSEERLEUVALGINASPETHR 660  
Db 2226 TACCTGTGGGAGAGATCCCGAGATGGAGCCACGTTGTGCGACCTGTGTGCGAGACACA 2285  
Qy 661 ARGIIIEHISLEUVALPROSEIRLEUASNPROASPGLYTYRGLUVALAJAIAAGINMETGLY 680  
Db 2286 CGCATCCACTGTGGCCCTCACTGMAACCTGATGGCTACAGAGTGGGAGCGCAGATGGGC 2345  
Qy 681 SERGLUPHEGLYASNPTRPALEUGLYLEUSTRPETHRGLUGIUGLYPHEAPPIIEPHEGLU 700  
Db 2346 TCAGAGTTTGGGAACCTGGGCGCTGGGACTGTGAGCTAGAGAGGGCTTTGACATCTTGAA 2405  
Qy 701 ASPPHEPROASPHEUASNPVALLEUTRPGIYVALAGIUGLUARGLYSTTRPVALPROTYR 720  
Db 2406 GATTTCCCGGATCTCAACTGTGTCTGTGGGAGCTGAGGAGAGAAATGGTCCCTTAC 2465  
Qy 721 ARGVALPROASNANLEUPROILEPROGLUARGTYRLEUSERPROEAPALATHRVAL 740  
Db 2466 CCGGTCCCAACATACTTGCCATCTGCGAACGCTACTTTGCGCAGATGGCAGGTA 2525

Qy 741 SETTHRGLUVALARGALAIIEIIEAATTPMERGLULYASNPPOHEVALLEUGLYALA 760  
Db 2526 TCACGAGAGGTCCGGGCGATCATTTGCTGATGAGAGAAACCCCTTCGTGTGGAGCA 2585  
Qy 761 ASNLEUASNGLYGLYGLUARGLEUVALSERTYRPROTYRASPHEVALAARGTHRPROTHR 780  
Db 2586 AATCTGAACGGCGGCGAGCCGCTATGATCTTACCCCTTACGATATGGCCGACGACCTTACC 2645  
Qy 781 GINGIUGIINLEUVALAJAIAIAMEVALAJAIAIARGGLYGLUASPGLUASPGLUVAL 800  
Db 2646 CAGAGAGAGCTGTGGCGGAGCCATGSCAGAGCAGCCCGGGGGAGGATGAGAGAGAGTCC 2705  
Qy 801 SERGLUVALAGIUGLUTHRPROASPHIEAALIEPHEARGTRPLEUVALIIESERPHEALA 820  
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Db 3006 ATGAGACAGGTGACCGCGGCATTTAAGGGGTGTGTACGAGACGACAGCAATCCCAT 3065  
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Qy 981 IIELEUVALARGSERASNPTRPLYSARGIIIEARGIUIIEWETALAMECANGLYASNARG 1000  
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Qy 1001 PROILEPROHISIIIEASNPPOSERARGPROMETHRPROGLINARGARGLEUGINGIN 1020  
Db 3306 CTTATCCACACATPAACCATTCGCGCCCTATGACCCCAACAGGAGAGCTGCAAGCAG 3365  
Qy 1021 ARGARGLEUGIINHISARGLEUARGLEUARGALAGIIMECARGLEUARGARGLEUASNALA 1040  
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Qy 1081 SERGLUTHRGLUTHRTHRGLUVALIETHRGUPHEGLYTHRGLUVALGIUPROGLU 1100  
Db 3546 TCAGAGACTGAGACTTACACAGAGGTGTGACAGATTTGGAGCCGAGGTGAGCCCGAG 3605



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Qy 561 AspPheArg11eHisSerTyrTyrAspMetArg15eLeuMetCysVal1Val1AsnGluGlu 580
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Db 1859 TGGCCCACTCAACCCGCACTTACAGCTGGGCAAGAGCTCACAGAGGCTCAAGATCTAT 1918
Qy 601 AlaMetGlu11eSerAspAsnProGlyGluHisGluLeuGlyGluProGlyUrpPheArgTyr 620
Db 1919 GCCATGAGATCTCAGACAACTCGGGGAGCATGAACTGGGGAGCCCGAGTTCCGCTAC 1978
Qy 621 ThrAlaGly11eHisGlyAsnGluVal1LeuGlyArgGlyUrpLeuLeuLeuMetGln 640
Db 1979 ACTGCTGGGATCCATGGCAACGAGTGTGGCCGAGAGCTTTGCTGCTGCTCATGACAG 2038
Qy 641 TyrLeuCyseArg15eTyrArgAspGlyAsnProArgVal1ArgSerLeuVal1GlnAspThr 660
Db 2039 TACCTGTGGCGAGAGTACCCGATGGGACCCAGTGTGGCGAGCTGGTGGAGGACACA 2098
Qy 661 Arg11eHisLeuVal1ProSerLeuAsnProAspGlyTyrGluVal1Aa1AaGlnMetGly 680
Db 2099 CGCATCACTGTGTGCTCTACAGAACCTGATGGCTACAGAGTGGGAGCGGAGATGGGC 2158
Qy 681 SerGluPheGlyAsnTyrAlaLeuGlyLeuTyrThrGluGluGlyPheAsp11ePheGlu 700
Db 2159 TCGAGATTGGGAATGGGCGCTGGAGCTGGAGCTGGAGAGGAGCTTTGACATCTTTGAA 2218
Qy 701 AspPheProAspLeuAsnSerVal1LeuTyrGlyAlaGluGluVal1ArgTyrProTyr 720
Db 2219 GATTTCCGGATCTCAACTGTGTGCTGGGAGCTGAGAGAGAAATGGTCCCTAC 2278
Qy 721 ArgVal1ProAsnAsnAsnLeuPro11eProGlyUrpTyrLeuSerProAspAlaThrVal 740
Db 2279 CGGGTCCCCAACAATTAATTTGCCATCCCTGAACGCTTTCGCCAGATGGCCAGCGTA 2338
Qy 741 SerThrGluVal1ArgAla1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e 760
Db 2339 TCCACGGAAGGTCCGGGCCATCATTTGCTGATGAGAGAGAACCCCTTCGTGCTGGAGCA 2398
Qy 761 AsnLeuAsnGlyGlyGlyUrpArgLeuVal1SerTyrProTyrAspMetAlaArgThrProThr 780
Db 2399 AATCTGAACGGCGGCGAGCGGCTAGTATCTTACCCCTACGATATGGCCGCGACCTTAC 2458
Qy 781 GlnGluGluLeuLeuAla1Aa1AaMetAla1Aa1AaArgGlyGlyUrpGluAspGlyUrpAl 800
Db 2459 CAGGAGCACTGCTGGCCGAGGACATGGCAGAGCCCGGGGGAGAGATGAGAGCGAGTCC 2518
Qy 801 SerGluAlaGlnGluThrProAspH1Aa11ePheArgTyrPheAla1e1e1e1e1e1e1e1e 820
Db 2519 TCCGAGGCCCAAGAGACTCCAGACCAAGCCATCTTCGGGTGGCTTGGCATCTCTTCGCC 2578
Qy 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840
Db 2579 TCCGACACCTCACTTGAACCGAGCCCTTACCGCGAGAGGCTGCCAAGCCCAAGCATACAC 2638
Qy 841 GlyGlyUrpGlyUrpVal1eVal1eAsnGlyAlaVal1eTyrAsnProArgThrGlyThr11eAsnAsp 860
Db 2639 GGGGGGATGGGATCTGTCAGACGGGGGCCAAGTGAACCCCGGACCGGATATCAATGAC 2698
Qy 861 PheSerTyrLeuHisThrAsnCyseLeuGluLeuSerPheTyrTyrGlyCysAspLysPhe 880
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Db 2699 TTGAGTTACTGATACCAACTGCTGAGACTCTCTTACTCGGGGCTGTACAAATTC 2758
Qy 881 ProHisGluSerGluLeuProArgGluTyrGluAsnAsnLysGluAlaLeuLeuThrPhe 900
Db 2759 CCTCATGAGATGAGCTGGCCCCGAGTGGGAGAAACAACAGAGAGCGCTGCTCACCTTC 2818
Qy 901 MetGluGluVal1HisArgGly11eLysGlyVal1Val1ThrAspGluGlnGly11ePro11e 920
Db 2819 ATGAGCAGAGGTGACCGCGCATTAAGGGGTGTGTACGAGCAGCAGAGCATCCCATTC 2878
Qy 921 AlaAsnAlaThr11eSerVal1SerGly11eAsnHisGlyVal1LysThrAlaSerGlyGly 940
Db 2879 GCCAAGGCCACATCTCTGTGAGTGGCATTTAAACGCGGTGAAGACAGCATGGTGTGT 2938
Qy 941 AspTyrTyrArg11eLeuAsnProGlyGlyUrpArgVal1ThrAlaHisAlaGluGlyTyr 960
Db 2939 GATTTACTGGGATCTTGAACCCGGGTGTGTATCCGCTGACAGCCACCGGAGGCTTAC 2998
Qy 961 ThrProSerAlaLysThrCysAsnVal1AspTyrAsp11eGlyVal1ThrGlnCysAsnPhe 980
Db 2999 ACCCCAGGCGCCAAAGCTGTGCAATGTGACTATGACATCGGGGCCCTAGTGCACCTTC 3058
Qy 981 IleLeuAlaArgSerAsnTyrLysArg11eArgGlu11eMetAlaMetAsnGlyAsnArg 1000
Db 3059 ATCTGTGCTGCTCCCACTGGAAGCCCATCCGGAGATCATGGCCATGAACGGGAACCGG 3118
Qy 1001 Pro11eProHis11eAspProSerArgProMetThrProGlnGluArgLeuGlnGln 1020
Db 3119 CTTATCCCAACATAGACCATGCGCCCTTATGACCCCAACAGAGCGCTCGAGCAG 3178
Qy 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgLeuAsnAla 1040
Db 3179 CGAGCCTTCAACACCGCTGTGGCTTGGGCAAGATCGGTGGGGCGCTCAACCGCC 3238
Qy 1041 ThrThrThrLeuGlyUrpHisThrVal1ProProThrLeuProProAlaProAlaThrThr 1060
Db 3239 ACCACCACTTACGCCCCCACTGCTGCTCCACGCTGCCCCCTGCGCACACAC 3298
Qy 1061 LeuSerThrThr11eGluProTyrGlyLeu11eProProThrThrAlaGlyTyrGluGln 1080
Db 3299 CTGAGCACTACATAGAGCTTGGGGCTCATATCCGCCAACACCCCTGGCTGGAGAGAG 3358
Qy 1081 SerGluThrGluThrTyrThrGluVal1Val1ThrGlnPheGlyThrGluVal1GluProGlu 1100
Db 3359 TCGGAGACTGAGACTTACACAGAGGTGTGACAGATTTGGAGCCGAGGTGGAGCCCGAG 3418
Qy 1101 PheGlyThrLysVal1GluProGluPheGluThrGlnLeuGluUrpProGluPheGluThrGln 1120
Db 3419 TTTGGGACCAAGGTGAGGCCCGAGTTTGAAGCCAGTTGGAGCTTGAAGTTCAGACCCAG 3478
Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
Db 3479 CTGGAACCCGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTGCG 3538
Qy 1141 GlnAlaPheProPheThrThrVal1GluThrTyrThrVal1AsnPheGlyAspPhe 1158
Db 3539 CAGGCAATTCCTTCAACAAGTAGAGACTTACAGTAGAATCTTGGGAGCTTC 3592
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RESULT 13  
US-10-264-049-490  
; Sequence 490, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birst et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133PI  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360



SOFTWARE: Patentin Ver. 3.1  
; SEO ID NO 490  
; LENGTH: 3523  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-049-490

## Alignment Scores:

Pred. No.:	0	Length:	3523
Score:	5725.00	Matches:	1054
Percent Similarity:	99.8%	Conservative:	2
Best Local Similarity:	99.6%	Mismatches:	2
Query Match:	91.3%	Indels:	0
DB:	7	Gaps:	0

US-10-642-946-3 (1-1158) x US-10-264-049-490 (1-3523)

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QY 101 LysGlyProLysValProLysGlySerLeuGlySerProArgProLysGly 120
DB 2 AAAGCCCCAAGTGTCCCAAGAGTCTTGAGGGGTCCCCAGCGCCGCAAGAGGG 61
QY 121 LysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAlaThrLys 140
DB 62 AAGGAGAACCCACCCCAAGGCCACCAAGAGCCCAAGAGAACCTTAAGGCCACCAAG 121
QY 141 LysProLysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAla 160
DB 122 AAGCCCAAGAGAACCCCAAGGCCACCAAGAGAACCCCAAGAGAACCCCAAGAGGCC 181
QY 161 ThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGlyThrLeuGly 180
DB 182 ACCAAGAACCCCGTCAGAGGAAGAGGCCCCCATTCGTGCTCCCTCAAGAACCTTGAG 241
QY 181 TrpProLysProProProSerProSerProGlyProGlyLysLeuProGlyLysAla 200
DB 242 TGCGCCACTGCCACCCACCCAGCCCTGGCCCGAGAGACTACCCAGAGAGGAGGGCG 301
QY 201 ProLeuSerAspAsnTrpGlnAsnProGlyLysGlyLysThrHisValGlyLysGlyLys 220
DB 302 CCCCTTCAATTAATCTGGCAAGATCCAGAGAGAGAACCCATGTGAGGCAAGAGAGC 361
QY 221 GlnProGlyLysProGlyLysGlyLysGlyLysProThrLeuAspTyrAsnAspGlyLys 240
DB 362 CAGCGTGAAGCCGAGAGAGAGGAGCCAGCAACCCAGCTGAGCTGACATGACCAATGAG 421
QY 241 ArgGlyAspTyrGlyLysAspPheGlyLysLysArgGlyLysGlyLysProArgProPro 260
DB 422 AAGGAGAGACTATGAGAGACTTTGAGTACATTCGGCCGAGAGAGAACCCAGGACCCCA 481
QY 261 SerArgArgArgArgProGlyLysArgValTrpProGlyLysProGlyLysLysAlaProAla 280
DB 482 AGCAGAGAGAGAGAGCCCGAGCGGATCTGGCCAGAGCCCTTGAGAGAGAGAGAGAGCC 541
QY 281 ProAlaProGlyLysGlyLysGlyLysGlyLysProProValLysProLeuLeuProProPro 300
DB 542 CCAAGCCCGGAGAGAGAGATGATGCTCGTGAAGCCTGCTGCCCCGCGTGGCCCTT 601
QY 301 AspTyrGlyLysAspGlyLysValLysProAsnTyrAspAspMetCysPyrTyrPheGlyPro 320
DB 602 GACTAGGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 321 ProProProGlyLysProAspAlaGlyLysArgLysThrAspGlyLysGlyLysGlyLys 340
DB 662 CTTCCGCCCGAGAGAGCCCGATGCTGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
QY 341 LysProLysLysGlyLysAspSerSerProLysGlyLysGlyLysThrAspLysTrpAlaValGlyLys 360
DB 722 AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
QY 361 GlyLysAspHisLysGlyLysProArgLysGlyLysGlyLysGlyLysGlyLysGlyLys 380
DB 782 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
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QY 381 GlyLysValLysCysProProLysGlyMetGlySerHisArgLysAlaAspAsnGlyLys 400
DB 842 GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTCAACCGTATTGAGAGACACCAAGATC 901
QY 401 ArgAlaSerSerMetLeuArgHisGlyLysGlyLysAlaGlyLysArgLysLeuAsnMetGly 420
DB 902 CGAGCTCTCCATGCTCGCCAGCGGCTGGGGGAGAGCGGCGGCGCTCAACATGAGAG 961
QY 421 ThrGlyAlaThrGlyLysAspTyrTyrAspGlyLysAlaTrpCysAlaGlyLysAspAlaArg 440
DB 962 ACCGTTGCCACTGAGAGAGAGTCACTATATATGATGATGATGATGATGATGATGATGATG 1021
QY 441 ThrGlnTrpLysGlyLysAlaAspThrArgArgThrThrArgPheThrGlyValLysThrGln 460
DB 1022 ACCCATGATGATGAGTGGAGACCAAGAGAGACTACCCGCTTCAAGGGGTCAACCCAG 1081
QY 461 GlyArgAspSerSerLysHisAspAspPheValThrPhePheValGlyPheSerAsn 480
DB 1082 GGCAGAGACTCCAGATCCATGACGATTTGTGACACCTTCTTGTTGGGCTTCAGCAAT 1141
QY 481 AspSerGlnTrpTrpValMetTyrThrAsnGlyLysGlyLysMetThrPheHisGlyLys 500
DB 1142 GACAGCCAGACATGGGTATGACCAACGCTATGAGAAATGACCTTTCATGAGAAC 1201
QY 501 ValAspLysAspThrProValLeuSerGlyLysLeuProGlyLysProValValAlaArgPheLys 520
DB 1202 GTGGACAGAGACACCCGCTGTGATGAGCTCCAGAGCGGCTGGCTGTTTCAATC 1261
QY 521 ArgLysLysProLeuThrTrpAsnGlySerLysCysMetArgLysGlyLysGlyLysCys 540
DB 1262 CGCATCTACCACTACCTGGAATGGCAGCTGTGCAAGCGCTGAGAGTGTGGGGTGC 1321
QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGlyLysValAlaThrAspAspLeu 560
DB 1322 TCTGTGGCCCTGTGTTACAGTACTACCAAGATGAGTGGTGGCCACCATGACCTG 1381
QY 561 AspPheArgHisHisSerTyrLysAspMetArgLysLeuMetLysValValAsnGlyLys 580
DB 1382 GATTTTGGGACCAACAGCTACAGAGACATGGGCCAGTTCATGAGTGGTGAACGAGAG 1441
QY 581 CysProThrLysThrArgThrTyrSerLeuGlyLysSerSerArgGlyLysLysLysLys 600
DB 1442 TGCCCCACCATCACCCGACTTACAGCTGGGCAAGAGACTCAAGGCTTCAAGATCAT 1501
QY 601 AlaMetGlyLysSerAspAsnProGlyLysGlyLysGlyLysGlyLysProGlyLysPheArgTyr 620
DB 1502 GCCATGAGATCTCAAGACACCTGGAGAGCTGGAACCTGGGGAGAGCCGAGTTCGCTAC 1561
QY 621 ThrAlaGlyLysHisGlyLysAsnGlyLysGlyLysArgGlyLysLeuLeuLeuMetGln 640
DB 1562 ACTGCTGGGATCATTGGCAAGAGTGTGGGCGAGAGCTGTGCTGCTCATGAGAG 1621
QY 641 TyrLeuCysArgGlyLysThrAspGlyLysAsnProArgValArgSerLeuValGlnAspThr 660
DB 1622 TACTGTGCGGAGATACCGGATGAGAACCCAGCTGTGGCAGCTGTGAGAGACACA 1681
QY 661 ArgLysHisLeuValProSerLeuAsnProAspGlyLysGlyLysValAlaAlaGlnMetGly 680
DB 1682 CGCATCTCACTGTGTCTCTCACTGAACCTGATGAGCTACAGAGTGGACGAGATGGGC 1741
QY 681 SerGlyPheGlyAsnTrpAlaLeuGlyLysLeuTrpThrGlyLysGlyLysPheAspLysPheGly 700
DB 1742 TCAGAGTTTGGGAATGGGCGCTGGGACTGTGAGCTGAGAGAGGCTTTGACATCTTGA 1801
QY 701 AspPheProAspLeuAsnSerValLeuTrpGlyLysAlaGlyLysGlyLysTrpValProTyr 720
DB 1802 GATTTCCCGGATCTCACTGTGTCTGTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1861
QY 721 ArgValProAsnAspAsnLeuProLysProGlyLysGlyLysSerProAspAlaThrVal 740
DB 1862 CGGATCCCCAATTAATCTGCTCCATCCCTGAACCTTCTTCCGACATGCCAGCTA 1921
QY 741 SerThrGlyValArgAlaIleIleAlaTrpMetGlyLysAsnProPheValLeuGlyAla 760
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Db      1922  TCCACGAGAGTCCGGGCATCATTTGCTGGATGGAGAAAGAACCCCTTCGTCGTGGAGCA 1981
Qy      761  AsnLeuAnnglylglyluhrgleuValSerTyProTyraPheMetAlaArgThrProThr 780
Db      1982  AATCTGAACGGCGCGGCGCTGTATCTTACCCCTTACGATATGAGCCCGCACCCCTACC 2041
Qy      781  GlngluGluInleuValaAlaMetAlaAlaAlaArgglyluuapGluuapGluVal 800
Db      2042  CAGAGAGAGCTGCTGGCGCGAGCCATGCGACAGACCCCGGGGGGAGATGAGAGAGAGTC 2101
Qy      801  SerGluuAglngluThrProAspHisAlaAlaPheArgTrpLeuAlaIleSerPheAla 820
Db      2102  TCCGAGGCCAGAGAGATCCAGACAGCCATCTCCGGTGGCTTGGCATCTCTTGGCC 2161
Qy      821  SerAlaHisLeuThrLeuThrGluProTyraArgglylycyGluuAgluAgnAspTyThr 840
Db      2162  TCCGCACACCTTCACCTTGACCGAGCCCTACCGCGAGAGCTGGCCAAAGCCAGACTACAC 2221
Qy      841  GlyGlyMetGlyIleValaAnglyAlaIleTyTrpAsnProArgTrpGlyThrIleAsnAsp 860
Db      2222  GGGGGCATGGGACATGTCACAGGGGGCCAAAGTGAACCCCGGACCGGGACTATCAAGAC 2281
Qy      861  PheSerTyLeuHisThrAsnCyAlaGluLeuSerPheTyLeuGlyCyAspTyPhe 880
Db      2282  TTCAGTTACCTGCATACCACTGCTGAGCTCTCTTACCTGGGCTGTGACAGTTC 2341
Qy      881  ProHisGluSerGluLeuProArgGlyTrpGluuAsnAsnlyGluAlaLeuThrPhe 900
Db      2342  CCTCATGAGAGTGGTGGCCCGCGAGTGGAGAAACAAGAGGGCGCTGCATCACCCTTC 2401
Qy      901  MetGluGluValHisArgglylyIleGlyValValThrAspGluGlyIleProIle 920
Db      2402  ATGAGAGAGGTGACCCGGCATTTAGGGGGTGTGTGCGAGCAGAGCAAGCATCCCAT 2461
Qy      921  AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly 940
Db      2462  GCCAAGGCCACATCTGTGTGAGTGGCATATATACGGCTGGAAGACGCAAGTGGTGT 2521
Qy      941  AspTyTrpArgIleLeuAsnProGlyGlyTrpArgValThrAlaHisAlaGluGlyTy 960
Db      2522  GATTACTGGCGGAATCTTGAACCCGGGTGAGTACCGCTGACAGCCCGGAGAGGCTAC 2581
Qy      961  ThrProSerAlaIleAspThrCyAsnValAspTyThrAspIleGlyAlaThrGlnCyAsnPhe 980
Db      2582  ACCCCAGAGCCCAAGACCTGCAATGTGACTATGACATCGGGCCACTGCTCAACATTC 2641
Qy      981  IleLeuAlaArgSerAsnTrpIleArgIleArgGlyIleMetAlaMetAsnGlyAsnArg 1000
Db      2642  ATCTGCTGCTGCTCCAACTGGAGCGCATCCGGGAGATCATGGCCATGAAACGGMAACGG 2701
Qy      1001  ProIleProHisIleAspProSerArgPProMetThrProGluGlnArgArgLeuGln 1020
Db      2702  CCTATCCCAACATAGACCATCGCGCTATATGACCCCAACAGGAGCAGCTGAGCAG 2761
Qy      1021  ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040
Db      2762  CGAGCGCTACAAACAGCGCTGCGGCTTCGGGCAAGATGGCGTGGCGCCCTCAACGCC 2821
Qy      1041  ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060
Db      2822  ACCACACACCTTAGGCCCCCACTGTGCTCCACAGCTGCGCCCTGCTGCCACACACC 2881
Qy      1061  LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGln 1080
Db      2882  CTGAGCACTACCATAGAGCCCTGGGGCTCATACCGCAACCAACCGCTGGCTGGAGAG 2941
Qy      1081  SerGluThrGluThrTyThrArgIleValValThrGluPheGlyThrGluValGluProGlu 1100
Db      2942  TCGAGAGCTAGACCTTACACAGAGGTGTGACAGAGTTTGGAGCCGAGGTGGAGCCGAG 3001
Qy      1101  PheGlyThrIleValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120

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Db      3002  TTTGGAGCAAGGTGAGAGCCCGAGTTTGAGACCCAGTTGAGAGCTGATTGAGACCCAG 3061
Qy      1121  LeuGluProGluPheGluGluGluGluGluGluGlyIleGlyGluGluValIleAspGly 1140
Db      3062  CTGGAACCCGAGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCCACTGGC 3121
Qy      1141  GluAlaPheProPheThrThrValGluThrTyThrValAsnPheGlyAspPhe 1158
Db      3122  CAGGCACTCCCTTCAACAGATGAGACCTTACAGATGAATTTTGGGACTTC 3175

RESULT 14
US-10-101-510-345
; Sequence 345. Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: MAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 3170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-345

Alignment Scores:
Pred. No.: 0 Length: 3170
Score: 4925.50 Matches: 922
Percent Similarity: 94.8% Conservative: 6
Best Local Similarity: 94.2% Mismatches: 14
Query Match: 78.5% Indels: 37
DB: 7 Gaps: 3

US-10-642-946-3 (1-1158) x US-10-101-510-345 (1-3170)
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Qy      201  oLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGlnIleHisG 221
Db      74  AATGGGCCCATC-----CA 88
Qy      221  nPro-GluProGluGluGluThrGluGlnProThrLeuAspTyraAsnAspGlnIleGlu 241
Db      89  GCCTTGGGCGCCACTGTGAGCCAGCCTCCCTCCAGCT----- 126
Qy      241  rgluAspTyrgluAspPheGluTyrlleArgArgGlnIleGlnProArgProProPro 261
Db      127  -----GATACATTGGCGCCAGAGCAACCAAGCCACCCCAA 166
Qy      261  exArgArgArgArgProGluArgValTrpProGluProProGluGluIleAlaProAla 281
Db      167  GCGAAGAGAGAGAGCCCGAGCGGGTGTGGCAAGACCCCTGAGAGAGAGAGCCGGGCC 226
Qy      281  roAlaProGluGluArgIleGluProProValIleProLeuLeuProProLeuProPro 301
Db      227  CAGCCCGGAGAGAGAGATTTGAGCCCTCTGTAAAGCTCTGCTGCCCGCTGCCCTCG 286
Qy      301  sPTyrglyAspGlyTyValIleProAsnTyraAspPheAspTyTyTrpPheGlyPro 321
Db      287  ACTATGTATGTGTATCGATCCCACTACGATGACATGGAATTTACTTTGGGCTTC 346
Qy      321  roProProGluIleProAspAlaGluArgGlnThrAspGluGluIleGluGluLeuVal 341
Db      347  CTCGCCCCAGAAAGCCCGATGCTGAGCGCCAGACGGAAGAAAGAGAGAGCTGAAGA 406

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OY	341	yPvPvolyeIyagIuApsSeSerPvolyeIuIuThraSpIyPThraValaValaGIuIyG	361
Db	407	AAccCAAAAGAGAGACAGCACCCCAAGAGAGAGACCAAGAGAGAGAGAG	466
OY	361	lyLyAaSPHhIvlyeGIuPvPvAqLyvSGIyGIuGIuLeuGIuGIuGIuTTPThPvProThG	381
Db	467	GCAAGAGACCAAAAGAGCCCGAAAGGCGAGAGAGTTGAGAGAGAGTGGAGCCCTACGG	526
OY	381	luLyvVallyeCyAePvProIleGIyMeGIuSerHsaGIleGIuAePaengInIea	401
Db	527	AGAAAGTCAGTGTCCCCCATTTGGAGTGAAGTACACCGTATTGAGGACCAACAGATCC	586
OY	401	rgAlSeSerMeLeuAghIeGIyLeuGIyAlaGInArgIyArdLeuAeMeGIuT	421
Db	587	GAGCTCCCTCCATGTGTGGCCACCGGCTGGGGGCAAGGCGGCGGCTTCAATGACAA	646
OY	421	hrgIyAlathrgIuAaPvAryTyTyAaSPGIyAlaTTPCyvAlaGIuAaPvAlaAqT	441
Db	647	CCGATGCCACTAGAGACGACTACTATGATGTGTGGTGTGTGCGGAGAGAGTCCAGGA	706
OY	441	hrgInTrrpIleGIuValAaPThraArgThrThzArPheThrgIyValIleThrGInG	461
Db	707	CCAGATGATTAAGGTGGACACCAAGAGAGACTACCGGTTCACAGGCGTCAATCCACAG	766
OY	461	lyArqAaSPSeSerIleHIsaAaPvPheValThrThrPhePheValGIyPheSeSaAa	481
Db	767	GCAGAGACTCCAGATCCATGAGATTTGTGTGCCACTTCTTCGTGGGCTTCAGCAAG	826
OY	481	apSeSerIuThrThrpValMeTyTrThAaNGIyTyGIuGIuMeTThrPheHIsGIyAaTy	501
Db	827	ACAGCGACAGATGGGATGATGACCAACAGGCTATAGAAATGACTTTCATGGAGAG	886
OY	501	aIaSPlySaPThrPvAlleuSeSerGIuLeuPvProGIuPvProValValaIaArGPheIleA	521
Db	887	TGGACAAAGACACACCCGTGTGAGTGAAGTCCCAAGCGGAGGTGGCTCGTTTATCC	946
OY	521	rgIleTyTrPvProLeuThrTPvAaNGIySeLeuCyMeCArgLeuGIuValLeuGIyCyS	541
Db	947	GCATCTACCCACTGCACCTGAAATGGCAGGCTGTGTGAGGCTGTGGAGTGTGGGTGTCT	1007
OY	541	eValAlaPvAlaTySeSerTyTyTyAlaGIaSPInIuValaIaATTPvAaPvLeuA	561
Db	1007	CTGTGGCCCCCTGTCTACAGCTACTAGCAACAGATAGGTGGGGCCACGAGTACCTGG	1067
OY	561	apPheArghIeHIsaSeTyTyLySaPMeArGIuLeuMeTySaValaIaSPNGIuIc	581
Db	1067	ATTTCGGGACCAACAGCTACAAAGAGATGCGCCAGCTCATGAAGGTGTGAAGAGAGGT	1127
OY	581	yAPvProThrIleThraArgThrTySeSerLeuGIyLySeSeSaArgIyLeuValIeTyTA	601
Db	1127	GCCCCACATACACCCGCACTTACAGGCTGGGCAAGAGCTCACAGAGGCTTCAGATCTAG	1187
OY	601	lAeMeGIuIleSeSaPvAaNPvProGIyGInHIsGIuLeuGIyGIuPvProGIuPvAaGT	621
Db	1187	CCATGAGATCTACAGAACCCCTGGGAGAGTAACTGGGGAGGCCGAGTCCGCTACG	1247
OY	621	hrgAlaGIyIleHIsaGIyAaNGIuValLeuGIyAArgGIuLeuLeuLeuLeuMeGIuT	641
Db	1247	CTGTGTGGATCCATGGCAAGAGTGTCTGGGCCGAGAGCTGTTCGTGTCTATACAGT	1307
OY	641	yTLeuCyAaArgIuTyTyAaSPGIyAaNPvAaArgyValaArgSeLeuValGIaSPThra	661
Db	1307	ACCTGTGCGAGAGTACCGCGATGGGAGACCAAGTGTGGCGACGCTGTGTCAAGACAC	1367
OY	661	rgIleHIsaIeValPvProSeSaAaNPvAaSPGIyTyGIuValaIaAlaGIuMeGIyS	681
Db	1367	GCATCCACTGTGGCTCCCTCACTGAACCTGTATGTCTACGAGGTGGAGCGCCAAATGGCT	1427
OY	681	eArgIuPheGIyAaNTTPvAlaLeuGIyLeuTyTrThrgIuGIuGIyPheAaPvIlePheGIuA	701
Db	1427	CAGAGTTTGGAACTGGGCGCTGGAGCTGTGACTGAGAGAGGCTTTGACATCTTTGAG	1487
OY	701	apPhePvAaPvLeuAeSaValleuTrrpIyAlaGIuGIuAryTyPvAlaProTyza	721

Db	1487	ATTTCCCGGATCTCACTCTGTGCTCTGGGGAGCTGAGGAGAGAAATGGGTCCCTTACC	1546
OY	721	rgValProaAnAsnAnLeuProIleProGluarGlyrLeuSerProAspAlaThrValS	741
Db	1547	GGGTCCCAACAATPACTTGCCCTATCCCTCAAGCTACTTGGCCAGATGCCAGGTAT	1606
OY	741	erThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla	761
Db	1607	CCAGGGAGGTCCTGGGCGCATATGGCTTGATGAGGAAGAACCTCTTGCTGTGGACCA	1666
OY	761	snLeuAnGlyGlyGluarGluValSerTyrProTyrAspMetAlaArgThrProThrG	781
Db	1667	ATCTGAACGGGGGAGAGGCTAGTATCTTACCCTTACGATATGTGCCGACGCTTACC	1726
OY	781	InGluGluLeuLeuAlaAlaMetAlaAlaIaArgGlyGluAspGluAspGluValS	801
Db	1727	AGGAGCAGCTGCTGTGGCCGACGCATGTGACAGAGCCCGGGGGAGAGTAGAGACAGAGTCT	1786
OY	801	erGluAlaGlnGluThrProAspHisAlaAlaIlePheArgTrpLeuAlaIleSerTheAs	821
Db	1787	CCGAGGCCCAAGAACTCCAGACCAACCCCATCTCTCCGTGGCTTGGCATCTCTTCCTCT	1846
OY	821	erAlaHisLeuThrLeuThrGluProTyrTrpArgGlyGlyCysGluAlaGluAspTyrThrG	841
Db	1847	CCGACACCTTACTTGTACCGAGCCCTTACCGGAGGCTGCCAAGCCACGACTTACACG	1906
OY	841	lyGlyMetGlyLysValAsnGlyValaLysTrpAsnProArgThrGlyThrIleAsnAsp	861
Db	1907	GGCGCAATGGGATGCTGTCACAGGGGCCAAAGTGAAACCCCGGACCGGAGCTATCAATGACT	1966
OY	861	heserTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPheP	881
Db	1967	TCAGTTTACTGTCATACCAACTGCTCTGAGGCTCTCTCTACTCGGCTGTGTACAAAGTCC	2026
OY	881	roHisGluSerGluLeuProArgGlyLutTrpGluAsnAsnLysGluAlaLeuLeuThrPheM	901
Db	2027	CTCATGAGAGACTGTGCCCCGAGAGTGGAGAACACAAAGAGGCGCTGCTCACTTCA	2086
OY	901	ecGluGluValHisArgGlyLysLeuGlyValValaThrAspGluGlnGlyLysProIleA	921
Db	2087	TGGAGCAGGTCCACCGTGGCATTTAAAGGGGGGTGGTGAAGACAGACAAAGGATCCCAATGG	2146
OY	921	laAsnAlaThrTyrIleSerValSerGlyLysAsnHisGlyValaLysThrAlaSerGlyGlyA	941
Db	2147	CCAACGCCACCATCTGTGTGATGGCATTTATCAACGGGTGTGAACACGCCAGTGGTGGT	2206
OY	941	spTyrTrpArgGluLeuAsnProGlyGluTyrArgValaThrAlaHisAlaGluGlyTyrT	961
Db	2207	ATTACTGGCGAATCTTGAAACCCGGGTGTAGTACCCGCTGACAGCCACCGGAGGGCTTCA	2266
OY	961	hrProSerAlaLysThrCysAsnValaAspTyrAspIleGlyAlaThrGlnCysAsnPheI	981
Db	2267	CCCCGAGGGCCAAAGACCTGGCAATTTGACTATGTACATCGGGGCCACTAGTGAACTTCA	2326
OY	981	leLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArgP	1001
Db	2327	TCTGTGGCTCGCTCCAACTGGAAGGCAATCCGGGAGATCATCGCATGTAAACGGGAACCGGC	2386
OY	1001	rolleProHisIleAspProSerTrpProMetCThrProGlnGluArgArgLeuGlnGlnA	1021
Db	2387	CTATTCACCAATAGAACCCATCGGCGCTTATGACCCCCCAACAGAGAGGCTTGACGACGAC	2446
OY	1021	rgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAlaT	1041
Db	2447	GAGCGCTTCAACAACCGCTGGCGCTTGGGGACAGATCGGGCTCGCGGCTTCAACGCGCA	2506
OY	1041	hrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThrL	1061
Db	2507	CCACGACCTTAGGCCCCACACTGTGCTCCACAGCTGCCCCCTGCGCTCCACACACCC	2566
OY	1061	euserThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGluS	1081



Db 9453 GGGAGGCTTTGGGCCCCATGTCCTTCTTTGATGGCAGTTGGAGGGATGACCAAGATG 9394  
 QY 84 ----- 84  
 Db 9393 CTCTCCAGGCTGGATGGCTAGTCACCTCTCTGCCCCCTTCTGTGCCAGAAACAAATA 9334  
 QY 84 ----- 84  
 Db 9333 GTGGAGGAGTGGATGACTAAGAAACCCCTATTGAGGTTTGGCAGGTTGGGGGAGTAGGGC 9274  
 QY 84 ----- 84  
 Db 9273 CTCCCCCTGGGAAGCTGGAAACCTAGAGCTCAGCTTTAGAGAGTTGAGATTGGTGTC 9214  
 QY 84 ----- 84  
 Db 9213 CAGCCCCAGACTTGCAGACAGAAATCTGGGTCGGATCCGATTCGCACTTGGGCANA 9154  
 QY 84 ----- 84  
 Db 9153 TGACTTAACCTCTCAGTTGCTGATCCGACCTGGGAATGACAAAGATCCCTGTGCCAG 9094  
 QY 84 ----- 84  
 Db 9093 GTTCTGGGCACTAGAGAGGGGCTCATGGGGGACAGAGCTGCTCTGTCAATTGACA 9034  
 QY 85 -----ValProProGluThyThyAspLysGlyLysLysGlyLys 98  
 Db 9033 CGAGTCTGATCTTGAGACAGATGCTCCGGAAAAGACAAAGACAAAGGAGAAAGGCA 8974  
 QY 98 slyAspLysGlyProLysValProLysGluSerLeuGluLysProArgProLys 118  
 Db 8973 GAAAGCAAAAGGCCCAAGGTGCCCAAGAGTCTTGGAGGGGTCCCCAGGCGGCCCA 8914  
 QY 118 slyGlyLysGluLysProLysAlaThyLysLysProLysGluLysProLysAla 138  
 Db 8913 GAAAGGGAAGGAAGCAACCCCAAGGCCAACAAAGGCCAAAGAGAACCACTTAAGGC 8854  
 QY 138 AthrLysLysProLysGluLysProLysAlaThyLysLysProLysGluLysProLys 158  
 Db 8853 CACCAAGAAAGCCCAAGAGAGCCACCAAGGCCCAAGAACCCCAAGAGAACCCAC 8794  
 QY 158 olvAlaAlaThyLysProLysArgProLysAlaThyLysProLysAlaProLys 178  
 Db 8793 CAAGGCCAACAAAGGCCCTCTCAAGAGAGAGGCCCTCTGAGCTCTCTCAAGAAC 8734  
 QY 178 rLeuGluTrpProLysProLysProLysProLysProLysGluLysProLysGlu 198  
 Db 8733 CTGGAGTGGCCACTGCCCCCAGCCCCAGCCTGGCCCCGAGAGACTAACCCAGAGG 8674  
 QY 198 Y----- 198  
 Db 8673 AGGTTTGGCCGGCTCTCTGGGGTGAAGGGCTCTGACTGCTCTCGGAGAGGCA 8614  
 QY 198 ----- 198  
 Db 8613 GGGAGTGGAGGAGGTTTCTGGGGCCCTCTCTAATAGACTTAAGCTTCCCACTGGA 8554  
 QY 198 ----- 198  
 Db 8553 TGGGAACCTCACTTTGTATAAATTACAAATTTGATGGTGGCTCCTCAGTGTGT 8494  
 QY 198 ----- 198  
 Db 8493 AGCCTTTTGGTAGGAGAGGAGCTTGGCAGCCTTTGGTGGAGCTTGTCTCTCAG 8434  
 QY 198 ----- 198  
 Db 8433 GCCCCTGCCAATGTCCTGGGCTCTGAGCCATGAGTTCCCTCTGCTTCTCCCG 8374  
 QY 198 ----- 198  
 Db 8373 TGGGACAGCTTTGTGTAGGGCTCCAGCAGACAGTAGATTCCCAAGAGGTGGGCC 8314

QY 198 ----- 198  
 Db 8313 AGCTCTGGGCCCATGAGATGCCAGACGATGCTGAAGGCCAGAGAGCTCAGGCTCC 8254  
 QY 198 ----- 198  
 Db 8253 TTGGAGTAGGCTCGGCTCAGAGAGGTGTCCACAGGCTCTGTGTGGCTTAATGGGTGC 8194  
 QY 198 ----- 198  
 Db 8193 TGTGGCTGAGGCTCCCAAGGTGTCAAGCAGGCTCCGCCCACTGCTTTCGAAC 8134  
 QY 199 -----GlyAlaProLeuSerAsnAsnTrpGlnAsnProGluGluThrHi 214  
 Db 8133 TCTGTGTTCAGGGCG-CCCCCTCAATAATACCTGGAGAAATCCAGAGAGAGACCA 8075  
 QY 214 sValGluAlaGlnGluHisGlnPro----- 222  
 Db 8074 TGTGAGGCAACAGAGACACAGCTGTGAGTGGCCGATCCGCTGGCCTTGGGGCCA 8015  
 QY 222 ----- 222  
 Db 8014 GCTGCCCTGGCTGTGACTGAGGCTTCCCAAGTAGGCTTGGGTGGTTCAG 7955  
 QY 223 -----GluProGluGluGluThrGluGluProThyLeuAspT 235  
 Db 7954 CAGCTACACAGCGCTTTCCTCCACAGGCCGAGAGAGAGACCAAGCAACCACTGACT 7895  
 QY 235 yAsnAspGlnIleGluArgGluAspTyArgLysPhe----- 247  
 Db 7894 ACAATGACCAATTCAGAGGGAGGACTATGAGACTTTGATGAGGTCTTCGACCCCA 7835  
 QY 247 ----- 247  
 Db 7834 CTTGGGTGGAACCTTGGCTGGGGATGTGCCAATGGGCCCATCCAGCCTTGGCCCC 7775  
 QY 248 -----GluTyrlLeuArgGlnLysGlnProArgProP 259  
 Db 7774 ACTTGAGCAGACCTTCCCCCTCAAGTGAATCTCGGCCCAAGAACCAAGCCAGCCAC 7715  
 QY 259 roProSerArgArgArgProGluArgValTrpProGluProGluGluLysAlaP 279  
 Db 7714 CCCCAAGCAGAGAGAGGAGGCCGAGCGGTCTGACAGAGCCCTTGAGAGAGAGGCC 7655  
 QY 279 roAlaProAlaProGluGluArgIle----- 287  
 Db 7654 CGGCCCCAGCCCGAGAGAGAGATTGTAGAGTGGGGGACAGAGAGAGGTGCCATGG 7595  
 QY 288 -----GluProProValLysProL 294  
 Db 7594 CCAAGCGCTTGGGCCCTCTTAACCTCCCGCTCCCAAGCTCTCTGTGAAGCTTC 7535  
 QY 294 euLeuProProLeuProProAspTyArgLysGlyTyValIleProAsnTyAspAsp- 313  
 Db 7534 TGTGCCCCCGCTGCCCCCTGACTATGTGATGATTACGTGATCCCACTACGATGACA 7475  
 QY 313 ----- 313  
 Db 7474 GTGAGTACCAGACCCAGAGCTGAGAGACATAGGAGAGTGGGGGTGGGGGT 7415  
 QY 313 ----- 313  
 Db 7414 GTGTACAGAGCAGCTGGGGCACTCAACCCACTTGCAACCCCACTGTGCCGTGTT 7355  
 QY 313 ----- 313  
 Db 7354 ACCTGCTGTCCCTGTGCTCTGTGCTGACCAACCCAGCACTGCTGTCTCTGCTCC 7295  
 QY 313 ----- 313  
 Db 7294 CTGAGGTGTCTTCTTCTTGGCGGCTTCTCTGTCTCTGCTTGTGCTGACCCCAAG 7235

[illegible]

Db	6154	CTGGCCCATGTGCACAAACAGAGCCCAAGTCCCGGAAACCTTTCTACTCAGATTCTTG	6095
QY	383	-----	383
Db	6094	GGACCAGAGGAGGGGCCCGGGAGCCAGATAGCTGCCTTGCTGGCCCCAGCCCT	6035
QY	383	-----	383
Db	6034	GGACCCCAAGCTGGCCTGCTCTTAGAGAGGTGACAGCTCCCAAGGCCCTTAGTGCTGGG	5975
QY	383	-----	383
Db	5974	CGTGTAGAGGAGAGACCTGGGGCCTTGTTGGGAGTGAAGACCTCAGAGTACCTTCACAG	5915
QY	383	-----	383
Db	5914	GTATCCCTCAGAGGCCATTGTGCAGACGGTCCCATCTGATGACATCTGTGCTGCGCC	5855
QY	383	-----	383
Db	5854	CTGGGGAGCTCTACCTGTGATTTTCAGTGTTGTCCCTGAGAGTGGGATGTGACGCC	5795
QY	383	-----	383
Db	5794	GTTCTCAGATGAGGAGCTGAGGCCACAGGAGGGGAAACACAGGCTGGATTGGAACA	5735
QY	383	-----	383
Db	5734	GCTCTGGGCTTGCTTGTGATGTCAATTCAGGTGGGCTGTGTGACAGGACCAAGGAGCCAC	5675
QY	383	-----	383
Db	5674	CAGCTGACAGAGCTGCCCTCTGACTGTGACCCCGAGTGTGCCGGAGTGGGCTTGAGGCT	5615
QY	383	-----	383
Db	5614	CCTTGGTTCTGGGTTGTGTGAGGAGGAAGATGAGCTAGTGAGCCACCATTTCTGGGTAC	5555
QY	384	-----Lys-CysProProlIegIYmeGluSerHisArgIleGluAspAsnGlnIle :::	400
Db	5554	GCGTCTCAGAGTGTCCCCCATTTGGATGAGTACACACGTTATTTGAGACACCAACATC	5495
QY	401	ArgIAserSerMetLeuArgHisGlyLeuGlnValArgIleArgGlyLeuAspMet--	419
Db	5494	CGAGCTCTCATAGCTGTGCGCCACGAGCTGGGGCACAGCGCGGCTCAACATGACAG	5435
QY	419	-----	419
Db	5434	GTGGGCATTGGGATGGGCCCATCTCCCACTGGGATTAAGGACCTCTCCGCCCATGCTCA	5375
QY	420	-----GlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTr 	433
Db	5374	GCTTCCCCCTGCCCTGGACAGACCGGTGGCCACTGAAGAGCAGTCACTATGATGTGGGTG	5315
QY	433	PCyEAlaGluAspAspAlaArgThrGlnTrpIleGluValAspThrArgThrArg	453
Db	5314	GTGTGCGGAGGACCATGCCAGAGACCAAGTGTATGAGTGAACCAAGAGAGACTACCG	5255
QY	453	GPhetThrGlyValIleThrGlnGlyArgAspSerSerIleHis-----	467
Db	5254	GTTCAACAGGCTCATCACCCCAAGGCAAGACTCCAGATCCAGTGGGTGGCCAGGCTCAT	5195
QY	467	-----	467
Db	5194	GGATAGTTGACAGAGGGAGTGTACTATAGGACATGCTCTGTGTCCATTAAAGAGATT	5135
QY	467	-----	467
Db	5134	CCAAGTGGGCCCTTTTGTGGCCCAAGCCAAAGAAGCCAAAAAGATCAAGTAGGAGACTACC	5075
QY	467	-----	467

Db 5074 CTGCCATCCCACTCTGAGCTGTCAGTACAGCCCTGTGTCTGATAGACATAGT 5015  
 QY 467 -----  
 Db 5014 TTAGGACAGATCACTGCCCATGTCTATGTGACGGGCATAGACCCAGCTCAACACT 4955  
 QY 467 -----  
 Db 4954 GGGCCGTGACAGACCACTCTGACTTAATTTCTTGGGGCTCGGAAGAGGAGCTTC 4895  
 QY 467 -----  
 Db 467 -----  
 QY 467 -----  
 Db 4894 AGGCCACTGAGGGCGTGGAGGGGAGAGACCTTGCTCTGACCACTGCTCACTCCAG 4835  
 QY 468 -AspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTrpValne 487  
 Db 4834 TGACGATTTTGTGACCACTTCTTGTGGGCTTCAGCAATGACAGCAGACATGGGTGAT 4775  
 QY 487 TTYrThrAsnGlyTYrGluGluMet----- 495  
 Db 4774 GTACACCAAGGCTTATGAGAAATGGTGGGACCAATGCCAGGCTCTTGCTCTCCC 4715  
 QY 495 -----  
 QY 495 -----  
 Db 4714 ATTGTGGGCGAGGGGTGGGCTCTCAGAGGGCTGGAGTACTGCTTGAGGCTGCT 4655  
 QY 496 -----ThrPheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProG 513  
 Db 4654 CTCGCCAGACCTTTCATGGGACGTGACAGAGACACCCGTGCTGAGTGAAGTCTCCAG 4595  
 QY 513 IuProValValAlaAspPheIleArgIleTYrProLeuThrTrpAsnGlySerLeuCyM 533  
 Db 4594 AGCGGTGTGGTCTGTTTCATCCGATCTACCACTCACTGAAATGGCAGCTGTGA 4535  
 QY 533 eArGleuGluValLeuGlyCySerVal----- 542  
 Db 4534 TGGGCTGGAGGTGTGGGTGTCTGTGGCCGTGAGTGTGAGGGCTGGCAGGGGCTC 4475  
 QY 542 -----  
 Db 4474 TGAGTAGAGTGGGTGTGAGGTGGGCCAGCCGGACCCAGCTAAAGACACCCGCT 4415  
 QY 543 -----AlaProValTYrSerTYrTYrAlaGlnAsnGluValValAlaThrAspAspLeu 561  
 Db 4414 CCTTGACGCTGTCTACAGCTACTACGACAGAAATGAGTGTGGCCACCGATGACTGG 4355  
 QY 561 sPheAspIleHisAspTYrLysAspMet----- 570  
 Db 4354 ATTTCCGGACACACAGCTACAGAGACATGGCCAGTTGGAGCATATATCTGGGGCTG 4295  
 QY 570 -----  
 Db 4294 GGGGTGGACCTGTCTGTGGGTGACGGAGTGTGTGCTGTGCTTCTGTCACTGGGCC 4235  
 QY 570 -----  
 Db 4234 AGTCCCTACTGTTCAGAGGATGTGTGCTCTCCCTACCTTAGAAGAGGCCAATACCT 4175  
 QY 570 -----  
 Db 4174 GGGGCTGCGTGAAGGGGTCAATCCCGTCCCTGCGCATAGACAGGCCCTGGAAGTGA 4115  
 QY 571 -----Arg 572  
 Db 4114 GGGGATGTGACGGGGGACGAGTTGATGATTGATTCAGCTCTCCCTCGTGGGCC 4055  
 QY 572 IuLeuMetLysValValAsnGluGlyCyProThrIleThrArgThrTYrSerLeuGlyL 592  
 Db 4054 AGCTCATGAAGGTGTGAACGAGAGTGGCCCAACATCAACCCGACCTTAAGCTGGGCA 3995  
 QY 592 ysSerSerArgGlyLeuLysIleTYrAlaMetGluIleSerAspAsnProGlyGluHisG 612  
 Db 3994 AGAGCTCAGAGGCTCAAGATCTATGCTGATGAGATCTCAGAACCTTGGGGAGCATG 3935

QY 612 IuLeu----- 613  
 Db 3934 AACTGGGAGAGGTGTGTGGGGGCCAGACGCTGCTCTGCTGTGATGTGACAGCTCA 3875  
 QY 613 -----  
 Db 3874 CTGCTCCGCTGTTCGGAGCCCTCTGGGGGATTCTGGCTTGTCTTAACAGGCCCTAG 3815  
 QY 613 -----  
 Db 3814 GAGCCAGCTGTCCCCAGACCTTCGGGTATGAGTGGGTCTGGTCTTCCTCAGCTG 3755  
 QY 614 -----GlyIuProGlu 617  
 Db 3754 CCCTGGGCTCGGAGACTGAGTGTCTACGTAGAGCTCCCGCCCTTGACAGGAGCCCGAG 3695  
 QY 618 PheArgTYrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeu 637  
 Db 3694 TTCCGCTACACTGTGGGATCCATGCAACGAGGTGTGGGCCGAGAGCTGTGCTGTG 3635  
 QY 638 LeuMetGlnTYrLeuCyAspArgIuTYrArgAspGlyAsnProArgValArgSerLeuVal 657  
 Db 3634 CTCATGCAGTACTGTGTGCGAGAGTACCGCATGGGAACCCAGTGTGGCAGCCTGTG 3575  
 QY 658 GlnAspThrArgIleHisGluValProSerLeuAsnProAspGlyTYrGluValAlaAla 677  
 Db 3574 CAGGACACAGCATCCACTGTGTGCTCAGTAAACCTGATGGCTACGAGGTGGCAGCG 3515  
 QY 678 GlnMet----- 679  
 Db 3514 CAGATGTGTGGTGAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3455  
 QY 680 -----GlySerGluPheGlyAsnTrpAl 687  
 Db 3454 GTGGGTAGCCGATGCTACCTGCTGCTGCCACAGAGGCTCAGATTGGGAACCTGGGC 3395  
 QY 687 AleuGlyLeuTYrTrpThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsn 707  
 Db 3394 GCTGGGACTGTGAGACTGAGAGAGGCTTGTGACATCTTGAAGATTTCCCGGATCTCAACTC 3335  
 QY 707 rValLeuTrpGlyAlaGluGluArgIuAspTYrValProTYrArgValProAsnAsnAsnLe 727  
 Db 3334 TGTGCTCTGGGAGCTGAGAGAGGAATGGTCCCTACCGGGTCCCAAAATTAATCTT 3275  
 QY 727 uProIleProGluArgTYrLeuSerProAspAlaThrVal----- 740  
 Db 3274 GCCCATCCCTGAACGCTACCTTTCGCCAGATGCCACGGT-GAGGCTACAGCTGCTGAA 3216  
 QY 740 -----  
 Db 3215 AGGGCAGAGGAGACAGCTGACCTCGGGGTCTGTGTCTTGGGCTTGGGGTGGGGCT 3156  
 QY 740 -----  
 Db 3155 GACGGTCTGAATCCAGACGCTGAGGCTTGGGGTGTGGGGACAGGGATCTGTGCA 3096  
 QY 740 -----  
 Db 3095 GTACTGTGTGAAGCTTCAATGAGAGGTGATCGGGCTAGGTTGGGATAGTGGCCGAGCT 3036  
 QY 741 -----SerThrGluValArgAlaIleIle 748  
 Db 3035 GCAGCCCTGGCTCACACGCTGTGGCACTCCAGAGTATCCAGAGAGTCCGGCCATCAT 2976  
 QY 748 eAlaTrpMetGluLysAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLe 768  
 Db 2975 TGCCTGATGAGAAAGAACCTTGTGTGTGGAGCAAAATCTGAACGCGCGGAGGGGCT 2916  
 QY 768 uValSerTYrProTYrAspMetAlaArgThrProThrGlnGluIuLeuValAlaAla 788  
 Db 2915 AGTATCTAACCTTCAAGATATGGCCGACGCTTACCCAGAGACAGCTGTGCGCCAGC 2856

QY 788 aMeAlaAlaAlaArgLysIleuAspGluuAspGluValSerGluValIleuGlnIleuThrProAs 808  
 Db 2855 CATGGCGACGACCCGGGGGAGATGAGACGAGAGTCTCGAGGCCAGAGAGCTTCAGA 2796  
 QY 808 PHIsAlaIleuPheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeuThrG1 828  
 Db 2795 CCAAGGCATCTCCGGGTGGCTGGCATCTCTGGCTCCGACACCTCACTTGGACGA 2736  
 QY 828 uProTyrArgGlyGlyCysGlnAlaGlnAspTyrThrGlyGlyMetGlyIleValAlaGln 848  
 Db 2735 GGCCTTACCGCGAGGCTGCCAGAGCCAGAGCTACACCGCGGCATGGGCATCGTCAACGG 2676  
 QY 848 yAlaLeuTyrAsnProArgTrpArgIleThr----- 857  
 Db 2675 GGCCMACTGAAACCCCGAGCCGAGAGTGAAGTCACTCGGAGGGGCTGTGGCGGGGCC 2616  
 QY 858 -----IleAsnAsp 861  
 Db 2615 TGGTCCGAGAGGGGCTGACTTTGGTCTGATCTGTCCTCCGCGCAGCTATCATGACTT 2556  
 QY 861 eSerTyrLeuHisThrAsnCybLeuGluLeuSerPheTyrLeuGlyCysAspLysPhePr 881  
 Db 2555 CAGTTTACCTGCATACCAACTGCTCGAGCTCTCTTCTACCTGGGCTGTGACAAGTTCCC 2496  
 QY 881 oHisGluSerGluLeuProArgIleuTrpGluAsnAsnLysGluAlaLeuLeuThrPhe 901  
 Db 2495 TCAATGAGAGTGAAGTGCCTCCCGAGAGTGAAGAACAAAGAGGCGTGTCTCACTTCAT 2436  
 QY 901 tGluGln----- 903  
 Db 2435 GGAAGCAGGTGGGGTGGCTAGGGCAATGCTGGGGAGAGAGGCTGCACAGGCTCTGGAT 2376  
 QY 903 ----- 903  
 Db 2375 GGGCGGAGGAGGAGGAGCGGACCACTTGACCTTCTGAGAGACGAGCCCTCACTGC 2316  
 QY 904 -----ValHisArgGlyIleLeuGlyValValThrAspGluGlnGlyIleProIleA 921  
 Db 2315 TTCCCTTAGGTGACCGGGCGGCTTAAAGGGGTGGTGAAGAGAGCAAGGCAATCCCATGG 2256  
 QY 921 IaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAla----- 937  
 Db 2255 CCAAGCGCACCATCTCTGTGAAGTGCATTATATCAGCGCGTGAAGACAGG--TACCTAGTGT 2197  
 QY 937 ----- 937  
 Db 2196 GCACACCTTACCCCATCTTCTGAGGAGAGACCCGCAAGAGGTGGGGCTTGAGGA 2137  
 QY 937 ----- 937  
 Db 2136 ACTCAGCGAGAGGTAGTCTGGGAGACCTGGGGGCGAAATTCAAGAGGAGAGCGGT 2077  
 QY 937 ----- 937  
 Db 2076 GCTGGGGGCGGAACTCAGAGGGGGAGGGGGCTGGGGGCAAGACTGATGGAGGGT 2017  
 QY 938 -----SerGlyG 940  
 Db 2016 GGGGGCTGGAGGGGCGCTCTGGGGGAGCGCGATCTCTTCCCTCCGACGAGTGTG 1957  
 QY 940 lYAspTyrTrpArgIleLeuAsnProGlyIleuTyrArgValThrAlaHisAlaGluGlyT 960  
 Db 1956 GTGATTACTGGCGAATCTTAAACCGGGTGAAGTACCGGTGAACGCCACGCGAGGGCT 1897  
 QY 960 yThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsn 980  
 Db 1896 ACAACCGGAGCGCAACCTGCAATGTATGACTATGCAATCGGGCCACTCAGTGCACCT 1837  
 QY 980 heIleLeuAlaArgSerAsnTrpLysArgIleArgGlyIleMetAlaMetAsnGlyAsnA 1000  
 Db 1836 TCATCTCGGTCTGCTCCAACTGGAAGCGCATCCGGGAGATCATGGCCATGAACGGGAACC 1777  
 QY 1000 rGProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLysGlnG 1020

Db 1776 GGCCTTATCCACATAGAACCATCGGCTCTATGACCCCCCAACAGGACGGCTGACG 1717  
 QY 1020 lArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnA 1040  
 Db 1716 AGCGAGCGCTTAAACAACCGGCTGCGGCTTGCGGACAGATGGGGCTGGCGCTCAAG 1657  
 QY 1040 lAthrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrT 1060  
 Db 1656 CCACACACACCTTAGGCCCCCACAACATGTGCTCTCCAGCGCTGCCCCCTGCCACCA 1597  
 QY 1060 hLeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluG 1080  
 Db 1596 CCTTGAGCACTATACATAGACCTTGGGGCTCTTACCGCCACACCGCTGGGAGG 1537  
 QY 1080 lSerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProG 1100  
 Db 1536 AGTCGAGACTGAGACTTACACAGAGGTGTGACAGATTGGGACCGAGGTGGAGCCG 1477  
 QY 1100 lPheGlyThrLysValGluProGluPheGluThrGluLeuGluProGluPheGluThrG 1120  
 Db 1476 AGTTTGGGACCAAGGTGAGGCCGAGTTTGAAGACCAAGTTGAGCTTGAAGTTCGAGGCC 1417  
 QY 1120 lLeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluIleAlaThrG 1140  
 Db 1416 AGCTGAAACCGGATTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCACTG 1357  
 QY 1140 lYglnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158  
 Db 1356 GCCAGGCAATTCCTTCAACAAGTAGAGCTTACACAGTGAACCTTGGGGACTTC 1301

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 Job time : 2878 secs

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OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 1, 2006, 00:05:23 ; Search time 519 Seconds

(without alignments)

6175.889 Million cell updates/sec

Title: US-10-642-946-3

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Delop 6.0, Delext 7.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: 4741290

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database: Published Applications NA New:

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.Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	6272	100.0	3935	8 US-11-266-748A-22822	Sequence 22822, A
2	3744	59.7	2268	8 US-11-266-748A-184697	Sequence 184697, A
3	3744	59.7	2268	8 US-11-266-748A-192181	Sequence 192181, A
4	3421	54.5	2065	8 US-11-266-748A-184695	Sequence 184695, A
5	3421	54.5	2065	8 US-11-266-748A-192179	Sequence 192179, A
6	2125	33.9	1193	8 US-11-266-748A-98157	Sequence 98157, A
7	2125	33.9	1193	8 US-11-266-748A-150968	Sequence 150968, A

8	2066	32.9	2490	9 US-11-376-589-1	Sequence 1, Appl1
9	1946	31.0	1437	8 US-11-266-748A-192182	Sequence 192182, A
10	1946	31.0	1437	8 US-11-266-748A-226230	Sequence 226230, A
11	1735.5	27.7	2452	8 US-11-242-505A-22	Sequence 22, Appl1
12	1733	27.6	2388	6 US-10-196-749-457	Sequence 457, Appl
13	1731	27.6	2205	8 US-11-242-505A-23	Sequence 23, Appl
14	1453	23.2	1184	8 US-11-266-748A-226229	Sequence 226229, A
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19	1167	18.6	1003	8 US-11-266-748A-184696	Sequence 184696, A
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21	1150	18.3	1008	8 US-11-266-748A-184698	Sequence 184698, A
22	1150	18.3	1008	8 US-11-266-748A-192184	Sequence 192184, A
23	1120	17.9	1003	8 US-11-266-748A-192189	Sequence 192189, A
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25	988	15.8	557	8 US-11-301-554-918	Sequence 918, Appl
26	916	14.6	1751	8 US-11-266-748A-256837	Sequence 256837, A
27	916	14.6	1751	8 US-11-266-748A-317354	Sequence 317354, A
28	897.5	14.3	2181	8 US-11-266-748A-26926	Sequence 26926, A
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35	868	13.8	520	8 US-11-266-748A-289924	Sequence 289924, A
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37	780.5	12.4	1000	8 US-11-266-748A-189986	Sequence 189986, A
38	743	11.8	1168	8 US-11-266-748A-9811	Sequence 9811, Appl
39	686	10.9	415	8 US-11-266-748A-64109	Sequence 64109, A
40	686	10.9	415	8 US-11-266-748A-66941	Sequence 66941, A
41	636	10.1	2362	6 US-10-539-228-230	Sequence 230, Appl
42	636	10.1	433	8 US-11-266-748A-169326	Sequence 169326, A
43	633.5	10.1	5188	6 US-10-669-920-1128	Sequence 1128, Appl
44	633.5	10.1	2085	6 US-10-511-937-395	Sequence 395, Appl
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#### ALIGNMENTS

RESULT 1  
US-11-266-748A-22822  
; Sequence 22822, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnson, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptional Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266, 748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3



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## RESULT 2

US-11-266-748A-184697  
; Sequence 184697, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266, 748A  
; PRIORITY FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
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; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
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; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (94)..(149)  
; OTHER INFORMATION: n is a, c, g, or t  
; US-11-266-748A-184697  
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US-10-642-946-3 (1-1158) x US-11-266-748A-184697 (1-2268)

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DB	225	CCTGGAGGGCGCCCGAGACGGCTGACCGAGACGAGATCGAGAGTCTTCCAGGGC		284
QY	41	PhleuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProPro		60
DB	285	TTCTGTCTAGAGCTAAGACCTGAGCCCGGAGAGACGCTGAGAGCCCGCGCTCTCC		344
QY	61	GIUPROTHRPROARGVALARGLVSAAGLNAAGLYGLYBPARGLYLYSARGPROGLY		80
DB	345	GAGCCACCCCGGGGTCCGAAAGCCAGCGGGGGGCAAGCCAGGGAAGCGGCCAGG		404
QY	81	THRALAALAGLVALPROPROGLIULYSTRILYSASPGLYGLYLYSGLYLYSASP		100
DB	405	ACGGCCGAGAGTGTCTCGGAAAGACCAAGACAAAGGAGAAAGGCAAGAAAGAC		464
QY	101	LYSGLYPROLYVALPROLYSGLUSERTLEUGLUGLYSERPROARGPROLYSGLY		120
DB	465	AAAGGCCCAAGGTGCGCAAGAGTCTTGGAGGGGTCCCGCGCGCCCAAGAGGGG		524
QY	121	LYSGLYLYBPORPROLYSALATHRLYSLYBPORLYSGLYLYSBPORPROLYSALATHRLYS		140
DB	525	AAGGAAGAGCACCCCAAGGCCACCAAGAACCCCAAGAGAGACCTTAAGGCCACCAAG		584
QY	141	LYSPLYSGIUGLUPROPROLYSALATHRLYSLYBPORLYSGLYLYSBPORPROLYSAL		160
DB	585	AAGCCCAAGAGAGAGCCCAAGAGCCCAAGAGACCCCAAGAGAGAGCAACCAAGGCG		644
QY	161	THRLYLYBPORPROSERGLYLYSARGPROPROILEUVALPROSERGLUTHLEUGLU		180
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QY	181	TRPPOLEUPROPROPROSERPROGLYPROGLUGLULEUPROGLINGLUGLYVAL		200
DB	705	TGGCCACTGCCCCCACCACCCCAAGCCTTGCGCCCGAGAGCTACCCAGAGGGAGGGCG		764
QY	201	PROLEUSERASNAANTTRPGINASNPROGLYGLUGLUTHRLYVALGLIUALAGLNGLUIS		220
DB	765	CCCTCTCAATATACCTGGAGAT-CCAGAGAGAGACCCCATGTGAGGACGGAGACAC		823
QY	221	GLNPROGLUPROGLUGLUGLUTHRLUGLUNPROTHRLYBPTRYASNAPGINILEGLU		240
DB	824	CAGCCCTGAGCGGAGAGAGGAGACCGAGCAACCACTGACTACATGACCAAGTCGAG		883
QY	241	ARGGLYASPTYRGILUASPHEGILUTYRLIARGARGLNYAGLINPROARGPROPROPO		260
DB	884	AGGAGAGACTATAGAGACTTTAGTACATTGCGCGCAAGACCCCAAGCCACCCCA		943
QY	261	SERARGARGARGPROGLUARGVALITRPPROGLUPROPROGLUGLULYSALAPROAL		280
DB	944	AGGAGAGAGGAGGCGCCGAGCGGGTCTGGCCAGAGACCCCTGAGAGAAAGCCCGGCG		1003
QY	281	PROALAPROGLUGLUGLUGLILEGLUPROPROVALLYBPORLEULEUPROPROLEUPRO		300
DB	1004	CCAGCCCCCGAGAGAGGATTTGAGCTCTGTGAACCTCTGTGCCCCCGCGCCCT		1063
QY	301	ASPTRYGLYASPTYTRYVALIILEPROASNTRYASAPWECASPTRYTRYRPHGLYPRO		320
DB	1064	GACTTAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT		1123
QY	321	PROPROGLIULYBPORASPALAGLARGINTHRASPGLUGLULYSGIUGLULEUYS		340

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QY	361	GLYLYSASPSTLYSGLUPROARGLYSGLYGLUGLULEUGLUGLUGLUTHRTRPOTHR		380
DB	1244	GGCAAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		1303
QY	381	GIULYSVALYSBPORPROILEGLYMERGLUSERHISARGILEGLUASPANGINILE		400
DB	1304	GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTGCACACCGATTAAGAGACAAACAGATC		1363
QY	401	ARGALASERSEMERLEUARGHISGLYLEUGLYVALAGINARGGLYARGLEUASNMERGIN		420
DB	1364	CGAGCTCTCCATGCTCGGCCACCGCTGGGGGAGACAGCGCGCGCTCAACATGCAAG		1423
QY	421	THRGILYATHRGILUASPSPTRYTRYRASPGLYATRPYSAALAGLUASPAPALARG		440
DB	1424	ACCGTGCACCTGAGAGAGACTACTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		1483
QY	441	THRGINTRPILEGLUVALASPTHRARGTRTHRARGPHETHRGLYVALILETHRGLN		460
DB	1484	ACCCAGTGAATAGAGGTGAGACCAAGAGAGACTACCCCGTTCAACAGCGTCAACCCAG		1543
QY	461	GLYARGASERSETHIISASPAPHEVALTHRTRPHEPHEVALGLYPHESERASN		480
DB	1544	GGCAGAGACTCGAGATCAATGACATTTTGACACACTTCTTGAGGCTTCAGCAANT		1603
QY	481	ASPSEGINTHRTTRVALMERTYRTHRASNGLYTRYGLUGLUMERTPHEHISGLYASN		500
DB	1604	GACACCCAGACATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT		1663
QY	501	VALIAPLYSAPTRHPRIVALYSEUSERTLEUPROGLUPROVALIVALIARGPHEILE		520
DB	1664	GTGGAACAAGGACACCCGTGTGATGAGTCCAGAGCGGTGTGTGTGTGTGTGTGTGTGT		1723
QY	521	ARGILEYRPROLEUTHRTRASNGLYSEUSERTLEUCYSMERARGLEUGLVALLEUGLYCYS		540
DB	1724	CGCATCTACCACTACCTGAGATGAGAGCTGTGCATAGCGCTGAGAGTGTGGGGTGC		1783
QY	541	SERVALIAPROVALITYRSETRYTRYRAGLNASGLIUALIATHRASNAPLEU		560
DB	1784	TCTGTGCCCCCTGTACTACGACTACCAACAGATGAGTGTGTGTGTGTGTGTGTGTGTGT		1843
QY	561	ASPHEARGHISISERTYRILYASPMERARGINLEUMERTLYVALIANGLUGLU		580
DB	1844	GATTTCCGGCACACAGCTACAAAGACATGCCCGCTCATGAMAGTGTGTGAACGAGGAG		1903
QY	581	CYSPTOTRILETHRARGTRHTRYRSERTLEUGLYLYSERTSERARGLYLEUYSILETRY		600
DB	1904	TGCCACCATACCCGACCTTACAGCCTGGGCAAGAGTCTACAGAGCTCTCAAGATCTAT		1963
QY	601	ALAMETGLIULESERASPNPROGLYGLIUNISGLIULEUGLYGLUPROGLUPHEARGTYR		620
DB	1964	GCCATGGAGATCTAGACACCTCTGGGAGCATGAACCTGGGGAGCCGAGATTCCGCTAC		2023
QY	621	THRALAGLYLLEHISGLYASNGLIUALLEUGLYARGLULEULEULEULEULEUMERTGIN		640
DB	2024	ACTGCTGGATTCATAGGCAACAGAGTGTGTGGCCAGAGCTGTCTGTCTGTCTGTCTGT		2083
QY	641	TYRLEUCYARGGLUTYRARGASPGLYASNPROARGVALIARGSERLEUVALGINASPTRH		660
DB	2084	THACTGTGCGAGAGTACCGCATGAGAACCACTGTGTGCGACCTGTGTGAGAGACACA		2143
QY	661	ARGILEHISLEUVALPROSERLEUASNPROASPGLYTRYGLIUALIALAAGLIMERTGLY		680
DB	2144	CGCATTCACCTGTGTCCCTCACTGAACCTGTATGCTACGAGTG-CCAGCGCAGATGGCG		2202
QY	681	SERGLUPHEGLYASNTRPALALEUGLYLEUTRTHRGLUGLUGLYPHEASPTILEPHEGLU		700
DB	2203	TCAGAGTTTGGAACTGGGCGCTGGAGCTGTGAGCTGAGAGGCGCTTTGACATCTTTGAG		2262



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Qy 481 AAPPSEGINThrTTPyAlMeTyrThraAngLYTyrGlulMeThrPheHISglYasn 500  
Db 1604 GACAGCAGACATGGGTGATGTATACACCAACGCGCTATGAGAAATGACCTTTCATGGGAAAC 1663  
Qy 501 VALAAPPlyAspThrProValleuSerGluLeuProGluProValValAlaThraPhele 520  
Db 1664 GTGGACAAAGACACACCGGTGTGAGTGTCCAGACCGGTGTGGCTGTTCATC 1723  
Qy 521 ATGILETyrProleuThrTTPaAngLYSerLeuCYMeTyrGlulValleuGlyCys 540  
Db 1724 CCGATCTACCACTCACTGGATGACGCTGTGTGATCGCTGGAGGTGTGGGTGC 1783  
Qy 541 SerValAlaProValTyrSerTyrTyrAlaGlnAserGluValAlaThraPheleu 560  
Db 1784 TCTGTGGCCCCCTGTCTACAGCTACTACGACAGAAAGAGTGTGTGCCACCATGACCG 1843  
Qy 561 AAPPPhaArgHISerTyrLYsAspMetArgGlnLeuMetLYsValValAAsngluGlu 580  
Db 1844 GATTTCCGGACACCACTCAAGACATGCCCACTCAATGAAGTGTGAACAGAGAG 1903  
Qy 581 CySProThrIleThraArgThrTyrSerLeuGlyLYsSerSerArgGlyLeuYsIleTyr 600  
Db 1904 TGGCCACCATCACCCGCACTTACAGCTGGGCAAGAGCTCACAGGCTCAAGATCTAT 1963  
Qy 601 AlAmetGluIleSerAspAsnProGlyGluHISgluLeuGlyGluProGluPheArgTyr 620  
Db 1964 GCCATGAGATCTCAACACCACTCGGGAGCATGAACCTGGGGAGCCCAAGTCCCTAC 2023  
Qy 621 ThrAlaGlyIleHISglYAsngluValleuGlyArgGlyLeuLeuLeuLeuMetGln 640  
Db 2024 ACTGCTGGATCATGAGCAACAGAGTGTGGCCGAGAGCTGTGCTGCTCTCATGCAAG 2083  
Qy 641 TTYLeuCYsArgGlyuTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
Db 2084 TACCTGTGCCAGAGATACCGCGATGGGAACCCACGTGTGGCGAGCTGTGGCAGACACA 2143  
Qy 661 ArgIleHISleuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680  
Db 2144 CGCATCACCCTGTGTGCTCTCATGAACTCGATGGCTTACAGAGG-GCACGCGAGATGGGC 2202  
Qy 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700  
Db 2203 TCAGATTTGGGAATCTGGGCGCTGGAGCTGTGACCTGAGAGGCTTTGACATCTTGAG 2262

RESULT 4  
US-11-266-748A-184695  
/ Sequence 184695, Application US/11266748A  
/ Publication No. US20060134663A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Harkin, Paul  
/ APPLICANT: Johnston, Patrick  
/ APPLICANT: Mulligan, Karl  
/ TITLE OF INVENTION: Transcription Microarray Technology and  
/ TITLE OF INVENTION: Methods of Using the Same  
/ FILE REFERENCE: 55815-0102 (319189)  
/ CURRENT APPLICATION NUMBER: US/11/266,748A  
/ CURRENT FILING DATE: 2005-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105479.2  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105482.6  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105483.4  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105507.0  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105485.9  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: EP 04105484.2  
/ PRIOR FILING DATE: 2004-11-03  
/ PRIOR APPLICATION NUMBER: US 60/662,276  
/ PRIOR FILING DATE: 2005-03-14

/ PRIOR APPLICATION NUMBER: US 60/700,293  
/ PRIOR FILING DATE: 2005-07-18  
/ NUMBER OF SEQ ID NOS: 483996  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 184695  
/ LENGTH: 2065  
/ TYPE: DNA  
/ ORGANISM: Homo Sapiens  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: (182)..(1884)  
/ OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-184695

Alignment Scores:  
Pred. No.: 5,95e-163 Length: 2065  
Score: 3421.00 Matches: 647  
Percent Similarity: 95.94 Conservative: 0  
Best Local Similarity: 95.94 Mismatches: 28  
Query Match: 54.5% Indels: 1  
DB: Gaps: 0

US-10-642-946-3 (1-1158) x US-11-266-748A-184695 (1-2065)

Qy 447 AAPPThraArgThrThraPheThrGlyValIleThraGlnLYsArgAspSerIle 466  
Db 40 GACACAGAGAGATACCCGCTTACAGGCGTATCACCCAGGAGACATCCAGCATC 99  
Qy 467 HISAspAspPheValThrThraPheValGlyPheSerAsnAspSerGlnThrTTPyAl 486  
Db 100 CATGACGATTTGTGTACACACTTCTGTGGGCTTCAGCAATGACAGCCAGACATGGGTG 159  
Qy 487 MetTyrThraAngLYTyrGluLeuMetThrPheHISglYAsnValAspLYsAspThrPro 506  
Db 160 ATGTACACCAAGGCTATGAGAAATGACTTTCATGGGAAGTGGACAAAGACACACCC 219  
Qy 507 VALleuSerGluLeuProGluProValValAlaArgPheIleArgIleTyrProleuThr 526  
Db 220 GTGCTGAGTGAAGCTCCAGAGCGGTGTGGCTGTTCATCGCATACCACTCACCC 279  
Qy 527 TTPaAngLYSerLeuCYsMetArgLeuGluValleuGlyCYsSerValAlaProValTyr 546  
Db 280 TGGAAATGGCAGCTGTGTGATGCTGCGCTGGAGGTGTGGGTGTGTGCCCCCTGTCTAC 339  
Qy 547 SerTyrTyrAlaGlnAsngluValAlaThraAspAspPheArgHISHisSer 566  
Db 340 ACTTACTACGACAGAAATGAGGTGTGTGCCACCATGACTGATTTCCGACACACAGC 399  
Qy 567 TTYLYsAspMetArgGlnLeuMetLYsValValAAsngluGluCYsProThrIleThraArg 586  
Db 400 TCAAGGACATCGCCAGCTCATGAAGGTGTGAACGAGAGTGGCCCACTACCCGCGC 459  
Qy 587 ThrTyrSerLeuGlyLYsSerSerArgGlyLeuLYsIleTyrAlaMetGluIleSerAsp 606  
Db 460 ACTTACAGCTGTGGCAAGAGCTCACAGAGCTTCAAGATTTAGCCATGAGATCTGAGC 519  
Qy 607 AAsnProGlyGluHISgluLeuGlyGluProGluPheArgTyrThraGlyIleHISglY 626  
Db 520 AACCTGTGGGACATGAAGTGTGGGAGCCCGAGTTCCGTACACTGCTGGATCCATGGC 579  
Qy 627 AAsngluValleuGlyArgGluLeuLeuLeuLeuMetGlnTyrLeuCYsArgGlyTyr 646  
Db 580 AACGAGGTGTGGGCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 639  
Qy 647 ArgAspGlyAsnProArgValArgSerLeuValGlnAspThrArgIleHISleuValPro 666  
Db 640 CGCGATGGGAACCACTGTGTGCGAGCCGTGGAGGACACACGATTCACCTGAGTGGCC 699  
Qy 667 SerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGlySerGluPheGlyAsnTrp 686  
Db 700 TCATGTAACTCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759  
Qy 687 AlAleuGlyLeuTrpThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsn 706

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Db 760 GCCTGGAGTGTGAGTGAAGAGGCTTTGACATCTTTGAAGTTCCCGGATCTAC 819
Qy 707 SerValLeuTrpGlyAlaGluGluValArgLeuTrpValProAsnAsn 726
Db 820 TCTGTCTCTGGGAGCTGAGAGGAAATGGTCCCTACCGGGTCCCAACAATAC 879
Qy 727 LeuProIleProGluArgTrpLeuSerProAspAlaThrValSerThrGluValArgAla 746
Db 880 TTCCCATCCCTGAACCTTACCTTTCCGAGATGCCAGGATCCAGAGAGTCCGGGCC 939
Qy 747 IleIleAlaTrpMetGluLeuAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlu 766
Db 940 ATCATTCCTGGATGGAGAAAGAACCTTCCTGCTGGAGCAAACTGAAACGGCGGAG 999
Qy 767 ArgLeuValSerTrpProTrpAspMetAlaArgThrProThrGluGluLeuVal 786
Db 1000 CGGCTAGTATCTTACCCCTACGATATGCGCGCTACCCAGAGAGAGCTGTGGCC 1059
Qy 787 AlaAlaMetAlaAlaAlaArgGlyValAspGluAspGluValSerGluAlaGluThr 806
Db 1060 GCAGCATGGCAGACGCCGGGGAGAGATGAGACAGAGTCTCCGAGGCCAGAGACT 1119
Qy 807 ProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeu 826
Db 1120 CAGACACAGCCCATCTTCGGGTGGCTTGCCATCTCTCCGCTCCGACACTCACCCTTG 1179
Qy 827 ThrGluProTrpArgGlyGlyCysGluAlaGluAspTrpThrGlyMetGlyLeuVal 846
Db 1180 ACCGAGCCCTACCGCGAGGCTGCCAAGCCAGACTACACCGCGCATGGGATGTC 1239
Qy 847 AsnGlyAlaAlaArgTrpAsnProArgThrGlyThrIleAsnAspPheSerTrpLeuHisThr 866
Db 1240 AAGGGGACCAAGTGAACCCCGGACCGGACATACATACCTTACCTTCCGATACC 1299
Qy 867 AsnCysLeuGluLeuSerPheTrpLeuGlyCysAspLysPheProHisGluSerGluLeu 886
Db 1300 AACTGCTGAGAGCTCTCTCTTACCTGAGCTGACAGTCTCCCTCATGAGAGTGAAGCTG 1359
Qy 887 ProArgGluTrpGluAsnAsnLeuValLeuLeuThrPheMetGluGluValHisArg 906
Db 1360 CCGCGGAGTGGAGAAACAACAAGAGCGCTGCTCATTCATGAGAGGTCACCGC 1419
Qy 907 GlyIleLeuGlyValValThrAspGluGluGlyIleProIleAlaAsnAlaThrIleSer 926
Db 1420 GGCATTAAAGGGGTGGTGAAGCAGCAGCAAGCATCCCATTCGCAACGACCATCTCT 1479
Qy 927 ValSerGlyIleAsnHisGlyValLysThrAlaSerGlyValAspTrpArgIleLeu 946
Db 1480 GTGAGTGGCTTAATACCGCGCTGAAGACAGCCAGTGGTGTATTACTGGCAATCTTG 1539
Qy 947 AsnProGlyValTrpArgValThrAlaHisAlaGluGlyTrpThrProSerAlaLysThr 966
Db 1540 AACCCGGGTGAGTACCGCGTGAACAGCCACGCGAGGGTACACCCCGAGCGCAAGACC 1599
Qy 967 CysAsnValAspTrpAspIleGlyAlaThrGluCysAsnPheIleLeuAlaArgSerAsn 986
Db 1600 TCGAAATGTGACTATACATCGGGGACACATGCAATCTTCTCGCTCCCTCCAC 1659
Qy 987 TrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArgProIleProHisLeuArg 1006
Db 1660 TGGAGCGCTTCCGGAGATCATGGCCATGAAGGAAACGGGCTTATCCACATAGAC 1719
Qy 1007 ProSerArgProMetThrProGluGluArgArgLeuGluGluValArgLeuGluHisArg 1026
Db 1720 CCATCGCGCCCTATGACCCCAACAATCGACGCTGATCAGGAGCGCTTACACACCGC 1779
Qy 1027 LeuArgLeuArgAlaGluMetArgLeuArgArgLeuAsnAlaThrThrLeuGlyPro 1046
Db 1780 CTGGGCTTCGGGACAGATGCGCTGCGGCTCAACCCNNNNNNNNNNNNNNNNNNNN 1839
Qy 1047 HisThrValProProThrLeuProProAlaThrThrLeuSerThrTrpIleGlu 1066
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Db 1840 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1899
Qy 1067 ProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGluSerGluThrGluThrTyr 1086
Db 1900 CCTGGGGCTCTATACCGCAACACCGCTGCTGGAGAGAGTGAAGTGAACCTTAC 1959
Qy 1087 ThrGluValValThrGluPheGlyTrpThrGluValGluProGluPheGlyThrLysValGlu 1106
Db 1960 ACAGAGTGTGACAGAAATTTGGGACCGAGTGAAGCCGAGTTTGGGACCAAGGTGAA 2019
Qy 1107 ProGluPheGluThrGluLeuGluProGluPheGluThrGluLeu 1121
Db 2020 CCGGA-TTTGAACCAAGTTGAGCTTGAAGCTTGAACCTACTG 2063

RESULT 5
US-11-266-748A-192179
; Sequence 192179, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192179
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1822)..(1884)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-192179

Alignment Scores:
Pred. No.: 5,95e-163 Length: 2065
Score: 3421.00 Matches: 647
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 28
Query Match: 54.5% Indels: 1
DB: 8 Gaps: 0

US-10-642-946-3 (1-1158) x US-11-266-748A-192179 (1-2065)
Qy 447 AspThrArgArgThrThrArgPheThrArgValIleThrGluGlyArgAspSerIle 466
Db 40 GACACCGAGAGGCTACCGGTTTACAGGCGTATCACCAGGAGAGACTTCACACTC 99
Qy 467 HisAspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTrpVal 486
Db 100 CATGACGATTTTGTGACCACTTCTTGTGGGCTTACGCAATGACAGCCAGACATGGTG 159
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Db 310 TTCTGCGCTTCAATGCATGAAGACCTTAGGGTGGAGGAGCAGAGAACGACGACCGCAC 369  
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Db 370 CACACAGGCGCCACGAACCTCCCAAGAGGCCATCAAGCCCAAGAAAGGCTCCCAAGAG- 426  
Qy 371 GtUGtUleuGtUglUGtUtrPthrProthRgLYs----- 382  
Db 427 GAGAAgTtAGTtGCAGAGACCGCTCCACCGATMAAATAGCAACAGAAAAGCAGAGAA 486  
Qy 382 ----- 382  
Db 487 AGCAAGATCTTGAAAGCTGCGACAGATGATGATGATGATGATGATGATGATGATGATGAT 546  
Qy 383 -----VallyeCySPPrpOileGlyMeCgUserHisArgIleGluAAspAAsnGlnIle 400  
Db 547 GTCAGAGAGAGTGGCCACCTCTGTGTGTAACATTAATAATCAAGACTTCCAGCTG 606  
Qy 401 ArgAlAsSerSerMetLeuAArgHsGlyLeuGlyValAglInArgGlyAArgLeuAAsnGln 420  
Db 607 CATGCTCCACATCGAAGCGTTATGGCTGGAGGCCACCGGGGAGACTCAACATCCAG 666  
Qy 421 ThrGlyAlaThrGluAAspAAspTYrTYrAspGlyAlaATrPCyAlaGluAAspAlaArg 440  
Db 667 GCAGGCAATTAAAGAAATGACTTTTACGATGGGGCTGTGTCTGTGTGTGTGTGTGTGTGT 726  
Qy 441 ThrGlnTrpIleGluValAAspThraArgArgThrThraArgPheThrglyValIleThrgln 460  
Db 727 CATCATGTGATCCAGAGGTGATGCGCGCGCTGACCAAGTTCCAGGGGTCAATACCCAA 786  
Qy 461 GlyAArgAspSerSerIleHisAAspAAspPheValThrThraPhePheValGlyPheSerAAsn 480  
Db 787 GGAAGAACTCTCTGCTGCTGAGTACTGGGTGATCATCTTAATAAGTCATGTGTGAGCAAT 846  
Qy 481 AspSerGlnThrTrpValMetTYrThraAsnGlyTYrGluGluMetThraPheHisGlyAAsn 500  
Db 847 GACAGCACACATGGGTACTGTGAAGAAATGATCTGGCAGCATGATATTGAAGAAAC 906  
Qy 501 ValAAspLYhAspThrProValLeuSerGlyLeuProGluProValValAlaArgPheIle 520  
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Qy 521 ArgIleTYrProLeuThrP-----AAsnGlySerLeuCyMetAArgLeuGluValIle 538  
Db 967 CGGATTAACCTCAAGTCTGTGTTGATTAACGGAAGCATCTGCATGAGATGAGATCTTG 1026  
Qy 539 GlyCySerValAlaProValTYrSerTYrTYr---AlaGlnAAsnGluValAlaIleThr 557  
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Qy 558 AspAAspLeuAAspPheArgHsHisSerTYrLYhAspMetAArgGlnLeuMetLYsVal 577  
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Qy 578 AAsnGluGlyProThrIleThraArgThrTYrSerIleGlyLYsSerSerAArgLYleu 597  
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Db 1207 AATTTATATGCGGTAGATCTCTGACACCTCTGGGGAACATGAATGTGTGAGCCGAG 1266  
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Qy 638 LeuMetGlyTYrLeuCyAspArgLYlyrAArgAAspGlyAAsnProArgValAAspSerLeuVal 657  
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Qy 658 GlnAAspThraArgIleHisLeuValProSerLeuAAsnProAAspGlyTYrGluValAla 677  
Db 1387 GAGAGACTCGAATCCACATTTACCTCTCCATCTGATGCTATGAGAAAGGCTTAT 1446

Qy 678 GlnMetGlySerGluPheGlyAAsnTrpAlaLeuGlyLeuTrpThrgluGluGlyPheAAsp 697  
Db 1447 GAGAGAGCTTCCAGATTTGGAGAGCTGTCTGGGAGCTTGGACCTCATATGATGCATGCAT 1506  
Qy 698 IlePheGluAAspPheProAAspLeuAAsnSerValIleTrpGlyValAglUGtUtrAArgLYsTPr 717  
Db 1507 ATCAACAACAATCTTCGGATTTAACTGCTGCTGTGGAGGCAAGAGACGACGAAT 1566  
Qy 718 ValProTYrAArgValProAAsnAAsnLeuProIleProGluAArgTYrLeuSerProAAsp 737  
Db 1567 GCCCAAGAGAGGTCCCAACCACTACATTCATCCATGAGTTCCTGTGTGTGTGTGTGTGTGT 1626  
Qy 738 AlaThraValSerThrgluValAArgAlaIleIleAlaTrpMetGlyLYsAAsnProPheVal 757  
Db 1627 GCCACAGTGGCCACAGAGACCAAGAGCGCATGCTGTGATGAGAAATCCCGTTTGTG 1686  
Qy 758 LeuGlyAlaAAsnLeuAAsnGlyGlyGluAArgLeuValSerTYrProTYrAAspMetAlaArg 777  
Db 1687 CTGGAGGCACTTACAGGGGGGTGAGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1746  
Qy 778 ThrProThrgluGluGluLeuValAlaAlaMetAlaAlaAArgGlyGluAAspGlu 797  
Db 1747 TCCCTGTGAAGACCCAG----- 1764  
Qy 798 AspGluValSerGluAlaGlnGluThrProAAspHisAlaIlePheAArgTrpLeuAlaIle 817  
Db 1765 -----GAGCACACCCCAACCTGATGATCATGTGTTCCTGCTGCTGCTGCTGCTGCT 1812  
Qy 818 SerPheAlaSerAlaHisLeuThrLeuThrgluProTYrAArgGlyLYsGlnAlaGln 837  
Db 1813 TCTACGCTTCACTACCGCTCATGACAGATGCCAGAGAGGGAGGTGCCACACGAA 1872  
Qy 838 AspTYrThrglyLYsMetGlyIleValAAsnGlyAlaLYsTrpAAsnProAArgThrglyThr 857  
Db 1873 GATTTTCAGAGAGAGAGGACCCGTCATATGGGCTTCTGCGACACAGTGGCTGAAGT 1932  
Qy 858 IleAAspAAspSerTYrLeuHisTrpAAsnCYsLeuGluLeuSerPheTYrLeuGlyCYs 877  
Db 1933 CTAAAGATTTACGCTACCTCCATCAACAACTGCTTTGAGCTGTCCATCAACGTTGGCTGT 1992  
Qy 878 AspLYsPheProHisGluSerGluLeuProAAspGluTrpGluAAsnAAsnLYsGluAlaLeu 897  
Db 1993 GATTAATCCACACAGAGAGAGCTGCCGAGAAATGGAGAAATACCGGAGTCTTG 2052  
Qy 898 LeuThraPheMetGluGluValHisArgGlyIleLYsGlyValValThraAspGluGlnGly 917  
Db 2053 ATTGTCTCATGAGAGAGGTTTATGAGGATCAAGGATGATGAGATTTACAAAGG 2112  
Qy 918 IleProIleAlaAAsnAlaThrIleSerValSerGlyIleAAsnHisGlyValLYsThraAla 937  
Db 2113 AAAGGATTTCAATGCTCTCATCTCTGTGAAGGTGTTAACCATGACATCCGAGACGCC 2172  
Qy 938 SerGlyLYsAAspTYrThraArgIleLeuAAsnProGlyGluTYrAArgValThraAlaHisAla 957  
Db 2173 AGGATGGGATTAATCTGCGTCACTAAGAACCTGGGAAATATGTGTCAACAGCAAGGG 2232  
Qy 958 GtUGtUtyrThraProSerAlaLYsThraCYsAAsnValAAspTYrAAspIleGlyAlaThrgln 977  
Db 2233 GAAAGCTTATACCTTCCACCAAGAACTGCATGAGTTGGCTATGATATGGAGATTACTCG 2292  
Qy 978 CyAAsnPheIleLeuAlaArgSerAAsnTrpLYsArgIleAArgGluIleMetAlaMetAAsn 997  
Db 2293 TGTGACTTCACTCCCAAAAGCAACCTGCGTAGATTAAGAAATTTATGGAGCATTT 2352  
Qy 998 GlyAAsnArgProIleProHisIleAAspProSerAArgPrometThraProGlnGlnAArg 1017  
Db 2353 GGAAGCACCTGTACGCTA-----CCTTCAGG----- 2382  
Qy 1018 LeuGlnGlnAArgLeuGlnHisAArgLeuAAsnAArgAlaGlnMetAArgLeuAArg 1037  
Db 2383 -----CGCTGAAGCTGCGGGGAGCGGAAAGCGGCGACGCT 2418

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QY      1038 LeuAenAlaThrThrThreuglyProhiStrValProProThreupProAlaPro 1057
      |||||
Db      2419 GGGTACCTGTGCGACACTTGAAGACATAC-----CCGACCGG 2457
QY      1058 AlaThrThreuserThrThrile 1065
      |||||
Db      2458 TCGAATAAATAATCCACTCCAGTA 2481

RESULT 9
US-11-266-748A-192182
; Sequence 192182, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192182
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1063)..(1102)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-192182

Alignment Scores:
Pred. No.:      3,39e-89      length:      1437
Score:          1946.00      Matches:      365
Percent Similarity: 96.3%      Conservative: 1
Best Local Similarity: 96.1%      Mismatches: 14
Query Match:    31.0%      Indels:      0
DB:              8      Gaps:      0

US-10-642-946-3 (1-1158) x US-11-266-748A-192182 (1-1437)
QY      779 ProThGInGluGInleuAaAlaAlaMeValAlaAlaArgGlyGluAerGluAer 798
      |||
Db      28 CCCCCAAGAGAGAGAGCTGCTGGCGCAGCATGCGAGCAGCCCGGGGGAGATGAGGAC 87
QY      799 GluValSerGluAlaGInGluThrProAerPhAlaAlaIleheArgTrpLeuAlaIleSer 818
      |||
Db      88 GAGGTTCGAGAGCCCGAGGAGACTCCAGACACAGCCATCTTCGGTGGCTTGCCATCTCC 147
QY      819 PheAlaSerAlaIleSerThreuserThrGluProTyArgGlyGlyCysGlnAlaGlnAer 838
      |||
Db      148 TTGGCTTCGGACACACTCACTTGAACCGAGCCCTTACCGGAGAGGCTGCCAAGCCGAGAC 207
QY      839 TyThrGlyGlyMetGlyIleValAlaGlyAlaLysTrpAsnProArgThrGlyThrile 858
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Db      208 TACACCGGCGCATGGCGATCGTCACACGGGCGCAAGTGAAACCCCGGACCGGCGCATATC 267
QY      859 AenAerPheSerTyThrLeuHiStrhAnCyLeuGluLeuSerPheTyThrleuGlyCysAer 878
      |||||
Db      268 AATGACTTCAGTTACTCTCATACATACAGTGCCTGGGGCTCTCTTACTTACCTGGGCTGTGAC 327
QY      879 LysPheProHiSGluserGluLeuProArgGluTrpGluAenAerGluAlaLeuLeu 898
      |||||
Db      328 AAGTTCCTCATGAGAGTGAAGTGTCCCGGAGTGGAGAACACACAGAGGCGCTGCTCC 387
QY      899 ThrPheMetGluGlnValHiStrArgGlyIleGlyGlyValIleThrAerGluGlnGlyIle 918
      |||||
Db      388 ACCTTCATGAGCAGAGTGCACCGCGCATTTAAGGGGTGTGTACCGAGACAGAGGCGATTC 447
QY      919 ProIleAlaAenAlaThrIleSerValSerGlyIleAenHiSGlyValIleThrAerLaser 938
      |||||
Db      448 CCCATGTGCACAGCCACCATCTCTGTAGTGCATTATACGGGCTGAAGACAGCCACT 507
QY      939 GlyGlyAerTyTrpArgIleLeuAerProGlyGlyTyArgValThrAlaHiSGlyAglu 958
      |||||
Db      508 GGTGTGATTTACTGGCGAATCTTGAAACCGGTGATACCGGCTGACAGCCACAGCGGAG 567
QY      959 GlyTyThrProSerAlaLysThrCysAenValAerTyTrpAspIleGlyAlaThrGlnCys 978
      |||||
Db      568 GGTACACCCCGAGCGCCAAAGACTGCAATGTGACTATGACATCGGGGCCACTCAGTGC 627
QY      979 AenPheIleuAlaArgSerAsnTrpLysArgIleAerGluIleMerAlaMerAerGly 998
      |||||
Db      628 AACTTATCTGTGGCTGTGCTCCCACTGAAGGCCATCGGAGATCATGGCCATGAACGAG 687
QY      999 AenAerProIleProHiSGluserPheSerAerProMetThrProGlnGlnAerGlu 1018
      |||||
Db      688 AACGGGCTATCCACACATAGACCATCGGCGCTTATGACCCCAACAGGAGCGGCTG 747
QY      1019 GInGlnAerGluGluGlnHiStrGluAerGluAglAglMeAerGluAerGlu 1038
      |||||
Db      748 CAGCAGCGAGCGCTCAACACCGCTGCGGCTTGGGACAGATCGGCTGGCGGCTTC 807
QY      1039 AenAlaThrThrThreuglyProhiStrValProProThreupProAlaProAla 1058
      |||||
Db      808 AACGCCACACACCTTAGGCCCCCACACTGTGCTCCACGCTGCCCCCTGCTGCTGC 867
QY      1059 ThrThrLeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrp 1078
      |||||
Db      868 ACCACCCGAGACATACATAGAGCCCTGGGCTCATACGCCCAACACCCCTGGCTGG 927
QY      1079 GluGluSerGluThrGluThrTyThrGluValIleThrGluPheGlyThrGluValGlu 1098
      |||||
Db      928 GAGGAGTCGAGACTGAGACTTACACAGAGGTGTGACAGAGTTGGAGCCGAGAGTGAG 987
QY      1099 ProGluPheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGlu 1118
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Db      988 CCGGAGTTTGGACACAGGTGAGGCCGAGTTTGAGACCAAGTTGAGGCTGAGTTGAG 1047
QY      1119 ThrGlnLeuGluProGluPheGluGluGluGluGluGluGluGluGluIleAla 1138
      |||||
Db      1048 ACCGAGCTGGAACCCGAGTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTAGCC 1107
QY      1139 ThrGlyGlnAlaPheProPheThrThrValGluThrTyThrValAenPheGlyAerPhe 1158
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RESULT 10
US-11-266-748A-226230
; Sequence 226230, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
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Qy 271 -----ProGluProGluGluVala---ProAlaProAlaProGluGluArg 266
Db 86 TCGGGAGCCCGGAGCCACCAAGTCCAGGCTGACCCGGCTTCATAGCAGCCGG 145
Qy 287 ILGluProValLysProLeuLeuProLeuProLeuProLeuArgLysArgLys 306
Db 146 CA-CAGCCGCGGAGAGACAGCT----- 168
Qy 307 ValLeuProLeuValLeuProLeuValLeuProLeuProLeuProLeuPro 326
Db 169 -----AACGGAGCTCAGAACAGCATGT-CCG 194
Qy 327 AspAlaGluArgLysLeuArgLysGluLysGluLysGluLysGluLysGluLys 346
Db 195 GATTCAGATCATCA-----GAGAGAAAGGTATTATGAAAGGAGAGAGAGCTAAC 248
Qy 347 Ser---SerProLysGluGluLysLeuLysLeuLysLeuLysLeuLysLeu 365
Db 249 TCTAACTCGCCGCCACCCAGCTGGTGACTGGCCGGCCCTGTGTGACCCCACTCCAGCAG 308
Qy 366 GluProArg-LysGluGluGluLysGluGluLysGluLysGluLysGluLys 385
Db 309 GACCTTCGACCCGCTGAGAA-----CAGAGAACAGGCTG 344
Qy 385 sPProLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 405
Db 345 TCCTCTCTTGGGCTGGAGTCCCTGCGAGTTTCAGATGCGGCTTGAAGCATCCAGCAG 404
Qy 405 LLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGluLys 425
Db 405 CCACTCTCTTGGGCTGGAGTCCCTGCGAGTTTCAGATGCGGCTTGAAGCATCCAGCAG 464
Qy 425 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 445
Db 465 CGGAGTCTATATGATGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
Qy 445 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 465
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Qy 465 LLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 485
Db 585 CTGAGAGTATGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
Qy 485 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 503
Db 645 GTGGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 704
Qy 503 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 523
Db 705 AGAAATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
Qy 523 rProLeuLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 541
Db 765 GCCCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 824
Qy 541 rValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 560
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Db 885 AGAAATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 944
Qy 580 uCyPProLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 600
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Qy 600 rAlaLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 620
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Db 1125 GTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1184
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Qy 720 rArgValProLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 740
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Qy 740 LLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 760
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Qy 760 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 780
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Qy 800 LLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 820
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Qy 820 ValLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 840
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Qy 840 rGluGluGluLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 860
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Db 1851 CCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1910
Qy 919 oLLeuArgLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 939
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US-11-266-748A-226229  
; Sequence 226229, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 226229  
; LENGTH: 1184  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (780)..(813)  
; OTHER INFORMATION: n 1a a, c, g, or t  
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Pred. No.: 1,42e-64 Length: 1184  
Score: 1453.00 Matches: 272  
Percent Similarity: 94.8% Conservative: 2  
Best Local Similarity: 94.1% Mismatches: 15  
Query Match: 23.2% Indels: 0  
DB: 8 Gaps: 0  
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Db 12 AAAGTGGCTTCTTACCTTGAGCTTGACAGTTCCCTCATGAGTGAAGCTGCCCCCGAG 71  
Qy 890 TrpGluAsnAsnLygluAlaLeuLeuThrPheMetGluGlnValHleArGlyIleLy 909  
Db 72 TGGGAACAACAAGAGGCGCTCACCCTTATGAGAGAGGTGACCGCGCATTTAAG 131  
Qy 910 GlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGly 929  
Db 132 GGGGTGTGACGAGCAGCAAGGCATCCCATTTGCCAACGCCACATCTCTGTGAGTGGC 191

Qy 930 IleAsnHStleValLyThrAlaSerGlyLyAspYrTrpArG1leLeuAsnProGly 949  
Db 192 ATTAAATCAGCGCGTGAACAGACAGCCAGTGTGTATTTCTGGCGAATCTTGAAACCGGGT 251  
Qy 950 GluYrArGValThrAlaHleAlaGluGlyYrThrProSeArAlaLyThrCyAsnVal 969  
Db 252 GAGTACCGCGTGAACAGCCAGCGGAGGTACACCCGAGGCGCAACAGCTGCATGTT 311  
Qy 970 AspYrArP1leGlyAlaThrGlnCyAsnPheIleAsnAlaXSerAsnTrpLyArG 989  
Db 312 GACTATGACATCGGGGCACTCATTTGCACTTCACTGTGCTCCAACTGGAAAGCGC 371  
Qy 990 IleArGluIleMetAlaMetAsnLyAsnArGProIleProHStleAspProSeArG 1009  
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Qy 1010 ProMetThrProGlnGlnArGLeuGlnGlnArGArGLeuGlnHleArGLeuArGLeu 1029  
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Qy 1030 ArGAlaGlnMetArGLeuArGLeuArGLeuAsnAlaThrThrThrLeuGlyProHStHVal 1049  
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Qy 1050 ProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIleGluProTrpGly 1069  
Db 552 CTTCCACGCTGCCCTCGCCCTCCACACCCCTGAGACATACATAGAGCCCTGGGCG 611  
Qy 1070 LeuIleProProThrThrAlaGlyYrTrpGluSerGluThrGluThrYrThrGluVal 1089  
Db 612 CTCATACCGCCCAACACCGCTGCGGAGGAGTGGAGACTGAGAACCTACACAGAGGCG 671  
Qy 1090 ValThrGluPheGlyThrGluValGluProGluPheGlyYrThrValGluProGluPhe 1109  
Db 672 GTGACAGATTTGGAGCGAGGTGAGCCCGAGTTTGGACCAAGGTGAGCCGAGTTT 731  
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Qy 1130 GluGluGluLyGluGluGluIleAlaThrGlyGlnAlaPheProPheThrYrValGlu 1149  
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Db 852 ACCTACACAGTAGACTTTGGGAGCTTC 878  
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US-11-266-748A-167870  
; Sequence 167870, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 48396  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 157870  
LENGTH: 950  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (782)..(815)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-167870

## Alignment Scores:

Pred. No.:	2,31e-63	Length:	950
Score:	1427.00	Matches:	275
Percent Similarity:	94.5%	Conservative:	1
Best Local Similarity:	94.2%	Mismatches:	13
Query Match:	22.8%	Indels:	3
DB:	8	Gaps:	0

US-10-642-946-3 (1-1158) x US-11-266-748A-167870 (1-950)

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DB 11 GAGGTCTCTTCTTACCTGGGCTGTGACAGATTCCTCATGAGAGTGAGTGGCCGCGAG 70  
QY 890 TrpGluAsnAsnLysGluAlaLeuLeuThrPheMetGluGluValHisArgGlyIleLeu 909  
DB 71 TGGAGAGAACAGAGAGGGGCTGTCTCATCTTGAGAGAGGTGACCGCGCATTAAG 130  
QY 910 GlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGly 929  
DB 131 GGGGTGTGACGGAGCGAGGATCCCATTCGCAACCGCACCATCTGTGTAGTGC 190  
QY 930 IleAsnHisGlyValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGly 949  
DB 191 ATTAATCACCGCGTGAAGACGACGCTGTGATTAATGCGCAATCTTGAAACCGCGGT 250  
QY 950 GluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLysThrCysAsnVal 969  
DB 251 GAGTACCGCTGTGACGCGAGGAGGCTACACCCGAGCGCCAGACCTGCAATGTT 310  
QY 970 AspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSerAsnTrpLysArg 989  
DB 311 GACTATGACATCGGGGCACTCACTGCACTTCACTGCTGCTCAACTGGAAGCGC 370  
QY 990 IleArgGluIleMetAlaMetLanGlyAsnArgProIleProHISleAspProSerArg 1009  
DB 371 ATCCGGGAGATCATGGCCATGAACGGGAGACCGGCTATCCACACATAGACCATCGCGC 430  
QY 1010 PromoterThProGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeu 1029  
DB 431 CTTATGACCCCGCAACGCGACGCTGTGACAGGAGGCTTACACACCGCTGCGGCTT 490  
QY 1030 ArgAlaGlnMetArgLeuArgArgLeuAsnAlaThrThrThrLeu-GlyProHISThrVa 1049  
DB 491 CGGGCACAGATGGGGCTGGCGGCTCAACGCCACACACCTAGGGCCCCCACTGT 550  
QY 1049 LProProThrLeuProProAlaProAlaThrThrLeuSerThrIleGluProTrpGlu 1069  
DB 551 GCCTCCACCGCTCGCTCGCTCGCTGACACCTGACCATAGAGCCCTGGGG 610  
QY 1069 YLeu-LIeProProThrThrAlaGlyTrpGluGluSerGluThrGluThrThrGluVal 1089  
DB 611 CTTCAATACCGCAACCGCTGCTGGAGAGGTGGAGACTGAGACTTACACAGAGG 670  
QY 1089 aIValThrGluPheGlyThrGluValGlu-ProGluPheGlyThrLysValGluProGlu 1108  
DB 671 TGGTCAACAGATTGGGACCGAGGTGAGCCCGAGTTTGGGACCAAGGTGAGCCCGAG 730

QY 1109 PheGluThrGlnLeuGluProGluPheGluThrGlnLeuGluProGluPheGluGlu 1128  
DB 731 TTTGAGACCCAGTTGGAGCTGTGAGTTGAGACCCAGCTGGAACCGAGTTTNNNNNNNN 790  
QY 1129 GluGluGluGluLysGluGluGluIleAlaThrGlyGlnAlaPheProPheThrVal 1148  
DB 791 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 850  
QY 1149 GluThrTyrThrValAsnPheGlyAspPhe 1158  
DB 851 GAGACCTACACAGTGAACCTTTGGGACTTC 880

Search completed: October 1, 2006, 00:15:22  
Job time : 592 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: September 30, 2006, 23:48:23 : Search time 17677 Seconds

(without alignments)  
5494.817 Million cell updates/sec

Title: US-10-642-946-3

Perfect score: 6272  
Sequence: 1 MAVRGAPLUSCLLALLALC.....TGGAFFTYETVYVNRGDF 1158

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/abes/ABSSMB.epool/US10642946/rnat.29092006.125310.12521/app.query.fasta\_1  
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-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
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5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_est12.\*  
12: gb\_est13.\*  
13: gb\_est14.\*  
14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	5081.5	81.0	3825	AK159377	Mus muscu
2	5081.5	81.0	3860	AK159409	Mus muscu
3	5077.5	81.0	3840	AK159330	Mus muscu
4	5077.5	81.0	3860	AK159342	Mus muscu

5	5075.5	80.9	3831	AK159957	Mus muscu
6	5070.5	80.8	3831	AK159774	Mus muscu
7	5009.5	79.9	3854	AK158276	Mus muscu
8	4912	78.3	3224	DQ035090	Homo sapi
9	4096	65.3	2836	AK004712	Mus muscu
10	2988	47.6	3211	DQ035091	Homo sapi
11	2074	33.1	3499	AK019509	Mus muscu
12	2033.5	33.4	2237	DQ051196	Homo sapi
13	1925.5	30.7	2917	HS080505	Homo sapi
14	1789.5	28.9	2169	DQ051197	Homo sapi
15	1751	27.9	2169	AY418884	Mus muscu
16	1738	27.7	2199	AY418884	Mus muscu
17	1738	27.7	2297	CR621966	full-length
18	1712	27.3	1107	CR598691	full-length
19	1642	26.2	2024	AY418885	full-length
20	1603	25.6	936	AL533357	full-length
21	1590	25.4	908	DV919324	full-length
22	1556	24.8	910	AL536370	full-length
23	1540	24.6	880	DT817537	full-length
24	1513	24.1	863	DT810893	full-length
25	1510	24.1	867	DT810026	full-length
26	1508	24.0	876	DV817015	full-length
27	1501	23.9	894	BQ884305	full-length
28	1483	23.6	844	DV926117	full-length
29	1476	23.5	862	CD514819	full-length
30	1457.5	23.2	1666	AK132611	full-length
31	1455	23.2	972	AL542558	full-length
32	1452	23.2	834	DV916664	full-length
33	1452	23.2	846	DV923633	full-length
34	1444	23.0	1006	BX444373	full-length
35	1441	23.0	1004	B1410327	full-length
36	1439.5	22.9	871	CD359998	full-length
37	1434	22.9	822	DT810385	full-length
38	1419.5	22.6	836	BQ897584	full-length
39	1419	22.6	914	CD245277	full-length
40	1414	22.5	841	BX102854	full-length
41	1402	22.4	977	DV921162	full-length
42	1396	22.3	905	CR852604	full-length
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44	1384.5	22.1	797	BM008065	full-length
45	1380	22.0	820	B1769923	full-length

## ALIGNMENTS

RESULT 1  
AK159377  
LOCUS  
DEFINITION  
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:1420018014 product:AE binding protein 1, full insert sequence.  
ACCESSION  
AK159377  
VERSION  
AK159377.1 GI:74196951  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathu; Muridae; Muridae; Murinae; Mus.  
REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
2 Carninci, P., Shibata, Y., Hayashizaki, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE	JOURNAL	PUBMED	AUTHORS	CONSRMT	REFERENCE
1			Kono, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashinaga, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
2			Riken Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
3			Genome Res. 10 (11), 1757-1771 (2000)		
4			11076861		
5			Kawai, T., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Fleschmann, W., Gaasterland, T., Gissi, C., Kling, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stambli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Maehima, J., Mazzarelli, J., Mombarts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Wetz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.		
6			Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.		
7			Riken Genome Exploration Research Group Phase II Team and the FANTOM Consortium		
8			Functional annotation of a full-length mouse cDNA collection		
9			Nature 409 (6821), 685-690 (2001)		
10			11217851		
11			Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J., Brad, D., Brusc, V., Chertuk, C., Corbani, L.E., Cousins, S., Dalla, E., Dragan, T.A., Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, J., Kawasawa, Y., Kedzierecki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravaei, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempole, C.A., Seton, M., Shimada, K., Sultana, R., Takemura, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, I., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayakawa, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakakuma, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.		
12			FANTOM Consortium		
13			Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
14			Nature 420 (6915), 563-573 (2002)		
15			12466851		
16			Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fritsch, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aldin, V., Allen, J.E.,		
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URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>

## FEATURES

## Source

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## CDS

## Alignment Scores:

Pred. No.: 0 Length: 3825  
Score: 5081.50 Matches: 964  
Percent Similarity: 87.6% Conservative: 55  
Beet Local Similarity: 82.9% Mismatches: 107  
Query Match: 81.0% Indels: 37  
DB: 6 Gaps: 12

US-10-642-946-3 (1-1158) x AK159377 (1-3825)

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21 ProGlyGlyArgProGlyInThrValLeuThrAspAspGlu11GluGluPheLeuGluGly 40  
257 CCAAGAGGGAACCCACAGAGCGTCTGACGACGACGAGATCGAGAGTTCCTGAAGGC 316  
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 DB 1901 GTCAATGAGAGGTGCCCAATCACTCCGACATACAGCCTGGGCAAGATTACAGAGGG 1960  
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 DB 3581 GGGGACTTC 3589  
 RESULT 2  
 AKI59409 3660 bp mRNA linear HTC 21-SRP-2005  
 LOCUS AKI59409  
 DEFINITION Mus musculi osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:1420019106 product:AE binding protein 1, full insert sequence.  
 ACCESSION AKI59409  
 VERSION AKI59409.1 GI:74197010  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculi (house mouse)  
 ORGANISM Mus musculi  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
 AUTHORS  
 TITLE High-efficiency full-length cDNA cloning



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PUBMED  
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AUTHORS
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- JOURNAL  
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- JOURNAL  
PUBMED  
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AUTHORS
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- Direct Substitution
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QY 477 GlyPheSerAsnAspSerGlnThrTrpValMetThrAsnGlyTrpGluMetThr 496  
 DB 1631 GGCTTCAGCAATGACACCGACCTGGGTGATGACCAATGGCTACGAGAAATACC 1690  
 QY 497 PheH1sGlyAsnValAspLysAspThrProValIleuSerGluLeuProGluProVal1 516  
 DB 1691 TTCTATGAAATGTCAGCAAGACACACTGTGCTGAGCGAGCTCCCGAGCCAGTTGTG 1750  
 QY 517 AlaArgPheH1leArgIleThrProLeuThrTrpAsnGlySerLeuGlyMetArgLeuGlu 536  
 DB 1751 GCCCGTTTCATCCGCATCTTACCACTCAGATGGTGTGCTGCTCAGCCGCTGGAG 1810  
 QY 537 ValIleuGlyCysSerValAlaProValIleuSerThrTrpAsnGluValAla 556  
 DB 1811 GTGCTAGGCTGCCCCGAGACCCCTGTCTACAGCTACGACCAAAATGAGGTGTA 1870  
 QY 557 ThrAspAspLeuAspPheArgH1sH1SerThrLysAspMetArgIleuMetLysVal 576  
 DB 1871 ACTGACAGCTGAGCTTCCGGACACACAGCTACAAAGACATGGCCGAGTGAAGCT 1930  
 QY 577 ValAsnGluGluCysProThrIleThrArgThrTrpSerLeuGlyLysSerSerArgGly 596  
 DB 1931 GTCAATGAGAGTGGCCCAACATCACTCGCAATACAGCTGGGCAAGATTCAAGAGG 1990  
 QY 597 LeuLysIleThrAlaMetGluIleSerAspAsnProGlyLysGluLeuGlyPro 616  
 DB 1991 CTCAAGTCTTACCGAATGAAATCTCAGACACCTGGGATCTGAACTGGGGAGACC 2050  
 QY 617 GluPheArgThrAlaGlyIleH1sGlyAsnGluValIleuGlyArgGluLeuLeu 636  
 DB 2051 GAGTTCGGCTACACAGCCGGGATCCACGGCAATGAGGTGCTAGGCCGAGGCTCTGCT 2110  
 QY 637 LeuLeuMetGlnTrpLeuGlyArgGluTrpArgAspGlyAsnProArgValArgSerLeu 656  
 DB 2111 CTGCTCATGCAAACTCATGCGCAGAGTACCGCGATGGGAACCGAAGTGGCAACTG 2170  
 QY 657 ValGluAspThrArgIleH1sLeuValProSerLeuAsnProAspGlyTrpGluValAla 676  
 DB 2171 GTTCAGAGACACAGCATCTCAGTGTGCTCGCTCGTGAACCTGTAGCTTGAAGTGGCA 2230  
 QY 677 AlaGluMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPhe 696  
 DB 2231 GCCAAGATGGGCTCAGAGTTTGGGAATGGGCACTGGGGCTGTGGACTGAGGAGGGCTTT 2290  
 QY 697 AspIlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLys 716  
 DB 2291 GACATCTTCCAGGACCTCCAGATCTCACTGTGTGGGCAAGCTGAGGAGAAAGAA 2350  
 QY 717 TrpValProThrArgValProAsnAsnLeuProIleProGluArgTrpLeuSerPro 736  
 DB 2351 TGGGTCCCTACAGGGTCCCAACAAATACCTGCAATCCCTGAACCTTACCTGTCCCA 2410  
 QY 737 AspAlaThrValSerThrGluValArgAlaIleLeuLeuTrpMetGluLysAsnProPhe 756  
 DB 2411 GATGCCACGGCTCCACAGAAATCCGGGCATTAATTCCTGGATGAGAAAGAACCTTT 2470  
 QY 757 ValIleuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTrpProTrpAspMetAla 776  
 DB 2471 GTCTGTGGTGAATCTGAACGGGTGTGAGCGGCTGTGTCTTATCCCTTATGACATGGCC 2530  
 QY 777 ArgThrProThrGluGluGluLeuLeuAlaAlaMetAlaAlaArgGlyGluAsp 796  
 DB 2531 CGGACACCTTACGAGGAGGAGCTGTGGCCGAGGACCTGGACGTGCCCGGAGAAAGAT 2590  
 QY 797 GluAspGluValSerGluAlaGluGluThrProAspH1sAlaIlePheArgTrpLeuAla 816  
 DB 2591 GATGACGGGGTGTCTGAGGCCACGAGACCTCAAGATCAACCTATTTCGCTGGCTGGCC 2650  
 QY 817 IleSerThrAlaSerAlaH1sLeuThrLeuThrGluProTrpArgGlyGlyCysGlnAla 836  
 DB 2651 ATCTCATTTTCCCTCCGCACTTCACATGACGAGCCCTTACCGGGAGGGGTCCAGGCC 2710  
 QY 837 GluAspTrpThrGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGly 856

DB 2711 CAGGACTACACACGCGGATGGGCAATTTCTAAAGGGGCCAAGTGAATCTCCCTCTGGG 2770  
 QY 857 ThrIleAsnAspPheSerTrpLeuH1sThrAsnGlyLeuIleuSerPheTrpLeuGly 876  
 DB 2771 ACTTTCATGATGACTTGTAGCTACTGTGACACAACTGTCTGGAGCTCCGTAATACCTGGG 2830  
 QY 877 CysAspLysPheProH1sGluSerGluLeuProArgGluTrpGluAsnLeuAsnGlyAla 896  
 DB 2831 TGTGACAAATTTCCCAACGAGATGAGCTTACCCCGAAGATGGAGAAACAAGAAAGCG 2890  
 QY 897 LeuLeuThrPheMetGluGluValH1sArgGlyIleLysGlyValValThrAspGluGln 916  
 DB 2891 CTGCTACCTTCAATGAGACAGGTGACCGGTGATTAAGGTGTGTGACAGATGAGCA 2950  
 QY 917 GlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnH1sGlyValLysThr 936  
 DB 2951 GGCATCCCACTTCCCAATGACCAATCTCTGTGATGGCATCAACCATGGGTGGAAGACA 3010  
 QY 937 AlaSerGlyGlyLysAspTrpTrpArgIleLeuAsnProGlyGluTrpArgValThrAlaH1s 956  
 DB 3011 GCAAGTGAAGTACTTACCTGGCGCATTTCTGAACCCGGGTGATGACCTGTGACAGCTCAC 3070  
 QY 957 AlaGluGlyThrProSerAlaLysThrCysAsnValAspTrpAspIleGlyValAlaThr 976  
 DB 3071 GCAAGGGCTTACACTCAAGTCCCAAGATTCGAAATGTGACTACATATTGGGGCCACT 3130  
 QY 977 GluLysAsnPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMet 996  
 DB 3131 CAGTGCACATTCATCTCTGGCTCGATCCCACTGGAACCGCATTTGGGAGATCTTGGCTATG 3190  
 QY 997 AsnGlyAsnArgProIleProH1sIleAspProSerArgProMetThrProGluGlnArg 1016  
 DB 3191 AAGGGAAACCGTCCATTTCTCCAGATGACCCCTCAGACCCCAAGCCCGAGCGG 3250  
 QY 1017 ArgLeuGluGluArgArgLeuGlnH1sArgLeuArgLeuArgIleMetArgLysArg 1036  
 DB 3251 CGCATGACAGGCGCCGTCTACAGTACCGGCTCCGATGAGGAACAGATGCATGCTGT 3310  
 QY 1037 ArgLeuAsnAlaThrThrThrLeuGluProH1sThrValPro---ProThrLeuProPro 1055  
 DB 3311 CGCCTCAATTCATCCGCA-----GGCCCTGCACAAAGCCCACTGCTGCTTATGAGCT 3364  
 QY 1056 AlaProAlaThrThrLeuSerThrThrIleGluProTrpGlyLeuIleProProThrThr 1075  
 DB 3365 CCCCCTTCCCTTACACACGACCATTAATCTGAGGCGCTGGAAATTTCTACCACTACACT 3424  
 QY 1076 AlaGlyTrpGluGluSerGluThrGluThrTrpGluValValThrGluPheGlyThr 1095  
 DB 3425 GCAAGCTGGAGAGTCAAGACTGAGACTGAGACTTATACAAAGTACTGACAGATTT----- 3478  
 QY 1096 GluValGluProGluPheGlyThrLysValGluProGluPheGluThrGluLeuGluPro 1115  
 DB 3479 -----GAGACAGATATGAGGACTGACTAGAGGTGGA----- 3511  
 QY 1116 GluPheGluThrGluLeuGluProGluPheGluGluGluGluGluGluGluGluGlu 1135  
 DB 3512 GAGATGAG-----GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3550  
 QY 1136 GluIleAlaIleGluAlaPheProPheThrThrValGluThrTrpThrValAsnPhe 1155  
 DB 3551 GAGATGACACAGGCTTACATTTCCATTTCAACACAGTGAAGCTTACACAGTGAACCTTT 3610  
 QY 1156 GlyAspPhe 1158  
 DB 3611 GGGGACTTC 3619

RESULT 3  
 AK159330  
 LOCUS  
 DEFINITION  
 AK159330 3840 bp mRNA linear HTC 21-SEP-2005  
 Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched  
 library, clone:1420016E21 product:AE binding protein 1, full insert  
 sequence.

AKI59330	AKI59330.1	GI:74192966	
VERSION	AKI59330.1	GI:74192966	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotic Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Scuriognathi; Murioidea; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (10), 1617-1630 (2000)	
PUBMED	10349636		
REFERENCE	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (10), 1617-1630 (2000)	
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (10), 1617-1630 (2000)	
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (11), 1757-1771 (2000)	
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flisberg, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuhl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Straub, F., Suzuki, R., Tomita, M., Wagner, R., Washio, T., Sakai, K., Okido, T., Furuno, M., Kono, H., Baldarelli, R., Barsh, G., Blake, J., Botelli, D., Boulcova, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombae, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (11), 1757-1771 (2000)	
PUBMED	11076861		
REFERENCE	5		
AUTHORS	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flisberg, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuhl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Straub, F., Suzuki, R., Tomita, M., Wagner, R., Washio, T., Sakai, K., Okido, T., Furuno, M., Kono, H., Baldarelli, R., Barsh, G., Blake, J., Botelli, D., Boulcova, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombae, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (11), 1757-1771 (2000)	
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REFERENCE	6		
AUTHORS	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flisberg, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuhl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Straub, F., Suzuki, R., Tomita, M., Wagner, R., Washio, T., Sakai, K., Okido, T., Furuno, M., Kono, H., Baldarelli, R., Barsh, G., Blake, J., Botelli, D., Boulcova, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombae, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.		
JOURNAL	Genome Res.	10 (11), 1757-1771 (2000)	
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JOURNAL	Genome Res.	10 (11), 1757-1771 (2000)	
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TITLE  
JOURNAL

## COMMENT

Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/

FEATURES  
source

Location/Qualifiers  
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Best Local Similarity: 82.8%  
Query Match: 81.0%  
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Gaps: 12

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VERSION	AK159342.1	GI:74196887	
KEYWORDS	HTC; CAP trapper.		
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ORGANISM	Mus musculus		
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			Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency, full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itch, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	11042159		
TITLE	3		
JOURNAL	Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
PUBMED	Komno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itch, M.,		
REFERENCE	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Hazada, A.,		
AUTHORS	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
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	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,		
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	Genome Res. 10 (11), 1757-1771 (2000)		
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PUBMED	4		
REFERENCE			
AUTHORS	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y.,		
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	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohseuki, S.		
	and Hayashizaki, Y.		
CONSTRM	RIKEN Genome Exploration Research Group Phase II Team and the		
TITLE	FANTOM Consortium		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409 (6821), 685-690 (2001)		
REFERENCE	11217851		
AUTHORS	5		
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	Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,		
	Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,		
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	Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,		
	Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,		
	Rogers, J., Birney, E. and Hayashizaki, Y.		
CONSTRM	FANTOM Consortium		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
JOURNAL	of 60,770 full-length cDNAs		
PUBMED	Nature 420 (6915), 563-573 (2002)		
REFERENCE	12466851		
AUTHORS	6		
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	Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J.,		
	Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L.,		
	Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,		
	Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H.,		
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	Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavoni, G.,		
	Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J., Ring, B. Z.,		
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	Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C. A., Seno, S.,		
	Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D.,		
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	Brusic, V., Quackenbush, J., Wahlestedt, C., Matlock, K., Silva, D.,		
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	Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itch, M.,		
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	Watanabe, A., Okamura-Oh, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.		
CONSTRM	FANTOM Consortium		
TITLE	The transcriptional landscape of the mammalian genome		
JOURNAL	Science 309 (5740), 1559-1563 (2005)		
PUBMED	16141072		
REFERENCE	7		
AUTHORS	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakatsishi, M.,		
	Nakamura, M., Nishida, H., Yap, C. C., Suzuki, M., Kawai, J., Suzuki, H.,		









QY 1096 GIUValGIuProGIuPheGIuThryValGIuProGIuPheGIuThryGluInleuGIuPro 1115  
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 QY 1116 GIUuPheGIuThryGluInleuGIuProGIuPheGIuGIuGIuGIuGIuGIuGIuGIu 1135  
 DB 3511 GAGATGAGAG-----GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3549  
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 ACCESSION AK159957  
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 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 PUBMED 10349636  
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 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
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 TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer  
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 PUBMED 11076861  
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CONSRTM  
 TITLE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium  
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 PUBMED Nature 409 (6821), 685-690 (2001)  
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 AUTHORS 5  
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 TITLE FANTOM Consortium  
 JOURNAL Analysis of the mouse transcriptome based on functional annotation  
 PUBMED of 60,770 full-length cDNAs  
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 FANTOM Consortium  
 The transcriptional landscape of the mammalian genome  
 Science 309 (5740), 1559-1563 (2005)  
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 RIKEN Genome Exploration Research Group  
 Antisense transcription in the mammalian transcriptome  
 Science 309 (5740), 1564-1566 (2005)  
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8 (bases 1 to 3831)  
 Arakawa, T., Carninci, P., Fukuda, S., Haseizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-fes@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 Location/Qualifiers  
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 putative"

CDS

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 PSAGKSTYAPTKKPKKPKATKKPKPKATKKPKPKATKKPKPKATKK  
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## Alignment Scores:

Pred. No.: 0 Length: 3831  
 Score: 5075.50 Matches: 963  
 Percent Similarity: 87.5% Conservative: 55  
 Best Local Similarity: 82.8% Mismatches: 108  
 Query Match: 80.9% Indels: 37  
 DB: Gaps: 12

US-10-642-946-3 (1-1158) x AK159957 (1-3831)

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 41 PheLeuSerGlnLeuGlnProGlu-----ProArgGluAspAspValGlnAlaProPro 58  
 318 TTCCTTCGAGTGGAGACCCAGTCCCGCCCGGGGAAGACGACGTGAAGTCCAGCCG 377  
 59 ProProGluProThrProArgValArgGlyAlaGlnAlaGlyGlyLeuProGlyLysArg 78  
 378 CTTCCCGAACCACCCAGCGTCCCGCCCAATCCAGACGAGGGGCAAG-----425  
 79 ProGlyThrAlaAlaGlnValProProGluLysThrLysAspLysGlyLysLys 98  
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QY 677 AlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPhe 696  
 DB 2202 GCGAGATGGGCTCAGATTTGGAACTGGGCACTGGGGCTGTGTGACCTGAGAGAGGCTTT 2261  
 QY 697 AspLysPheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLys 716  
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 DB 2862 GTGCTACCTTCATGAGAGGTGACCGTGGCATTTAGGGTGTGTGACATGACAA 2921  
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 DB 3042 GCAGAGGGCTACCTCAAGTCCCAAGATCTGCAATGTGACTATGATTTGGGGCACT 3101  
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 QY 997 AsnGlyAsnArgProLysProHisAlaLeuAspProSerArgProMetThrProGlnGlnArg 1016  
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Qy 1056 AAlAPrOAlaThrThrLseuSerThrThrTllegluProTlrglyLeuIleProProThrThr 1075

Db 3336 CCCCCCTTCCCTTACACCACTTATTCCTTGGAGCCCTGGAGAAAGTTTACCACCTACCT 3395

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Db 3396 GCGAGCTGGAGAGGTAGAGACTGAGAACCTTATCAGAAAGTATGACAGAGATT----- 3449

Qy 1096 GluValGluProGluPheGlyThrThrValGluProGluPheGluThrGluLeuGluPro 1115

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Qy 1116 GluPheGluThrGluLeuGluProGluPheGluGluGluGluGluGluGluGluGlu 1135

Db 3483 GAGATAGAG-----GAGAGAGAGAGAGAGAGAGAGAGAGAGAA 3521

Qy 1136 GluIleAlaThrGlyGlyAlaPheProPheThrThrValGluThrThrValAlaPhe 1155

Db 3522 GAGGTGACACAGGCTTACATTTCACTCACAACAGTGAGACTTACACAGTGAACTTT 3581

Qy 1156 GlyAspPhe 1158

Db 3582 GGGGACTTC 3590

RESULT 6  
AK159774 3831 bp mRNA linear HTC 21-SEP-2005  
LOCUS AK159774  
DEFINITION Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:1420030M05 product:AE binding protein 1, full insert sequence.

ACCESSION AK159774 GI:74204573  
VERSION AK159774.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

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Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Takaishi Ichikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge. Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

## FEATURES

source

CDS

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## Alignment Scores:

Pred. No.:	0	Length:	3831
Score:	5070.50	Matches:	962
Percent Similarity:	87.4%	Conservative:	55
Best Local Similarity:	82.7%	Mismatches:	109
Query Match:	80.8%	Indels:	37
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US-10-642-946-3 (1-1158) x AKI59774 (1-3831)

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QY	21	ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40
DB	258	CCTGAGGGGAACCCACACACGCTGTCAGACACACAGATGAGAGATTCCTCGAAGC	317
QY	41	PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro	58
DB	318	TTCCTTTCGAGATTGAGACCCAGTCCCGCCCGGGAAGACGAGTGAAGTCCAGCG	377
QY	59	ProProGluProThrProArgValArgValAspGlnAlaGlyGlyAspProGlyAspArg	78
DB	378	CTTCCGAAACCCACCGACGCTCCGCAATCCAGGACGAGGGGCGAAG-----	425
QY	79	ProGlyThrAlaAlaGluValProProGluGluThrAspGlyGlyAspGlyGlyAsp	98
DB	426	CAGCGGCGACGATGTTGAAAGTCCCTCCAGAAAACAAAGACAAAGAGAGAGAGAG	485
QY	99	LysAspGlyGlyProGlyValProGlyGluSerLeuGluGlySerProArgProProLys	118
DB	486	AAGGACAAAGGCCCAAGCCCAAGAA--CCCTCGAGGGCTTACCGAGGCCCAAG	542
QY	119	LysGlyLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla	138
DB	543	AAACCAAGAGAAAGCCACCCAGGCCACCAAGAGCCCAAGAGAAACACCCAGAGCC	602
QY	139	ThrLysLysProGlyGluGluProProLysAlaThrLysLysProLysGluLysProPro	158
DB	603	ACCAAGAAAGCCCAAGAGAGAGCCCAAGGCCACCAAGAGAGAGAGAGAGAGAGAG	662
QY	159	LysAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr	178
DB	663	AAGGCACATTAAGAGCCCTCCGACAGAAAGAAAGTCTCAACTGAGTGGCCCTTGGAA	722
QY	179	LeuGluThrProLeuProProProProSerProGlyProGluGluLeuProGluGluGly	198
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QY	199	GlyAlaProLeuSerAspAsnTrpGlnAsnProGlyGluGluGluThrIleValGluAlaGln	218
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[illegible]

sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

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RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium

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FANTOM Consortium

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of 60,770 full-length cDNAs  
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Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,



CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jaki, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kikuchi, H., Kikuchi, H., Kollmeier, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavani, W. J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempile, C. A., Seno, S., Sesca, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincal, B., Sperling, S., Stupka, E., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, B., Vezard, R., Wei, C. L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

PANTOM Consortium  
The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)  
16141072

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

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RIKEN Genome Exploration Research Group  
Antisense transcription in the mammalian transcriptome  
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16141073

TITLE  
JOURNAL

8 (bases 1 to 3854)  
Arakawa, T., Carninci, P., Fukuda, S., Hoshizume, M., Hayashida, K., Horii, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Niimura, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Substation  
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan [E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://pantom.gsc.riken.jp/.  
Location/Qualifiers

FEATURES  
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#### ORIGIN

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Score: 5009.50 Matches: 957  
Percent Similarity: 86.9% Conservative: 54  
Best Local Similarity: 82.2% Mismatches: 113  
Query Match: 79.9% Indels: 41  
DB: 6 Gaps: 10

US-10-642-946-3 (1-1158) x AK158276 (1-3854)

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Dd	723	CCCGATGCTGAGCGCCAGACGAGCAAGAGAGAGAGAGCTGAAGAAACCAAAAAAGAG 782
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Dd	783	GACAGCACCCCAAGAGAGAGACCAAGAGTGGGAGTGGAGAAAGGCAAGGACCAACA 842

[illegible]

QY	726	AsnLeuProIleProGluuArgTyrLeuSerProAspAlaThrValSerThrGluValArg	745
Db	1923	AACTGGCCATCCCTGGAACGCTACTCTTCCGCAGATCCACGGATATCAGAGAGTCCGG	1982
QY	746	AlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAlaAsnLeuAsnGlyGly	765
Db	1993	GCCATCATGCTGCTGATGGAGAGAACCCCTGCTGCTGGGAGCAATCTGAAACGGCGGC	2042
QY	766	GluArgLeuValSerTyrProTyrAspMetAlaArgThrProThrGluGluLeu	785
Db	2043	GAGCGGCTAGATCTCTACCCCTCAGATATGGCCCGGCAAGCTACCCGAGGACAGCTGCTG	2102
QY	786	AlaAlaIleMetAlaAlaAlaArgGlyGluAspGluAspGluValSerGlyuAlaGluGlu	805
Db	2103	GCCGAGCGCAAGGACGACGCCGGGGGAGAGTATGAGACAGAGGCTCCGAGAGCCAGAGG	2162
QY	806	ThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisIleuThr	825
Db	2193	ACTCCAGACCAAGCCATCTTCGGGTGGCTTCCATCTCTTCGCTCGCACACTCACC	2222
QY	826	LeuThrGluProTyrArgGlyGlyCysGluAlaGluAspTyrThrGlyMetGlyIle	845
Db	2223	TTGACCGAGCCCTACCGCGGAGGCTGCCAAGCCAGAGACTACACCGGCGCATGGCATC	2282
QY	846	ValAsnGlyAlaLysTrpAsnProArgThrGlyThrIleAsnAspPheSerTyrLeuHis	865
Db	2283	GTCAACGGGGGCAAGTGAGAACCCCGGACCGGAGCTATCAATGACTTCAGTACTTCAT	2342
QY	866	ThrAsnCySLeuGluLeuSerPheTyrLeuGlyCysAspLysPheProHisSGLuSerGlu	885
Db	2343	ACCAACTGCTCGAGCTCTCTTCTTACTGGGCTGTGACAAAGTTCCCTCATGAGAGTGAG	2402
QY	886	LeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheMetGluGluValHis	905
Db	2403	CTGCCCGCCGAGTGGAGAAACAACAAGAGGCGCTGCTCACTTCATGAGGAGGTGCAC	2462
QY	906	ArgGlyIleLysGlyValValThrAspGluGluGlyIleProIleAlaAsnAlaThrIle	925
Db	2463	CGCGGCATTTAAGGGGGGTGTGACGAGACGAGAACGGCATCCCATTTGGCAAGCCACATC	2522
QY	926	SerValSerGlyIleAsnHisSGLValLysThrAlaSerGlyGlyAspTyrTrpArgIle	945
Db	2523	TCTGTGAGTGGCATTAATCACGGGCTGAAAGACGACAGTGGTGTGATTACTGGCGAATC	2582
QY	946	LeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLys	965
Db	2583	TTGAACCGGGGAGGTACCGGCTGACAGCCACGCGAGGGGCTCAACCCGAGCGCCAG	2642
QY	966	ThrCysAsnValAspTyrAspIleSGLValaThrGluCysAsnPheIleLeuAlaArgSer	985
Db	2643	ACCTGCATATGTTGACTATAGACTCGGGGCCCTCAGTGCAACTTCATCTCGGCTGCCTCC	2702
QY	986	AsnTrpLysAspGlyIleArgGluIleMetAlaMetAsnGlyAsnArgProIleProHisIle	1005
Db	2703	AACTGAAAGCGATCCGGAATCATGTGCCATGAAACGGAAACGGACTATCCACACATA	2762
QY	1006	AspProSerArgProMetThrProGluGlnArgArgLeuGluGluGluArgLeuGluHis	1025
Db	2763	GACCATGCGCGCCATATGACCCCCCAACAGGAGCGCTGCAGCGACGCGCTCAACAC	2822
QY	1026	ArgLeuArgLeuArgAlaGluMetArgLeuArgArgLeuAsnAlaThrThrThrLeuGly	1045
Db	2823	CGCTCGCGGCTTCGGGCAACAGATCGGGCTGGCGGCTCAACGCGCACCAACCCCTGGGC	2882
QY	1046	ProHisThrValProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIle	1065
Db	2883	CCCAACACTGTGCTCCCAACGCTGCCCCCTGCCCCCTGCAACACCTGAGCATCACTATA	2942
QY	1066	GluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGluSerGluThrGluThr	1085
Db	2943	GAGCCCTGGGCTCATACCGGCAACACCGCTGCTGGAGAGGTGGAGAACTGAGAAC	3002
QY	1086	TyrThrGluValValThrGluPheGlyThrGluValGluProGluPheGlyThrLysVal	1105

Db 3003 TACACAGAGGTGTCGACAGACTTTGGACCGAGGTGAGCCCGAGTTTGGACCAAGCTG 3062

Qy 1106 GluProGluPheGluThrGlnLeuGluProGluPheGluThrGlnLeuGluProGluPhe 1125

Db 3063 GAGCCCGAGTTTGAGACCCAGCTGAGCTTGAAGCCGAGCTGGAACCCGAGTTT 3122

Qy 1126 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1145

Db 3123 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3182

Qy 1146 ThrThrValGluThrThrThrValAspPheGlyAspPhe 1158

Db 3183 ACAACAGTAGAGACTTACACAGTCACTTGGGACTTC 3221

RESULT 9  
AK004712 2836 bp mRNA linear HTC 02-SEP-2005  
LOCUS AK004712  
DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011K15 product:AE binding protein 1, full insert sequence.  
ACCESSION AK004712 GI:12836087  
VERSION AK004712.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraka, T., Horii, F., Imofani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
URL: http://dev.fantom.gsc.riken.jp/

FEATURES  
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Best Local Similarity: 86.0% Mismatches: 60  
Query Match: 65.3% Indels: 28  
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Qy 292 LysProLeuLeuProLeuLeuProLeuLeuProLeuLeuProLeuLeuProLeuLeuPro 311

Db 61 AAGCCCTG-----CTGCCCTCGAGCTATGAGGATAGCTACGTATCCCACTAT 111

Qy 312 AspAspMetAspThrThrThrGluProProProProGluGluGluGluGluGluGluGluGlu 331

Db 112 GATGACTTGAGACTATTTATTTCCCACTCCACCGCAGAACCTGATTTGGACAAGAG 171

Qy 332 ThrAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 351

Db 172 GTGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231

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OY	370	GIyGIuGIuLeuGIuGIuTrpThrProThrGIuLyVaLySeCyapProIleGI		389
Db	292	GGTAGAGAGCTGGAGAGAGTGGCGCCAGTGGAGAAAA	TCAAGTCCCACTTATGGG	351
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OY	410	LeuGIyLaGIaGIaNGyGIyArgLeuAaMeGIuInThrGIyVaLyThGIuAaSPaerPyTrYr		429
Db	412	CTGGAGGCCACGGGGGGCGGCTCAACATGACAGCGTGGCCAAATGAAATATACATAT		471
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OY	450	ArghTrThraGPhetheTrGIyVaLyIleThrGIuGIyAaSPaSerIleThIaSPaAP		469
Db	532	AGGAAACTCGGATTACGGGCGCTACATCATCGAGGCGGTGATCCAGCATTCATAGCAGC		591
OY	470	PhVaLItrThrPhaPhaVaLySeSerAaAaSPaSerGIuInThrTrpVaLyMeTrYrThr		489
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OY	510	GIuAaPProGIuProVaLyVaLaArGPhelIeArgIleTyProLeuArThrPaNGIy		529
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OY	530	SeLeuCyMeArGIuGIuVaLyLeuGIyCySeSerVaLaLaProVaLySeTrYrYr		549
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OY	590	LeuGIyLySeSerSerThrGIyLeuLyIleTyVaLaMeGIuIleSeArSPaSPaProGIy		609
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Homidae; Pan.  
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AUTHORS 1. (bases 1 to 3211)  
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civeallo, D.,  
White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE 2. (bases 1 to 3211)  
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civeallo, D.,  
White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
Direct Submision  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
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AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Mech. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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PUBMED 11076861  
REFERENCE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
AUTHORS Functional annotation of a full-length mouse cDNA collection  
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PUBMED 11076861  
REFERENCE The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.  
AUTHORS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
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PUBMED 11076861  
REFERENCE RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.  
AUTHORS Antisense transcription in the mammalian transcriptome  
JOURNAL Science 309, 1564-1566 (2005)  
PUBMED 11076861  
REFERENCE The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).  
AUTHORS The Transcriptional Landscape of the Mammalian Genome  
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PUBMED 11076861  
REFERENCE Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirata, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suuki, H., Tagami, Y., Tagawa, A., Takehashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamoto, M. and Hayashizaki, Y.  
AUTHORS Direct Submission  
TITLE Submitted (18-AUG-2000) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

COMMENT Fax: 81-45-503 -9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: <http://genome.gsc.riken.jp/>  
 URL: <http://fantom.gsc.riken.jp/>  
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REFERENCE 1 (bases 1 to 2237)  
Nijelsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
White,T.J., Snieksy,J.J., Adams,M.D. and Cargill,M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (ex) PLOS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
AUTHORS 2 (bases 1 to 2237)  
Nijelsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
White,T.J., Snieksy,J.J., Adams,M.D. and Cargill,M.  
DIRECT SUBMISSION  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
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COMMENT This sequence was made by sequencing genomic exons and ordering  
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DEFINITION	Homo sapiens mRNA, cDNA DKFZp666J235 (from clone DKFZp666J235).		
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VERSION	AL833732.1	GI:21734382	
KEYWORDS	HTC.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2917) Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and Wiemann, S.		
CONSRMT	The German cDNA Consortium		
TITLE	Direct Submission		
JOURNAL	Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp666J235) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp666J235 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.		
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ORIGIN

## Alignment Scores:

Pred. No.: 2,41e-134 Length: 2917  
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US-10-642-946-3 (1-1158) x HSM805045 (1-2917)

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Search completed: October 1, 2006, 04:45:29  
 Job time : 17813 secs





XX  
DR WPI: 2003-058567/05.

XX Novel isolated nucleic acid upregulated/downregulated in osteogenesis,  
PT useful for bone disease therapy in subject.

XX  
PS Claim 26; Page 146-147; 237pp; English.

XX The present invention relates to novel nucleotide sequences, which are  
CC differentially expressed in models of osteogenesis upon being put in  
CC contact with a stimulator of osteogenesis. The present sequence is one  
CC such sequence. This sequence can be used for diagnosing osteoporosis/bone  
CC disease in a patient, promoting osteogenesis and/or preventing  
CC osteoporosis/bone disease. The present sequence encodes an intracellular  
CC enzyme

XX  
SQ Sequence 3935 BP; 923 A; 1243 C; 1185 G; 584 T; 0 U; 0 Other;

Alignment Scores:

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US-10-642-946-3 (1-1158) x ABZ34770 (1-3935)

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QY 21 ProGlyValArgProGluInThrValLeuThrAspArgGluIleGluGluPheLeuGluGly 40  
DB 200 CCGGAGGGCGCGCGGAGCGGTGTCGACGACGAGATCGAGAGTTCCTCGAGGCG 259  
QY 41 PheLeuSerGluLeuGluProGluProArgGluAspValGluAlaProProProPro 60  
DB 260 TTCCTGTCAAGCTTAACCTGAGCCCGGAGAGAGAGCTGAGGCGCCGCGCTCC 319  
QY 61 GluProThrProArgValArgIysAlaGlnIleGlyIlyLeuProGlyIlyAspProGly 80  
DB 320 GAGCCCAACCCCGCGGTCCGAAAAGCCAGCGCGGGGCAAGCCAGGAAAGCGCCAGG 379  
QY 81 ThrAlaAlaGluValProProGluIlyThrIlyAspIlyGlyIlyIysGlyIlyAsp 100  
DB 380 ACCGCGCAGAAAGTGCCTCCGAAAAGCAAAAGAGAAAGGAAAGCAAAAGAAAGAC 439  
QY 101 LysGlyProIlyValProIlyGluSerLeuGluGlySerProArgProProIlyGly 120  
DB 440 AAAGGCCCAAGGTGCGCAAGAGTCTTGAGAGGGTCCCGCAGCGCGCCAAAGAGGG 499  
QY 121 LysGluIlyAspProProIlyAlaThrIlyIlyProIlyGluIlyAspProProIlyAlaThrIly 140  
DB 500 AAAGAGAAAGCAACCAAGGCAACCAAGAGCCCAAGAGAGCAACCTTAAGGCAACAG 559  
QY 141 LysProIlyGluIlyProProIlyAlaThrIlyIlyAspIlyGluIlyIysProProIlyAla 160  
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QY 161 ThrIlyLysAspProSerGlyIlyAspProProIleuAlaProSerGluThrLeuGlu 180  
DB 620 ACCAAGAGGCCCGCTCAGAGGAAGGCCCGCCATTCGTGCTCCCTCAGAAACCTTGAG 679  
QY 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyAla 200  
DB 680 TGGCCACTGCGCCCGCCAGCCCTGCGCCCGAGAGAGTACCCAGAGGAGGAGGGGG 739  
QY 201 ProLeuSerAspAsnThrProIlyAsnProGluGluGluThrIlyAlaGluIlyGluIly 220  
DB 740 CCCCTCTCAATTAATCGCAAGATCCAGAGAGAGCCCATGTGAGGAGCAAGAGGAC 799  
QY 221 GlnProGluProGluGluGluThrGluGluProThrLeuAspTyIysAspGlnIleGlu 240

DB 800 CAGCTGAGCCGGAGAGAGAGACCGAGCAACCACTGAGCTAACAATGACCAATCGAG 859  
QY 241 ArgGluAspTyIysAspPheGluTyIleArgArgGlnIlyGlnProArgProProPro 260  
DB 860 AGGAGAGCTATGAGAGCTTTGAGTACATTCGGCCCGCAAGAGCAACCAAGGCAACCCCA 919  
QY 261 SerArgArgArgArgProGluIlyArgValTrpProGluProProGluGluIlyAlaProAla 280  
DB 920 ACCAAGAGAGAGAGCCCGAGCGGCTTGCGCCAGAGCCCGCTGAGAGAGAGAGCCCGGCC 979  
QY 281 ProAlaProGluGluArgIleGluProProValIlyProLeuLeuProProLeuProPro 300  
DB 980 CCAGCCCGGAGAGAGAGATTGAGCTCTGCGAAGCCCTGCTGCGCCCGCGCTGCCCT 1039  
QY 301 AspTyIysAspGlyTyIValIleProAsnTyIysAspAspMetAspTyIysPheGlyPro 320  
DB 1040 GACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099  
QY 321 ProProProGluIlyProAspAlaGluArgInThrAspGluGluIlyGluIlyLeuIly 340  
DB 1100 CTTCCGCGCCAGAGCCCGATGCTGAGCGCCAGAGCGAGAGAGAGAGAGAGAGAGAG 1159  
QY 341 LysProIlyIlyGluAspSerSerProIlyGluGluIlyThrAspIlyTrpAlaIlyIly 360  
DB 1160 AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219  
QY 361 GlyIlyAspPheIlyGluProArgIlyGlyIlyGluIlyLeuGluIlyGluIlyTrpThrPro 380  
DB 1220 GGCAAGAGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279  
QY 381 GluIlyValIlyCysProProIleGlyIlyMetGluSerIlyAspIleGluIlyAspGlnIle 400  
DB 1280 GAGAAAGTCAAGTGTCCCGCATTTGGATGAGTCAACCGATTTAGAGAGACACAGAGTC 1339  
QY 401 ArgAlaSerSerMetLeuArgIleGlyIlyGluIlyAlaGlnArgIlyArgLeuAsnMetGln 420  
DB 1340 CGAGCTCTCATGCTGCGCCACGCGCTGGGGGACAGCGCGCGCGCTCAACATGACAG 1399  
QY 421 ThrGlyAlaThrGluAspAspTyIysAspGlyValaTrpCysAlaGluAspAspAlaArg 440  
DB 1400 ACCGGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459  
QY 441 ThrGlnTrpIleGluIlyAspThrArgArgTrpThrArgPheThrGlyValIleThrGln 460  
DB 1460 ACCAGTGAATGAGAGTGAACCAAGAGAGAGATACCGGTTCAAGGGCTATCACCCAG 1519  
QY 461 GlyArgAspSerSerIleIleAspAspPheValThrThrPhePheValGlyPheSerAsn 480  
DB 1520 GGCAGAGACTCCAGATCCATGACATTTTGTGACACACCTTCTGCGGCTTCAGCAAT 1579  
QY 481 AspSerGlnThrTrpValMetTyIysThrAsnGlyTyIysGluGluMetThrPheIleGlyAsn 500  
DB 1580 GACAGCCAGACATGGGTGATGATGACACCAAGGCTATGAGAAATGACCTTTCATGGAGAC 1639  
QY 501 ValAspIlyAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520  
DB 1640 GTGACAGAGAGACACCGGTGCTGAGTAGAGCTCCAGAGCGGTGGTCTGTTTCAATC 1699  
QY 521 ArgIleTyIysProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540  
DB 1700 CCGATCTACCCACTCAGCTGAGATGAGAGCTGTGATGAGCTGAGAGTGTGAGGGGTGC 1759  
QY 541 SerValAlaProValTyIysSerTyIysTrpIlyIlyIlyAsnGluValAlaThrAspAspLeu 560  
DB 1760 TCTGTGGCCCTGTCTACAGCTATACGACAGAAATGAGGTGGCCACCATGACTGCTG 1819  
QY 561 AspPheArgIleIleSerTyIysAspMetArgGlnLeuMetIlyValValAsnGluGln 580  
DB 1820 GATTTCCGSCACACACAGCTACAGAGACATGGCCAGCTCATAGAGTGGTGAACGAGAG 1879  
QY 581 CysProThrIleThrArgThrTyIysSerLeuGlyIlySerSerArgGlyLeuIlyIleTy 600

Db 1880 TGCCCCACCATCACCGCGACTTACAGCCTGGGCAAGAGCTCAGAGCGCTCAAGATCTAT 1939  
 QY 601 AlMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620  
 Db 1940 GCCATGAGATCTCAGACCAACCCCTGGGAGACATGAATGGGGAGCCCGATTCCGCTAC 1999  
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 Db 2180 TCGAGATTGGGAATCGGGCGCTGGGACTGTGACTGAGAGAGGGCTTTGACATCTTTGAA 2239  
 QY 701 AspPheProAspPheLeuAsnSerValLeuTyrGlyAlaGluGluValArgGlySerTyrValProTyr 720  
 Db 2240 GATTCCCGGATCTCAACTGTGTCTGTGGGAGCTGAGGAGAGAAATGGGTCCCTTAC 2299  
 QY 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740  
 Db 2300 CGGGTCCCAACATTAACCTTCCCATCCCGAACGCTTACCTTGCAGATGCACGGTAA 2359  
 QY 741 SerThrGluValArgAlaIleIleAlaTyrMetGluValAsnProPheValIleuGlyAla 760  
 Db 2360 TCCACGAGAGTCCGGGCGCATCATTTGCTGTGATGAGAAAGAACCTTTCGTGGAGGACA 2419  
 QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
 Db 2420 AATCTGAACGGCGGCGAGCGGCTAGTATCTTACCCCTACGATATGGCCCGCACGCTTACC 2479  
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 QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTyrLeuAlaIleSerPheAla 820  
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 QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly 940  
 Db 2900 GCCAAGCGCACCATCTGTGAGTGCATTAATCAAGCGCTGAAGACAGCACTGGTGGT 2959  
 QY 941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960  
 Db 2960 GATTACGCGGAATCTTGAACCGGGGTGAGTACCGGCTGACACCCACGCGGAGGGCTTAC 3019

QY 961 ThrProSerAlaIleThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980  
 Db 3020 ACCCCGAGCGCCAAAGACTGCAATGTGACTATGACATGGGGCCACTCAGTGCACTTCC 3079  
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 Db 3080 ATCTGGCTGCTCCACTGAACTGAAAGCCATCCGGAGATATGGCCATGAACGGAAACCGG 3139  
 QY 1001 ProIleProHisIleAspProSerArgPrometThrProGlnGlnArgLeuGlnGln 1020  
 Db 3140 CTTATCCACACATACATACCATCGGCTTATGAGACCCCAACAGAGAGCGCTGCAGCAG 3199  
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 QY 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProAlaProAlaThrThr 1060  
 Db 3260 ACCACCACTTGAAGCCCACTGTGCTCCACGCTGCCCTGCCCTGCACACACC 3319  
 QY 1061 LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGln 1080  
 Db 3320 CTGAGCACAACATTAAGCGCTGGGCTCATACGCCCAACACCGCTGGTGGAGAG 3379  
 QY 1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100  
 Db 3380 TCGAGACATGAGACTTACACAGAGGTGTGACAGAGTTGGGACCGAGGTGGAGCGCCGAG 3439  
 QY 1101 PheGluThrIleValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120  
 Db 3440 TTGGGACCAAGGTGAGCCGAGTTTGAAGCCCACTGAGCTGAGTTGAGACACCAG 3499  
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
 Db 3500 CTGGAAACCGGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCACTGGC 3559  
 QY 1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158  
 Db 3560 CAGGCAATTCCTTCAACAGATGAGACTTACAGTGAAGTGAAGTGGGAGCTTCC 3613

RESULT 2  
 ID ACCS0076 standard; cDNA; 3935 BP.  
 XX ACCS0076;  
 AC XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Breast cancer associated cDNA sequence SEQ ID NO:1.  
 XX  
 KW Human; breast cancer; cytostatic; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN W02003004989-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019669.  
 XX  
 PR 21-JUN-2001; 2001US-0299887P.  
 XX  
 PR 27-JUN-2001; 2001US-0301572P.  
 XX  
 PR 18-JUL-2001; 2001US-0306501P.  
 XX  
 PR 25-SEP-2001; 2001US-0325002P.  
 XX  
 PR 05-MAR-2002; 2002US-0362585P.  
 XX  
 PR 14-MAY-2002; 2002US-0380391P.  
 XX  
 PA (MILL-) MILLENIUM PHARM INC.  
 XX  
 PI Lillie J, Gannavarapu M, Glact K, Hoersch S, Kamatkar S;  
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;

XX MPI: 2003-210381/20.  
DR P-P5DB; ABR47386.  
XX  
PT Breast cancer diagnosis or treatment by comparing the level of expression  
PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.  
XX  
PS Claim 1, SEQ ID NO 1, 128bp; English.  
XX  
CC The present invention describes a method for assessing whether a patient  
CC is afflicted with breast cancer. The method comprises comparing the level  
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
CC ABR47386 to ABR47632) in a patient sample and the normal level of  
CC expression of the marker in a control non-breast cancer sample, where a  
CC significant increase in the level of expression of the marker in the  
CC patient sample and the normal level is an indication that the patient is  
CC afflicted with breast cancer. The breast cancer associated sequences from  
CC the present invention have cytostatic activities and can be used in gene  
CC therapy. The method is useful for diagnosing and treating breast cancer.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 3935 BP; 923 A; 1243 C; 1185 G; 584 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 1,77e-290 Length: 3935  
Score: 6272.00 Matches: 1158  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0  
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DB 140 ATGGCGGCGCTGGCGGGGGGCGCCCTGCTCAGCTGCTCTGCGCTTGGCGGCGCTGTGC 199  
QY 21 ProGlyGlyAArgProGlnThrValLeuThrAspAspGlnuileGluGluPheLeuGluGly 40  
DB 200 CCGGAGGGGGCGCCGAGAGCGGTGTCGACGACGAGATCGAGAGTTCTCCGAGGGC 259  
QY 41 PheLeuSerGluLeuGluPProGluPProArgGluAspAspValGluAlaPProPProPro 60  
DB 260 TTCCTGTCAAGCTAAGAACTGAGCCCGGAGAGACGACGTGAGGCGCCCGCGCTCC 319  
QY 61 GluPProThrProArgValArgLyAlaGlnAlaGlyLyLysPProGlyLysArgProGly 80  
DB 320 GAGCCACCCCGGGGTCCGAAAGCCGAGCGGGGGGCAAGCCAGGAAAGCGGCCAGGG 379  
QY 81 ThrAlaAlaGluValPProGluGlyLysAspLyGlyLysLyGlyLysLyAsp 100  
DB 380 ACCGCGCAGAGAGTGCCTCCGAAAAGACCAAGAACAAAGGAAAGGAAAGCAAGAGAC 439  
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DB 500 AAGGAAAGGCAACCAAGGCCAAGAGCCCAAGAGAGCCACTTAAGCCACCAAG 559  
QY 141 LysPProLysGlyLysPProLysAlaThrLyLysLyPProLysGlyLysPProLysAla 160  
DB 560 AAGCCCAAGAGAGAGCCCAAGAGCCCAAGAGCCCAAGAGAGAGCCCAAGAGGCG 619  
QY 161 ThrLyLysPProPProSerGlyLysArgPProPProLysLeuAlaPProSerGlyThrLeuGlu 180  
DB 620 ACCAAGAGGCGCGGTGAGGAAAGGCGCCCAATTCCTGCTCCCTCAAGAAACCTGAGAG 679  
QY 181 TrpPProLeuPProPProPProSerProGlyPProGluGluLeuPProGlnGluGlyAla 200

DB 680 TGGCCACTGCCCCCAAGCCCTGGCCCGAGAGAGCTAACCCAGAGAGAGGGCG 739  
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DB 740 CCCCTCTCAAAATTAATCTGGCAAAATCCAGAGAGAGAGCCCATGTGGAGGACAGAGAGAC 799  
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DB 800 CAGCTTGAGCCGGAGAGAGAGAGCCAGACCCACACTGAGACTACATAGACAGATTCAG 859  
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DB 860 AGGAGAGACTATGAGAGACTTTGAGTACATTGGGGCCAGAGAACCCAGGCGCACCCCA 919  
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DB 920 AGCAGAAAGAGAGAGCCGAGCGGGTCTGGCCAGAGCCCTGAGAGAAAGCCCGGGCC 979  
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QY 301 AspTyGlyAspGlyTyValilePProAsnTyAspAspMetAspTyTyPheGlyPro 320  
DB 1040 GACTATGGTATGATGTTACGTGATCCCACTACATGACATGACTATTACTTGGGCT 1099  
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QY 441 ThrGlnTrpLileGluValAspThrArgTrpThrArgPheThrGlyValileThrGln 460  
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DB 1700 CCGATCTACCACTACCTGAGATGAGCGCTGTGCAATCGGCTGAGAGGTGTGGGGTGC 1759  
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 Db 1940 GCCATGAGATCTCAGACCAACCTGGGAGACATGAATGGGGAGGCCGATTCGGCTAC 1999  
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 QY 641 TYrLeuCYsaRghIuTYrArGaAPGlyAaSPProArghValArghSerLeuValGlnaAPThr 660  
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 Db 2180 TCAGAGTTGGGAATCGGGCGCTGGGACTGTGACCTGAGAGGGGCTTTGACATCTTTGAA 2239  
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 Db 2840 ATGAGACAGGTGACCGCGGCAATTAAAGGGGTGTGTAGCGAGCAAGCAAGCAATCCCAT 2899

QY 921 AlaSPAlaThrIleSerValSerGlyIleAaSPHIsGlyValaIleThrAlaSerGlyGly 940  
 Db 2900 GCCAACGCCACATCTCTGTGATGCAATTAATCAAGGGGTGAAGACACAGCTGTGGT 2959  
 QY 941 AaPTTYrTrArghIleLeuAaSPProGlyGlyTYrArghValThrAlaHIsAlaGluGlyTYr 960  
 Db 2960 GATTACTGGGAATCTTGAACCCGGGAGATACCGGCTGACAGCCAGCGAGGGCTAC 3019  
 QY 961 ThrProSerAlaIleTYrThyAaSPValaAPTYrAaSPGlyAlaThrGlnCybAaSPhe 980  
 Db 3020 ACCCGAGCGCCAAAGCTCGCAATGTGACTATGATATGGGGCCACTCAGTGAATTC 3079  
 QY 981 IleuValaArghSerAaSPTrAlaGlyIleValaIleMeCAlaMeCAsnglyAaSPArgh 1000  
 Db 3080 ATCTGTGCTGCTCCCACTGAAGCGCATCCGGAGATCATGGCCATGAACGGGAACCG 3139  
 QY 1001 ProIleProHIsIleAaSPProSerArghProMetThrProGlnAlaArghLeuGlnGln 1020  
 Db 3140 CCTATCCACACATGAACCCATGCGCCTTATGACCCCCCAACAGCGAGCTTGACAG 3199  
 QY 1021 ArgArghLeuGlnHIsArghLeuArghAlaGlnMeCArgLeuArghLeuAaSPAla 1040  
 Db 3200 CAGCGCTTCAACACACCGCTGGGGCTTGGGCAAGATGGGCTGGCGGCTCAACGCG 3259  
 QY 1041 ThrThrThrLeuGlyProHIsThrValaProProThrLeuProProAlaProAlaThr 1060  
 Db 3260 ACCACACACCTTGGCCCCCACACTGTGCTCCACCGCTGCCCCCTGGCCACACAC 3319  
 QY 1061 LeuSerThrThrIleGluProTYrGlyLeuIleProProThrThrAlaGlyTYrTPbGlu 1080  
 Db 3320 CTGAGCACTACATGAAGCTTGGGCTCTCATACGCCCAACACGCTGGGAGAG 3379  
 QY 1081 SerGluThrGluThrTYrThrGluValaIleThrGluPheGlyTYrGluValaGluProGlu 1100  
 Db 3380 TCGGAGACTGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTAGC 3439  
 QY 1101 PheGlyThrLyValaGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120  
 Db 3440 TTTGGGACCAAGGTGAGGCCGAGTTTGAAGCCAGTTTGAAGCTTGAAGTTTCGAGAC 3499  
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
 Db 3500 CTGGAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTAGC 3559  
 QY 1141 GlnAlaPheProPheThrThrValaGluThrTYrThrValaAaSPHIsAaSPhe 1158  
 Db 3560 CAGGACTTCCCTTCAACAAGTGAAGACTTACACAGTGAACCTTTGGGGACTTC 3613  
 Db  
 RESULT 3  
 ADF90653  
 ID ADF90653 standard; DNA; 3935 BP.  
 XX  
 AC ADF90653;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human hepatic-fibrosis disease marker SEQ ID 115.  
 XX  
 KW Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;  
 XX  
 KW hepatic carcinoma; human; de.  
 XX  
 OS Homo sapiens.  
 OS  
 PN JP2003259877-A.  
 XX  
 PD 16-SEP-2003.  
 XX  
 PF 11-MAR-2002; 2002JP-00065013.  
 XX  
 PR 11-MAR-2002; 2002JP-00065013.  
 XX  
 PA (SUMU) SUMITOMO SEIRAKU KK.



D	1880	TGCCCCACCATCA	CCGCACTTACAGCCTGGGCAAGAGCTCA	CGAGGCTCAAGATAT	1339
Q	601	AlMeGluLiLeSerA	AsnProGlyLhiGluLeuGlyLpGluPheArgTy		620
D	1940	GCCATGAGATCTC	AGAACCCCTGGGACATGATGGGGAGCCCGATTCCGCTAC		1999
Q	621	ThcAlGlyLLeh	AsnGluValLeuGlyAArgGluLeuLeuLeuMeGln		640
D	2000	ACTGCTGGGATCC	ATGGCAAGAGTCTGGCCGAGAGCTGTGGCTGTCTCATGCA		2059
Q	641	TyrLeuCyAArgGly	LurYArgAspGlyAsnProArgValArgSerLeuValGlnAspThr		660
D	2060	TACCTGGCCGAG	AGTACCGGATGGGACCAAGTGTGGCAAGCCGTGGTGCAGACACA		2119
Q	661	ArgLLehLeuVal	ProSerLeuAsnProAspGlyTyTgLuValAlaAlaGlnMetGly		680
D	2120	CGCATCCACCTG	GGCTCTCATGAACTCATGATGGCTGACAGGGTGGCGCAGATGGGC		2179
Q	681	SerGluPheGlyA	AsnTPAlaLeuGlyLeuTPThGluGluGlyPheAspLLePheGlu		700
D	2180	TCAGAGTTGGGA	CTGGGCGCTGGACGTGGACTGAGAGGGCTTTGACATCTTGA		2239
Q	701	AspPheProA	AsnLeuAsnSerValLeuTPGlyAlaGluGluArgLysTPValProTy		720
D	2240	GATTTCCGGAT	CTCACTGTGCTGTGGAGCTGAGGAGAGAAATGGGTCCCTAC		2299
Q	721	ArgValProA	AsnAsnLeuProLLeProGluArgTyLeuSerProAspAlaThrVal		740
D	2300	CGGGTCCCAAC	ATAACTTGCCCATCCCTGAACGGTACTTTCGCAGATGCGCAGTA		2359
Q	741	SerThGluVal	ArgAlaLeileAlaTPMeGluLysAsnProPheValLeuGlyAla		760
D	2360	TCACGGAAGTCC	GGGCGCATCTGATGATGAGAGAACCTTCGCTGGTGGAGCA		2419
Q	761	AsnLeuAsnGly	LysGluArgLeuValSerTyProTyAspMeAlaArgThrProThr		780
D	2420	AATCTGAACGG	CGGCGAGCTAGTACTTACCCCTACGATATGGCCCGCAGCCTACC		2479
Q	781	GlnGluGlnLeu	LeuAlaAlaMetAlaAlaAlaArgGlyGluLysAspGluVal		800
D	2480	CAGGACAGCTG	CTGGCGCAGCATGGCAGCAGCCGGGGGAGGATGAGCAGAGTCC		2539
Q	801	SerGluAlaGln	LurProAAspAlaAlaLePheArgProLeuAlaLeSerPheAla		820
D	2540	TCGAGGCGCC	AGAGACTCCAGACAGCCATCTCCGGGCTTGCCCATCTCTTCGCC		2599
Q	821	SerAlaLLeu	ThrLeuThArgLurProTyArgGlyGlyCyAsGlnAlaGlnAspTyThr		840
D	2600	TCCGCAACACT	CACTTGACCGGCTTACCGGAGGCTGCCAAGCCCGAGACTACACC		2659
Q	841	GlyGlyMetGly	LLeValAsnGlyAlaLysTPAsnProArgThArgTyLLeAsnAsp		860
D	2660	GGGGCATGGG	CACTCAACGGGGCAAGTGGAACCCCGGACCGGACTATCAATGAC		2719
Q	861	PheSerTyLeu	LhiThArgAsnCyLeuGluLeuSerPheTyLeuGlyCyAsArgLysPhe		880
D	2720	TTTAGTTACCT	GAATCAACATGCTGAGCTCTCTTCACTGGGCTGTGACAGATTC		2779
Q	881	ProhLeGluSer	LurProArgGluTPGlyLysAsnLysGluAlaLeuLeuThPhe		900
D	2780	CCTCATGAGAG	TGAGTGCCTCCCGGAGTGGAGAAACAAGAGGCGCTGCCTACCTTC		2839
Q	901	MetGluGlnVal	LhiArgGlyLLeLysGlyValAlaThrAspGlnGlnGlyLeProLLe		920
D	2840	ATGAGACAGGT	GACCGGCAATTAAGGGGTGTGACGACAGCAAGGCATCCCAT		2899
Q	921	AlaAsnAlaThr	LLeSerValSerGlyLLeAsnGlyValLysThArgLysArgGly		940
D	2900	GCCAAAGCCCA	CTCTCTGTGAGGTATTAATCAAGGCTGAAGACAGCACTGTGGT		2959
Q	941	AspTyTPArgL	ysLeuAsnProGlyGluTyArgValThArgLhiAlaGlnGlyTy		960

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D	2960	GATTACTGGGA	ATTTGAACCCGGGTAGTACCGGGTGCACAGCCACGCGAGGGCTAC		3019
Q	961	ThrProSerAla	LysThCyAsnValAspTyArgAspLLeGlyAlaThArgLysAsnPhe		980
D	3020	ACCCGAGGCGC	AAAGACTTGCAATTTGACTATGACATGGGGCCACTCAGTGCACTTC		3079
Q	981	LLeuAlaArgSer	AsnTPLysArgLLeArgGluLLeMetAlaMetAsnGlyAsnArg		1000
D	3080	ATCTTGCTGCT	CCAATGGAAGCCATCCGGAGATCATGGCCATGAAGGGAACCGG		3139
Q	1001	ProLLeProh	isLLeAspProSerArgProMetThProGlnGlnArgArgLeuGlnGln		1020
D	3140	CTATCCACA	CACTAAGCCATGCGCCCTATGACCCCAACAGAGAGCGCTGCAGAG		3199
Q	1021	ArgArgLeuGln	LhiArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla		1040
D	3200	CGAGCCTACA	CACCGCTGCGGCTTCGGGCAAGATCGGCTGCGGCGCTCAACGCC		3259
Q	1041	ThrThrThrLeu	GlyProhLLeThValProProThLeuProProhLLeProhLLeThThr		1060
D	3260	ACCACCACTA	GGCCCCCACTGTGCTCCACGCTGCCCCCTGCCACACC		3319
Q	1061	LeuSerThrTh	LLeGluProTPGlyLeuLLeProProThThArgLLeArgTyTPGlyGlu		1080
D	3320	CTGAGCACTA	CACTAAGGCTGGGGCTCATACCGCCCAACCGCTGGTGGAGAG		3379
Q	1081	SerGluThGlu	ThThTyThArgLValAlaThrGluPheGlyThArgLValGluProGlu		1100
D	3380	TCGGAAGCTGA	CACTACACAGGTGTGACAGATTTGGGACCGAGGTGAGAGCCCGAG		3439
Q	1101	PheGlyThTh	ValGluProGluPheGluThArgLLeuGluProGluPheGluThArgL		1120
D	3440	TTTGGACCA	AGGTGAGCCGAGTTTGAAGCCAGTTGAGCTGAGTTCGAGACCAG		3499
Q	1121	LeuGluProGlu	PheGluGluGluGluGluGluGluGluGluGluGluGluLLeAlaThArgL		1140
D	3500	CTGGAACCGG	AGTTTAGGAAGAAGAGAGAGAGAGAGAGAGAGATAGCACTGGC		3559
Q	1141	GlnAlaPhe	ProPheThThValGluThTyThThValAsnPheGlyAspPhe		1158
D	3560	CAGGCACTTCC	CTTCAACAAGTAGAGACTACACAGTGAACCTTGGGAGACTTC		3613

RESULT 4

ID	ADZ26196	standard; DNA; 3935 BP.
AC	ADZ26196;	
DT	16-JUN-2005	(first entry)
XX		
DE	Human gene Nb1a21871 nucleotide sequence SEQ ID NO:162.	
XX		
KW	microarray; nervous system tumor; cytostatic; neoplasia;	
KW	neurological disease; gene; ds; chromosome-7.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2005030959-A1.	
XX		
PD	07-APR-2005.	
XX		
PF	24-SEP-2004; 2004MO-JP014441.	
XX		
PR	25-SEP-2003; 2003US-0505614P.	
XX		
PA	(CHIB-) CHIBA PREPECTURE.	
PA	(HISM) HISIMITSU PHARM CO LTD.	
PA	(NIGA) NGK INSULATORS LTD.	
XX		
PI	Nakagawara A, Ohira M, Ishii S, Goto T, Kubo H, Hirata T;	
PI	Yoshida Y, Yamada S,	
XX		
DR	WPI; 2005-273381/28.	



DR GENBANK: NM\_001129.  
XX Method and microarrays for assessing neuroblastoma prognosis based on  
PT probes hybridizable with gene transcriptional product, useful in  
PT diagnosis, therapy selection and management of patients.  
XX  
PS Claim 1, SEQ ID NO 162; 440bp; Japanese.  
XX  
CC The invention relates to microarrays for assessing the prognosis of  
CC neuroblastoma, which contains 25-45 good prognosis probes selected from  
CC among 96 polynucleotides which are hybridizable with a gene  
CC transcriptional product that shows accelerated expression in patients  
CC having good prognosis of neuroblastoma, which comprise the nucleotide  
CC sequences of AD226035-AD226130, their partial consecutive sequences or  
CC complementary chains, and 25-45 bad prognosis probes selected from among  
CC 104 polynucleotides which are hybridizable with a gene transcriptional  
CC product that shows accelerated expression in patients having good  
CC prognosis of neuroblastoma, which comprise the nucleotide sequences of  
CC AD226131-AD226234, their partial consecutive sequences or complementary  
CC chains. Also described is a method for assessing neuroblastoma prognosis  
CC comprising: (a) labeling a gene transcriptional product obtained from the  
CC tumor cells of patients with neuroblastoma; (b) contacting the labeled  
CC material with the microarray; and (c) measuring label signals from the  
CC hybridized gene transcriptional product. The patient is judged to show  
CC good prognosis when significant label signals are obtained from those  
CC hybridized with 25 good prognosis probes, but however when significant  
CC label signals are obtained from those hybridized with 25 bad prognosis  
CC probes, such patient is judged to have poor prognosis. The method and  
CC microarrays are for assessing neuroblastoma prognosis, and therefore are  
CC useful in diagnosis, therapy selection and management of patients  
CC suffering from neuroblastoma. The present sequence represents a human  
CC gene transcriptional product which shows accelerated expression in  
CC patients having good prognosis of neuroblastoma.  
XX  
SQ Sequence 3935 BP; 923 A; 1243 C; 1185 G; 584 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 1, 77e-290 Length: 3935  
Score: 6272.00 Matches: 1158  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 14 Gaps: 0  
US-10-642-946-3 (1-1158) x AD226196 (1-3935)  
QY 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20  
DB 140 ATGGCGGCGGTGGCGGGGCGCCCTGCTCAGCTGCTCTGCGCTGGCCCTGTGC 199  
QY 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGlnGlnPheLeuGlnGly 40  
DB 200 CCGGAGGGCGCGCGGAGACGGTGTACCGACGACGAGATCGAAGATTCCTCGAGGCG 259  
QY 41 PheLeuSerGlnLeuGlnProGlnProArgGluAspAspValGlnAlaProProPro 60  
DB 260 TTCCTTCAGAGCTTAACCTGAGCCCGGAGGAGACGACTGAGGCGCCCGGCTCC 319  
QY 61 GlnProThrProArgValArgGlyAlaGlnAlaGlyGlyLeuProGlyTyrAspProGly 80  
DB 320 GAGCCACACCGCGGGTCCGAAAGCCAGCGGGGGGCAAGCCAGGAAAGCGGCAAGG 379  
QY 81 ThrAlaAlaGlnValaProProGlnGlySerThrLeuAspLeuGlyValSerGlyValSer 100  
DB 380 ACCGCGCGCAAAATGCTCCCGGAAAGACCAAGAACAAAGGAAAGCAAGAAAGAC 439  
QY 101 LysGlyProLeuValProLysGlnSerLeuGlnGlySerProArgProProLysGly 120  
DB 440 AAAAGGCCCAAGGTGCCAAGAGTCTTGGAGGGGTCCCGGCGGCCCAAGAAAGGG 499  
QY 121 LysGlnLysProProLysAlaThrLysLysProLysGlnLysProProLysAlaThrLys 140  
DB 500 AAGGAAGAGCAACCAAGGCAACCAAGAGCCCAAGAGAAAGCCACTTAAGGCCACCAAG 559

QY 141 LysProLysGlnGlnProProLysAlaThrLysLysProLysGlnLysProProLysAla 160  
DB 560 AAGCCCAAGAGAGGCCCAAGGCCACCAAGAAAGCCCAAGAAAGCAACCCCAAGGCC 619  
QY 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGlnThrLeuGln 180  
DB 620 ACCAAGAAAGCCCGCTCAGGAGAGAGGCCCCCATTTGGCTCCCTCAGAAACCTGGAG 679  
QY 181 TrpProLeuProProProProSerProGlyProGlnGlnLeuProGlnGlnGlyVala 200  
DB 680 TGGCCACTGCCCCCAACCCCGAGCCCTGCGCGGAGGCTAACCCAGAGGAGAGGGGG 739  
QY 201 ProLeuSerAspAspThrGlnAspProGlyGlnGlnGlnThrLysValaGlnGlnGln 220  
DB 740 CCCCTCAAAATTAATGGAGATTCAGAGAGAGAGCCCATGTGGAGGACAGAGAC 799  
QY 221 GlnProGlnProGlnGlnGlnThrGlnGlnProThrLeuAspTyrAspAspGlnIleGln 240  
DB 800 CAGCCTGAGCGCGAGAGAGAGAGCCGAGCAACCACTGAGCTAATGACCAATCGAG 859  
QY 241 ArgGluAspTyrGluAspPheGlnTyrIleArgArgGlnLysGlnProArgProProPro 260  
DB 860 AGGGAGGACTATGAGAGACTTGTAGTACATTCGGCCGCAAGAACCAAGCCAGGCCCA 919  
QY 261 SerArgArgArgArgProGlnArgValaTrpProGlnProProGlnGlnLysAlaProAla 280  
DB 920 ACCAAGAGAGAGAGGCCCGAGAGGGTCTGGCCAGAGCCCTGAGAGAGAGGCCCGGCC 979  
QY 281 ProAlaProGlnGlnArgIleGlnProProValLysProLeuLeuProProLeuProPro 300  
DB 980 CCAGCCCGGAGAGAGAGATTAAGCTCTCTGGAAGCCCTGTGCTCCCGCTGCCCT 1039  
QY 301 AspTyrGlyAspGlyTyrValIleProAspThrAspAspMetAspTyrTyrPheGlyPro 320  
DB 1040 GACTATGGATGATGATTAAGTATCCCAACTACGATGACATGACTATTACTTTGGGCT 1099  
QY 321 ProProProGlnLysProAspAlaGlnArgGlnThrAspGlnGlnGlnGlnGlnGln 340  
DB 1100 CCTCGGCCCAAGAACCCGATCTGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1159  
QY 341 LysProLysLysGlnAspSerSerProLysGlnGlnGlnThrAspLysTyrAlaGlnLys 360  
DB 1160 AAACCCAAAGAGAGAGAGAGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1219  
QY 361 GlyLysAspPheLysGlnProArgLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 380  
DB 1220 GGCAAGAGACCAAGAGAGCCCGGAAAGGCGAGGAGTGGAGAGAGAGAGAGAGAGAG 1279  
QY 381 GlnLysValLysCysProProIleGlyMetGlnSerHisArgIleGlnAspAspGlnIle 400  
DB 1280 GAGAAAGTCMAGTGCTCCCGCATTTGGATGAGTCAACCCGATTTGAGGACAAACAGATC 1339  
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlnGlnAlaGlnArgLysArgLeuAspMetGln 420  
DB 1340 CGAGCCTCCTCATCTGTGGCCACGAGCTGGGGGACAGCGCGGCGGCTCAACATGACAG 1399  
QY 421 ThrGlyAlaThrGlnAspAspTyrTyrAspGlyAlaTrpCysAlaGlnAspAspAlaArg 440  
DB 1400 ACCGGTGCACAGAGAGACGACTATGATGATGTGGTGTGGCCAGAGACGATGCGAG 1459  
QY 441 ThrGlnTrpIleGlnValaAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460  
DB 1460 ACCCATGATGATGAGAGTGAACCAAGAGAGACTACCCGGTTACAGAGGCTCATCACCCAG 1519  
QY 461 GlyArgAspSerSerIleHisAspAspPheValaThrThrPhePheValaGlyPheSerAsn 480  
DB 1520 GGCAAGAGACTCAGACATCATGACATTTTGGACCACTTCTGTGGTGGCTTCAGCAAT 1579  
QY 481 AspSerGlnThrTrpValaMetTyrThrAspGlnGlyTyrGlnGlnMetThrPheHisGlyAsn 500  
DB 1580 GACAGCAACATGAGGTATGATACCAACAGGCTATGAGAAATGACTTTTATGAGGAAC 1639



QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaArgPheIle 520  
 DB 1640 GTGGACAGGACACCCGGTGTGAGTACCTCCAGGCGGGTGGTCTCTTCATC 1699  
 QY 521 ArgIleTyrProLeuThrTrpAengIYSerLeuCyMetArgLeuGluValLeuGlyCys 540  
 DB 1700 CGCATCTACCACTCACTGGAATGGCAGCTGTGACATGGCTGGAGGGTGGCTGGGGTGC 1759  
 QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaThrAspAspLeu 560  
 DB 1760 TCTGTGGCCCTCTCTCAACCTCACTACGACAGAACTAGGTGGTGGCCAGTGTGACTG 1819  
 QY 561 AspPheArgHisIleSerTyrLysAspMetArgIleuMetLysValAlaAsnGluGlu 580  
 DB 1820 GATTTCCGGACACACAGCTACAGAGACATGGCCAGCTCATGAAGGTGGTGAACGAGAG 1879  
 QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLeuLysIleTyr 600  
 DB 1880 TGGCCACCATCAACCCGCACTTACAGCTGGGCAAGAGCTCAAGAGGCTCAAGATCTAT 1939  
 QY 601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620  
 DB 1940 GCCATGAGATCTTCAGACAACTCTGGGGAGCATGAATGGGGAGCCCGAGTTCGGCTAC 1999  
 QY 621 ThrAlaGlyIleHisGluAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640  
 DB 2000 ACTGCTGGGATCCATGACCAAGAGTGTGGCCGAGAGCTGTGCTGCTGCATGACGAG 2059  
 QY 641 TyrLeuCyArgGlyTyrArgAspGlyLysProArgValArgSerLeuValGlnAspThr 660  
 DB 2060 TACCTTGGCGAGAGTACCCGCACTGGGAACTCAGTGTGGCAGCTGTGGCGAGGACACA 2119  
 QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAsnMetGly 680  
 DB 2120 CGCATCCACTGGTGGCTCTCACTGAACCTCATGAGCTACGAGGTGGCAGCGCAGATGGCG 2179  
 QY 681 SerGluPheGlyAsnThrAlaLeuGlyLeuThrThrGluGluGlyPheAspIlePheGlu 700  
 DB 2180 TCAAGATTTGGGAATCGGGGCTGGGACTGTGAGATGAGAGGGCTTTGACATCTTTGAA 2239  
 QY 701 AspPheProAspLeuAsnSerValLeuTyrGlyAlaGluGluArgLysTrpValProTyr 720  
 DB 2240 GATTTCCCGGATCTCACTCTGTGCTCTGGGAGCTGAGAGAGGAAATGGGCTCCCTAC 2299  
 QY 721 ArgValProAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740  
 DB 2300 CCGGTCCTCCCAACAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2359  
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 DB 2360 TCCACCGAGGTCCGGGCTCATCTGCTGATGAGAAAGAACCTTCTGCTGCTGCTGCTGCT 2419  
 QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
 DB 2420 AATCTGAAGCGCGGCGGAGCTAGTACTTACCTTACCTTACCTTACCTTACCTTACCT 2479  
 QY 781 GlnGluGlnLeuLeuAlaAlaMetValAlaAlaArgGlyGlyLeuAspGluAspGluVal 800  
 DB 2480 CAGGAGCACTGCTGGCCGACGATGAGCAGCCCGGGGGAGATGAGAGCAGAGTCC 2539  
 QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgThrLeuAlaIleSerPheAla 820  
 DB 2540 TCCGAGGCGGAGAGACTCCAGACCAAGCATCTTCCGGTGGCTGGCCATCTCTCTGCTG 2599  
 QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840  
 DB 2600 TCCGACACACTCACTTGAACCGAGCTTACCGGAGGCTGACAAACCGAGACTACAC 2659  
 QY 841 GlyGlyMetGlyTyrLeuAlaGlnGlyAlaLysTrpAsnProArgThrGlyThrIleAsnAsp 860  
 DB 2660 GCGGAGATGGGCAATCTCTCAACCGGGGCAAGTGGAAACCCCGGACCGGACTATCAATGAC 2719  
 QY 861 PheSerTyrLeuHisIleThrAsnCybLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880

DB 2720 TTCAGTTACCTGCATACCACTGCTGGAGCTCTCTTCTACTGGGCTGTGACAACTTC 2779  
 QY 881 ProHisGluSerGluLeuProArgGluTyrGluAsnAsnLysGluAlaLeuLeuThrPhe 900  
 DB 2780 CCTCATGAGAGTACGTGGCCCGGAGTGGAGAAACAACAGAGGCGCTGCTCACTTC 2839  
 QY 901 MetGluGlnValHisArgGlyTyrLeuGlyValValThrAspGluGlnGlyIleProIle 920  
 DB 2840 ATGAGCAGATGACCCGCGCATTTAAGGGGGTGTGTACGAGCAGACAGCATCCCATTT 2899  
 QY 921 AlaAsnAlaThrIleSerValSerGlyTyrLeuHisGlyValIleLysThrIleSerGlyGly 940  
 DB 2900 GCCAACGCCAATCTCTGTAGTGGCTATTATACGGGGTGAAGACAGCCAGTGGTGGT 2959  
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 DB 3020 ACCCGAGCGCCAAAGACTGCAATGTGACTATGACATCGGGGCCACTCAGTGCAACTTC 3079  
 QY 981 IleLeuAlaArgSerAsnThrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000  
 DB 3080 ATCTGGCTGTGCTCCAACTGAAAGGCATCCGGAGATATGACCCTGAACCGGAACTGG 3139  
 QY 1001 ProIleProHisIleAspProSerArgPrometThrProGlnGlnArgArgLeuGlnGln 1020  
 DB 3140 CCTATCCACACATGAGACCCATGTGGCCCTTATGAGCCCCCAACAGAGAGCTGTGACGAG 3199  
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 DB 3260 ACCACACCTTAGGCCCCACACTGTGCTCCACAGCTGCCCCCTGTGCACACACC 3319  
 QY 1061 LeuSerThrThrIleGluProThrGlyLeuIleProProThrThrAlaGlyTyrGluGlu 1080  
 DB 3320 CTGAGACATCACTAGAGCTTGGGGCCCTCATACCGCAACACCGCTGGTGGAGGAG 3379  
 QY 1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100  
 DB 3380 TCGGAGACTGAGACCTACACAGAGGTGTGACAGAGTTTGGGACCGAGGTGAGCCCGAG 3439  
 QY 1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120  
 DB 3440 TTTGGACCAAGGTGAGCCGAGATTGAGACCCAGTTGAGCCTGAGTTGAGAACCCAG 3499  
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
 DB 3500 CTGGAACCGGATTTGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGATACCACTGGC 3559  
 QY 1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158  
 DB 3560 CAGGATTCCTCCCTTACAACAGTAGAGACTACAGTAGAATCTTTGGGGGACTTC 3613  
 DB  
 RESULT 5  
 ID AD086121  
 ID AD086121 standard; cDNA; 3914 BP.  
 AC AD086121;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2993.  
 XX human; tumour-associated antigenic target; TAT; cytosstatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.  
 XX  
 OS Homo sapiens.



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Db 1220 GCGAAGACCAACAAGAGCCCGCAAGGCGAGAGTGGAGAGAGAGTGGACGCTACG 1279
Qy 381 GILuYValIyCyProProlIeGIYMeGlUSeRthIaRgIleGIuAaPaangIle 400
Db 1280 GAAAAAGTCAAAAGTGTCCCGCATTTGGAGTGAAGTCAACCGTATTGAGCAACCGATC 1339
Qy 401 ArgAlSeSerMetLeuAArgHISGlyLeuGIYValAGlnAArgIlyArGLeuaAmMetGln 420
Db 1340 CGAGCTCTCTCAATGCTGCGCCACGCGCTGGGGCAGACGCGCGCTCAACATGACG 1399
Qy 421 ThrGIYAlaThrGIuAaPaAerTYrTYrAaPGIYAlaTTPCySaIaGIuAaPaAaIaRg 440
Db 1400 ACCGGTGCCACTAGAGACGACTCTAATGATGCTGCGTGTGCTGCCAGAGACATGCCAG 1459
Qy 441 ThrGIuTTPleGIuValAaPthArAArgXThrThraRphThrGIYValIleThrGln 460
Db 1460 ACCAGTGGATTAAGGAGGACACCAAGAGAGACTACCGGTTCAAGGCGTCATCACCCAG 1519
Qy 461 GlYArAaPSeSerIleHISaAaPaAaPheValThrThraRphPheValGIYPhSeSerAa 480
Db 1520 GCGAGAGACTCCAGACATCCATGACGATTTGTGACCACTTCTTGCGGGCTTCAGCAAT 1579
Qy 481 AaPSeSerGIuThrTrpValMeCTYrThraAaNGIYTYrGIuGIuMeCTThraPheHISGlyAa 500
Db 1580 GACAGCCAGACATGGGTGATGACACCAACGCTATGAGAAATGACCTTTCATGGGAC 1639
Qy 501 ValAaPlyAaPthProValLeuSeRGIuLeuProGIuProValAlaIaArGpHeIle 520
Db 1640 GTGGACAAGACACACCGGTGTGAGTGAAGTCCCAAGCGGAGTGGGTCTGTTTCATC 1699
Qy 521 ArgIleTYrProleuThrTPAaNGIYSeRLeuCyMeCArgLeuGIuValIleuGIYCyS 540
Db 1700 CGCATTAACCACTCACTGGAATGGAGCTGTGATGCGCTGAGAGGTGCGGAGTGC 1759
Qy 541 SerValAlaProValTYrSeRTYrTYrAlaGIuAaNGIuValAlaIaThraPaAaPleu 560
Db 1760 TCTGTGGCCCTCTCTACAGCTACTACGACACAAATAGGTGGTGGCCACCGATGACTG 1819
Qy 561 AaPthArAArgHISeRTYrIlyAaPMeCArgGlnLeuMeIlySaIValaIaNGIuGIu 580
Db 1820 GATTTCCGGACACCAAGCTCAAGACATGCGCAGCTCATGAAGGTGGAGACGAGAG 1879
Qy 581 CyProThrIleThraRgThrTYrSeRLeuGIYlySeSerArGgIYLeuIlySeIleTYr 600
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Qy 601 AlaMeGIuIleSeRPaAaPProGIYGIuHISGlyLeuGIYGIuProGIuPhaArGYr 620
Db 1940 GCCATGGAATCTCAACAAACCTGGGGAGCATGAATGGGGAGGCCCAAGTTCCGCTAC 1999
Qy 621 ThrAlaGIYIleHISGlyAaNGIuValaIleuGIYArGIuLeuLeuLeuLeuMetGln 640
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Qy 661 ArgIleHISeRLeuAlProSeRLeuAaPProAaPGIYTYrGIuValAlaIaIaGIuMeGIY 680
Db 2120 CGCATCACTGTGTGCTCACTGAACCTCGATGCTCAAGAGTGGCAGCGCAGATGGGG 2179
Qy 681 SerGIuPhaGIYArAaPthAlaGIuGIYLeuTYrThrGIuGIuGIYPhaAaPleIlePhaGIu 700
Db 2180 TCAGATTTGGGAATCGGGCGCTGGGACTGTGACTGAGAGAGGGCTTTGACATCTTGA 2239
Qy 701 AaPthArAaPSeRLeuAaPSeRValLeuTYrThrGIYAlaGIuGIuArGlySTrPValProTYr 720
Db 2240 GATTTCCCGGATCTCAACTGTGCTCTGGGGAGCTGAGGAGAGAAATGGGTCCCTAC 2299
Qy 721 ArgValaProAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 740
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Qy 761 AaRLeuAaNGIYGIYGIuArGLeuValaSeRTYrTYrTYrAaPMeIlyAaRgThrProThr 780
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Db 2660 GCGGCATGGGACTGCTCAACGGGGCAAGTGGAAACCCCGGACCGGACTATCATGAC 2719
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Qy 981 IleuValaArgSeRAsaNTpIlySaRGIleArGIuIleMeCAlaMeCArgIlyAaAaRg 1000
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Qy 1041 ThrThrThrLeuGIYProHISThraValProProThrLeuProProAlaThrThr 1060
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Qy 1061 LeuSeRThrThrIleGIuProTYrGIYLeuIleProProThrThraIaGIYTPGIuGIu 1080
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Qy 1081 SerGIuThrGIuThrTYrThrGIuValaIThrGIuPhaGIYThrGIuValaGIuProGIu 1100
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QY 301 AspTyrGlyAspGlyTyrValIleProAsnTyrAspMetAspTyrTyrPheGlyPro 320  
DB 1040 GACTATGTAAGTGTACGTGATCCCAACTACATGACATGACTTATCTTGGGCT 1099  
QY 321 ProProGluInyProAspAlaGluArgGlnThrAspGluGluGluGluLeuLys 340  
DB 1100 CTTCGGCCCAAGAACCCGATGCTGAGCGCCAGACACAGAGAGAGAGAGAGCTGAG 1159  
QY 341 LysProLysAlaGluAspSerSerProLysGluGluThrAspLysTyrAlaValGluLys 360  
DB 1160 AAACCCAAAAGAGGAGACAGACGCCCAAGAGAGAGACCGCAAGTGGCGCATGAGAG 1219  
QY 361 GlyLysAspHisLysGluProArgLysGlyGluGluGluGluGluGluGluGluGlu 380  
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QY 381 GluLysValLysCysProPheIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400  
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QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyValGlnArgGlyArgLeuAsnMetGln 420  
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QY 441 ThrGlnTyrIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460  
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QY 601 AlaMetGluLysSerAspAsnProGluGluHisGluLeuGluGluProGluPheArgTyr 620  
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QY 641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
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QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680  
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QY 701 AspPheProAspLeuAsnSerValLeuTyrGlyAlaGluGluArgLysTyrValProTyr 720  
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DB 2540 TCCGAGGCCCAAGAGACTCCAGACACAGCATTTCCGGTGGCTTCATCTCTTCGCC 2599  
QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840  
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QY 841 GlyGlyMetGlyIleValAsnGlyAlaLysTyrAspProArgThrGlnIleAsnAsp 860  
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QY 981 IleLeuAlaArgSerAsnTyrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000  
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QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgLeuAsnAla 1040



Dh	1086	AGCAAGAGAGGAGCGCCGAGCGGGTCTGGCCAGAGCCCTTGAGAGAGAGGCCCGGCG	1145
Qy	281	ProAlaProGluGluAArgIleGluProProValIlyProLeuLeuProProLeuProPro	300
Dh	1146	CCAGCCCCGGAGAGAGAGTTGAGGCTCCTGTGAAGCCTCTGTGCCCCCGCTGCCCT	1205
Qy	301	AapTyrgIyAapGlyTyTyValIleProAenTyraAapMetAapTyTyTyPheGlyPro	320
Dh	1206	GACTATGGTGTATGGTTAGCTGTATCCCAACTACGATGACATAGCATATATCTTTGGGCT	1265
Qy	321	ProProProGluIlyProAapAlaGluTyrgIleProGluIlyAapGluGluIlyLeuLeu	340
Dh	1326	AAACCCAAAAGAGAGACAGACGCCCCAGAGAGAGACCGACMACTGGGCACTGGAGAG	1385
Qy	361	GlyTyAapAphIleTyGluProAArgIyGlyGluLeuGluGluGluIlyTyTyProThr	380
Dh	1386	GGCAAGGAGACCAAAAGAGCCCCGAAAGGGCGAGGTTGGAGAGAGATGGACGCTACG	1445
Qy	381	GlyIlyAapValIlyProProProIleGlyMetGlySerHisArgIleGluAapAapGluIle	400
Dh	1446	GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTACACCGTATTGAGAGACAAACAGATC	1505
Qy	401	ArgAlaSerSerMetLeuAArgHisGlyLeuGlyAlaGluAArgGlyAArgLeuAapMetGln	420
Dh	1506	CGAGCTCTCTCAATGCTGCGCCACGGCTGGGGGCGACGCGCGGCTCAACATGCGAG	1565
Qy	421	ThrGlyAlaThrGluAapAapTyTyTyraApyAlaTyProCyAlaGluAapAapAlaArg	440
Dh	1566	ACGGGTGCACACTAGAGACGACTACTATGATGGTGTGTGTGTGCGGAGAGCATGGCAGG	1625
Qy	441	ThrGlnTyPylleGluValAapThrAArgArgThrAArgPheThrGlyValIleThrGln	460
Dh	1626	ACCCAGTGAATAGAGGTGAGACCCAGGAGACTACCCGTTTCACAGGGTCATACCCAG	1685
Qy	461	GlyAArgAapSerSerIleHisAapAapPheValThrThrPhePheValGlyPheSerAap	480
Dh	1686	GGCAGAGACTCCAGATCCATGACGATTTGTGACCACTTCTGTGTGGCTTCACGCAAT	1745
Qy	481	AapSerGlnThrTyPylleValMetTyTyThrAangIlyTyrgIuGluMetThrPheHisGlyAap	500
Dh	1746	GACAGCCAGACATGGGTATGTATACCAACGACTATAGAGAAATGACCTTTCATGGGAGAC	1805
Qy	501	ValAapIlyAapThrProValLeuSerGluLeuProGluProValValAlaAapPheIle	520
Dh	1806	GTGGCAAGAGACACACCCGTGTGATGAGTCCACAGGCGGGTGTGGCTCGTTTCATC	1865
Qy	521	ArgIleTyTyProLeuThrTyPylleAangIlySerLeuCyMetAArgLeuGluValLeuGlyCys	540
Dh	1866	CGCATCTACCACTCACTCGAATGGACGCGCTGTGCATGCCCTCGAGAGTGTGGGGTGC	1925
Qy	541	SerValAlaProValTySerTyTyTyraGluAangIlyValAlaAapAapLeu	560
Dh	1926	TCTGTGGCCCTGTCTTCACTACGTAACCAACGAATAGATGTGTGGCCACCGAGATGACTG	1985
Qy	561	AapPheAArgHisAesTyTyTyraAapMetAArgGluLeuMetIlyValAapGluGlu	580
Dh	1986	GATTTCCCGGACACACAGCTTACAGGATCGCGCCAGCTCAGAAAGTGTGAACGAGGAG	2045
Qy	581	CysProThrIleThrAArgThrTyTySerLeuGlyIlySerSerAArgGlyIlyLeuIlyIleTy	600
Dh	2046	TGCCCCACCATCACCCGCACTTACAGCTGTGGCAAGACTCAGAGGCTTCMAATCTAT	2105
Qy	601	AlaMetGluIleSerAapAapProGlyIlyHisGluLeuGlyGluProGluIlyAArgTy	620
Dh	2106	GCCATGGAGATCTCAGACACCTCTGGAGCATGAATCGGGGAGGCCGAGATTCCGCTAC	2165
Qy	621	ThrAlaGlyIleHisGlyAapGluValLeuGlyAArgGluLeuLeuLeuLeuMetGln	640
Dh	2166	ACTGTGGGATTCATAGGACGAGAGGTGTGGGGCCAGAGCTGTGTCTCTCATCAG	2225

QY	641	lyrlenCySaRggluTyrraRgApGlYanP-oArGyVaLaRserleuValGlnaSPthr	660
Db	2226	TACCTGTCCGAGAGTACCGGATGGGAACCACTGTGGCCAGCTGTGTCAAGACCA	2285
QY	661	ArgIleHsleuValProSerleuAnPProAspGlyTYrGluValAlaAlGImetGly	680
Db	2286	CGCATCCACCTGTGTCCTCACTGAACCTGATGGCTACAGAGTGAGCCAGATGGGC	2345
QY	661	SerGluPheGlyAsnTPAlaLeuGlyLeuTPThrGluGluGlyPheAspIlePheGlu	700
Db	2346	TCAGAGTTGGGAACCTGGGCGCTGGGACTGTGGACTGAGAGAGGCTTTGACATCTTTAA	2405
QY	701	AspPheProAspLeuAsnSerValLeuTPGlyAlaGluValaGlyLeuTPValProThr	720
Db	2406	GATTTCCCGGAGTCTCACTGTGTGTCTGGGAGCTGAGAGAGAAATGGGTCCTTAC	2465
QY	721	ArgValProAsnAsnAsnLeuProIleProGluARgTYrleuSerProAspAlaThrVal	740
Db	2466	CGGGTCCCAACATTAATTGCGCATTCCTGAAGCTACCTTTGGCCAGATGCCAGGTA	2525
QY	741	SerThrGluValaRgAlaIlelleAlaTPMetGluYAsnProPheValleuGlyAla	760
Db	2526	TCACGGAGGTCCGGGCGCATTTGCCGTGATGAGAGAAACCCCTTGCTGGAGACA	2585
QY	761	AsnleuAnGlyGlyGluArgleuValSerTYrProTYrAspMetAlaArgThrProThr	780
Db	2586	AATCTGAACGGCGGAGAGCGGCTAGTATCTTACCTTCAGATATGCGCCAGCTTACC	2645
QY	781	GlnGluGluLeuLeuAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal	800
Db	2646	CAGGAGCAGCTGTGGCCGACCATGGAACAACCCCGGGGGAGATGAGAGACAGGTC	2705
QY	801	SerGluArgGluTPThrProAsnHsAlaIlePheArgTPleuAlaIleSerPheAla	820
Db	2706	TCCGAGGCCAGAGACTCCAGACCAGCCATCTTCGGTGGCTTGCATCTCTTGCC	2765
QY	821	SerAlaHsleuTPThrLeuThGluProTYrArgGlyGlyCysGluAlaGluAspTYrThr	840
Db	2766	TCCGAGACCTCACTTGACCGAGCCCTACCGGGAGGCTGCAAGCCCAAGACTACAC	2825
QY	841	GlyGlyMetGlyIleValAsnGlyAlaAlaYsTPAsnProArgThrGlyThIleAsnAsp	860
Db	2826	GCGGCGAAGGCGCATCTGTCAACGGGGCCAAAGTGAAACCCCGGACCGGACATCAATGAC	2885
QY	861	PheSerTYrleuHsIsthAsnCYleuGluLeuSerPheTYrleuGluCYAspLysPhe	880
Db	2886	TTCAATTAACCTGCATACCACTGCTGGAGCTTCTCTTCTTACCTGGGCTGTGACAGATTC	2945
QY	881	ProHsGluSerGluLeuProArgGluTPGluAsnAsnGlyAlaLeuLeuThrPhe	900
Db	2946	CCTCATGAGATGAGCTGCCCGCCGAGTGAGGAACAACAAGAGGCGCTGTCACTTC	3005
QY	901	MetGluGluValHsArgGlyIleLysGlyValValaThrAspGluGluGlyIleProIle	920
Db	3006	ATGAGACGAGTGACCGCGGCAATTAAGGGGGGTGTGACGAGCGAGCAAGGATCCCCATT	3065
QY	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHsGlyValaIlysthrAlaSerGlyGly	940
Db	3066	GCCAAAGCCACATCTCTGTGATGTGCATTATCAACGGCGTGAAGACAGCCAGTGTGCT	3125
QY	941	AspTYrTPArgIleLeuAsnProGlyGluTYrArgValaThrAlaHsAlaGluGlyTYr	960
Db	3126	GATTACTGGCCAAATCTTGAAACCGGGTGATGACCGCGTGACAGCCCAACGCGAGGCTTAC	3185
QY	961	ThrProSerAlaYsTPThrCYAsnValaAspTYrAspIleGlyAlaTPArgGluCYAsnPhe	980
Db	3186	ACCCGAGCGCCAAAGACTTGCATATGTGACTATACATCGGAGGCACTCACTGCACTTC	3245
QY	981	IleLeuAlaArgSerAsnTPLyAspGlyleArgGluIleMetAlaMetAsnGlyAsnArg	1000
Db	3246	ATCTCGGTGCTCTCACTGGAAACCGATCGGGAGATCATGAGCATGAACGGGAACCGG	3305







QY 301 AsPTyGlyAspGlyTyrValIleProAsnTyrAspMetAspTyrTyrPheGlyPro 320  
DB 1019 GACTATGGTAAAGTTTACGTGATCCCACTACAGATGACATGACTTATCTTGGGCGCT 1078  
QY 321 ProProProGlnIlyProAspAlaGluArgGlnThrAspGluGluIlyAspGluIlyLeu 340  
DB 1079 CTTCCGCGCCAGAAAGCCGATGGTGAAGCGCCAGACGAGACGAAAGAAAGAGAGCTGAA 1138  
QY 341 LysProIlyLeuGluAspSerSerProIyGluGluThrAspIlyTyrAlaValGluLys 360  
DB 1139 AAACCCAAAAGAGGACAGCAGCGCCCAAGAGAGAGCCACAAAGTGGGACGAGGAGAG 1198  
QY 361 GluLysAspHisIlyLeuGluProArgLysGluGluGluIlyGluGluGluIlyProThr 380  
DB 1199 GCGAAGGACCAAAAGAGCCCGAAAGGAGAGAGTGGAGAGAGAGAGAGCGCTACG 1258  
QY 381 GluLysValIlyAspProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400  
DB 1259 GAGAAAGTCAAGTGTCCCGCCATTGGGATGGAGTCAACCGGTATGAGAGCAACAGATC 1318  
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420  
DB 1319 CGAGCTCTCTCAATGCTGCCACAGGCTGGGGGACAGCGCGCGCTCAACATGCAG 1378  
QY 421 ThrGluValIleThrGluAspAspTyrTyrAspGlyAlaTyrProCysAlaGluAspAspAlaArg 440  
DB 1379 ACCGGGTGCCACTAGAGGACGACTACTATGATGTGCGTGTGCCAGAGGACGATGCCAG 1438  
QY 441 ThrGlnTyrIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460  
DB 1439 ACCCATGGATTAAGGTGGACACACAGAGAGACTAACCGGTTCACAGCGCTACACCCAG 1498  
QY 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480  
DB 1499 GGGAGAGACTCCGCAATCCATGACGATTTGTGACCACTTCTTCGGGGCTTCAACAT 1558  
QY 481 AspSerGlnThrTyrValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500  
DB 1559 GAGAGCCAGACATGGGTGATGATACCCAGCGCTATGAGGAAATGACCTTTCATGGAGAC 1618  
QY 501 ValAspLysAspThrProValIleuSerGluLeuProGluProValValAlaArgPheIle 520  
DB 1619 GTGGACAGAGACACCCCGTGTGAGTGAAGCTCCAGAGCGCGTGGTCTCTTTCATC 1678  
QY 521 ArgIleTyrProLeuThrTyrAsnGlySerLeuCysMetArgLeuGluValIleGlyCys 540  
DB 1679 CGCATCTACCCACTCACTGGAAATGGCAGCTGTGCATGCGCTGGAGGGTGTGGGGTGC 1738  
QY 541 SerValAlaProValIlySerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeu 560  
DB 1739 TCTGTGGCCCTGTCTTACAGTACTACGACACAGAAATGAGGTGTGGCCACCGATGACTG 1798  
QY 561 AspPheArgHisIleSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGln 580  
DB 1799 GATTTCCGGCACACAGCTTACAGACATGCGCACTCATGAAGTGGTGAACGAGAGAG 1858  
QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuIlyIleTyr 600  
DB 1859 TGGCCACACATCACCGGCACTTACAGCTGGGCAAGAGCTCAAGAGGCTCAAGATCTAT 1918  
QY 601 AlaMetGluIleSerAspAsnProGluGluHisGluLeuGlyGluProGluPheArgTyr 620  
DB 1919 GCCATGAGATCTCAACAAACCTGGGAGACATGAATCGGGAGGCGGAGTTCCCTCAG 1978  
QY 621 ThrAlaGlyIleHisGluAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640  
DB 1979 ACTGCTGGGATTCATGGAAACGAGGTGCTGGGCGGAGAGCTGTGCTGCTCCTCAGCG 2038  
QY 641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
DB 2039 TACCTGTGCGAGATGACCGGATGGAAACCCAGCTGTGCGAGCTGGTGCAGAGACACA 2098

QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaIleGlnMetGly 680  
DB 2099 CGCATCCAGCTGTGTGCTTCACTGAACCTGATGGCTACGAGGTGGACGCGAGTGGCG 2158  
QY 681 SerGluPheGlyAsnTyrAlaLeuGlyIleTyrThrGluGluGluIlyPheAspIlePheGlu 700  
DB 2159 TCAGATTTGGGAACCTGGGCGCTGGGACTGTGACATGAGAGAGGCTTTACATCTTTGAA 2218  
QY 701 AspPheProAspLeuAsnSerValIleTyrGlyAlaGluGluArgLysTyrValProTyr 720  
DB 2219 GATTTCCCGATCTCAACTGTGTCTGGGGAGCTGAGAGAGGAAAGGGTCCCTCAG 2278  
QY 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740  
DB 2279 CGGGTCCCAACATATCTTGCCATCCCTGAACGCTACTTTCGCAATGCCAGGTA 2338  
QY 741 SerThrGluValArgAlaIleIleAlaTyrMetGluLysAspProPheValIleGlyAla 760  
DB 2339 TTCACGAGAGTCCGGGCGCATTCCTGGATGGAGAAAGACCCCTTGGTGGGAGCA 2398  
QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
DB 2399 AATCTGAACGGCGCGCAGAGCGCTAGATCTTACCTTACGATATGCGCCGACGCTTACC 2458  
QY 781 GlnGluGlnLeuLeuAlaIleAlaMetAlaAlaIleArgGlyGluAspGluAspGluVal 800  
DB 2459 CAGAGACAGCTGTGGCCGACAGCATGGAGAGCGCGGAGGAGATGAGACGAGGTG 2518  
QY 801 SerGluAlaGlnIlyThrProAspHisAlaIlePheArgTyrPheValIleSerPheAla 820  
DB 2519 TCGAGAGCCCAAGAGACTCCAGACACGCGCATCTTCGGTGGCTTCCATCTTCGCG 2578  
QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840  
DB 2579 TTCGCACACCTCACTTGAACCGACTACCGCGGAGCTGGCAGAGCCAGACCTACACC 2638  
QY 841 GlyGluMetGlyIleValAsnGlyAlaLysTyrAsnProArgThrGlyThrIleAsnAsp 860  
DB 2639 GGGGAGATGGGATCTCTCAACGGGCGCAAGTGAACCCCGGACGGGACTATCAATGAC 2698  
QY 861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880  
DB 2699 TTCAGTACCTGATACCAATGCGCTGAGAGCTCTCTTCTTACCTGGGCTGTGACAACTTC 2758  
QY 881 ProHisGluSerGluLeuProArgLysTyrGluAsnAsnLysGluAlaLeuLeuThrPhe 900  
DB 2759 CCTCATGAGATGAGCTGCCCGCGAGTGGAGAAACAAGAGAGCGCTGCTCACTTC 2818  
QY 901 MetGluGlnValHisArgGlyIleLysGlyValIleThrAspGluGlnGlyIleProIle 920  
DB 2819 ATGAGACAGGTGCACCGCGGCAATTAAAGGGGTGTGTGACGAGACGACAGGCAATCCCATTT 2878  
QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIlyThrAlaSerGlyGly 940  
DB 2879 GCCAAGCCACCATCTCTGTGAGTGCATTATTCACGGGTGAAGACAGCCAGTGTGAT 2938  
QY 941 AspTyrTyrArgIleLeuAsnProGluGlyTyrArgValThrAlaHisAlaGluGlyTyr 960  
DB 2939 GATTAATCGGATCTTGAACCGGGGTGAGTACCGCGTGAACGCCACCGAGAGGCTTAC 2998  
QY 961 ThrProSerAlaLysThrCysAsnValAspTyrArgPheIleGlyAlaThrGlnCysAsn 980  
DB 2999 ACCCGAGGCGCAAGACTGCAATGTGACTATGACATCGGGGCACTCAGTGCAACTTC 3058  
QY 981 IleLeuAlaArgSerAsnTyrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000  
DB 3059 ATCTGGTGTGCTCCACTGAGAGGAGCATCCGGAGATATATGCGCATGAGAGGAAACGG 3118  
QY 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLysGlnGln 1020  
DB 3119 CCTATCCSACATATGACCATCGGCGCTTATGAGACCCCSAACAGAGAGCGCTGAGAGAG 3178  
QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgIleGlnMetArgLeuArgArgLeuAsnAla 1040

DB 3179 GCACCCCTTACACACCGCTGCGGCTTCGGGACAGATGCGGCTGCGGCTTCAACGCC 3238  
QY 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060  
DB 3239 ACCACCAACCTTGGGCCCCCACAACCTGCTCCCAAGCTGCCCCCTGCCCCCAACGCC 3298  
QY 1061 LeuSerThrThrTlLeuLupProTlPglLyleuLleProProThrThrAlaGlyTlPglLuu 1080  
DB 3299 CTGAGACTACCAATGAGGCTTGGGGCTTCATACCCCAACCAACCGCTGGCGGAGAG 3358  
QY 1081 SerGluThrGluThrTlThrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100  
DB 3359 TCGGAGACTGAGACCTTACACAGAGGTGTGACAGAGCTTGGAGCCAGGTGAGGCCGAG 3418  
QY 1101 PheGlyThrLysValGluProGluPheGluThrGluLeuGluProGluPheGluThrGlu 1120  
DB 3419 TTTGGGACCAAGGTGAGGCCGAGTTTGAAGCCAGTTGAGGCTGAGTTTGAAGACCAG 3478  
QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
DB 3479 CTGGAAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCCACTG 3538  
QY 1141 GlnAlaPheProPheThrThrValGluThrTlThrValAsnPheGlyAspPhe 1158  
DB 3539 CAGGCAATCCCTTTCACACAGTGAAGACCTTACAGTGAATCTTTGGGACTTC 3592

## RESULT 9

AAT97610  
ID AAT97610 standard; cDNA; 3854 BP.  
XX

AC AAT97610;  
XX

DT 27-MAR-1998 (first entry)  
XX

DE Human E2A-binding protein cDNA.  
XX

KW E2A-binding protein; E2A-BP; human; vascular smooth muscle cell;  
XX wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.  
XX

OS Homo sapiens.  
XX

FT Key Location/Qualifiers  
XX CDS 1027..3564  
XX FT /\*tag= a

XX MO9733900-A1.  
XX

XX 18-SEP-1997.  
XX

XX PD 14-MAR-1997; 97MO-US004117.  
XX

XX PF 15-MAR-1996; 96US-0013439P.  
XX

XX PR (HARD ) HARVARD COLLEGE.  
XX

XX PA Lee M, Haber E, Endege WO, Layne MD;  
XX

XX PI MPI; 1997-470808/43.  
XX

XX DR P-PSDB; AAW36816.  
XX

XX PT DNA encoding human and mouse E2A binding proteins - useful for inhibiting  
XX or stimulating growth of vascular smooth muscle cells, e.g. for wound  
XX healing or treatment of rheumatoid arthritis or retinopathic diabetes.  
XX

XX PS Claim 9; Page 55-60; 90pp; English.  
XX

CC This sequence represents a full-length nucleotide sequence that codes for  
CC human E2A binding protein (E2A-BP, see AAW36816). It was isolated from a  
CC human aortic RNA following 3 rounds of 5'RACE procedures. E2A-BP is  
CC expressed in vascular smooth muscle cells; mRNA is preferentially  
CC expressed in the aorta. E2A-BP interacts with E2A proteins in vivo, binds  
CC to both E12 and E47 and inhibits binding of E47 homodimer to an E-box

CC probe (see AAT97606). Mouse (see AAT97611) and rat (see AAT97612-13) E2A-  
CC BP sequences have also been isolated. E2A-BP nucleic acids may be used in  
CC gene therapy and antisense methods for treating vascular diseases such as  
CC arteriosclerosis, to produce transgenic or knock-out animals, as well as  
CC in methods of producing E2A-BP polypeptides that can be used  
CC therapeutically to promote vascular smooth muscle cell growth e.g. for  
CC wound healing, or to screen for modulator compounds useful e.g. for the  
CC treatment of arteriosclerosis and angiogenesis. The E2A-BP gene promoter  
CC can be used in gene therapy methods to direct vascular smooth muscle cell  
CC heterologous expression of the E2A-BP gene, antisense sequences or  
CC

SO Sequence 3854 BP; 899 A; 1214 C; 1161 G; 580 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,456-288 Length: 3854  
Score: 6227.00 Matches: 1149  
Percent Similarity: 99.84 Conservative: 1  
Best Local Similarity: 99.74 Mismatches: 2  
Query Match: 99.34 Indels: 0  
DB: Gaps: 0

US-10-642-946-3 (1-1158) x AAT97610 (1-3854)

QY 7 AlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCySProGlyValArgProGlu 26  
DB 106 GGGCCCTGCTCAGCTGCTCTCTGCGCTTGTGCGCTTGTGCGCTTGTGCGCGCGCGCG 165  
QY 27 ThrValLeuThrAspAspGluLeuGluPheLeuGluGlyPheLeuSerGluLeuGlu 46  
DB 166 ACGGTGTGACCGAGCAGCAGAGTCCAGAGAGTCTTCGAGGCGCTTCTGACAGCTAGAA 225  
QY 47 ProGluProArgGluAspAspValGluAlaProProProProGluProThrProArgVal 66  
DB 226 CCTGAGCCCCGGGAGAGAGAGCGTGAAGGCCCGCGCTTCCGAGCCCAACCCCGCGGTC 285  
QY 67 ArgLysAlaGlnAlaGlyGlyLysProGlyLysArgProGlyThrAlaAlaGluValPro 86  
DB 286 CGAAGAGCCCAAGCGGGGGGCAAGCCAGGAAGCGGCGGCAAGCGGCGGCAAGAGTGCCT 345  
QY 87 ProGluLysThrLysAspLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysValPro 106  
DB 346 CCGGAAAGACCAAGACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 405  
QY 107 LysGluSerLeuGluGlySerProArgProProLysGlyLysGlyLysLysProProLys 126  
DB 406 AAGAGTCTTGGAGGGGTCCCGAGCGCGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGG 465  
QY 127 AlaThrLysLysProLysGluLysProProLysAlaThrLysLysProLysGluPro 146  
DB 466 GCCACCAAGAACCCCAAGAGAGGACCTTAAGGCCACCAAGAGGCCCAAGAGAGGCCA 525  
QY 147 ProLysAlaThrLysLysProLysGlyLysProProLysAlaThrLysLysProProSer 166  
DB 526 CCAAGAGCCCAAGAACCCCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 585  
QY 167 GlyLysArgProProGluLeuAlaProSerGluThrLeuGluTlPProLeuProProPro 186  
DB 586 GGAAGAGAGGCCCCCAATTTGCTGCTCCCTCAAGAACTTGAATGCGCAATGCCCAACCC 645  
QY 187 ProSerProGlyProGluGluLeuLeuProGluGluGlyAlaProLeuSerAsnAsnTlP 206  
DB 646 CCAAGCCCTGGGCCCCGAGAGAGTACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 705  
QY 207 GlnAsnProGlyGluGluThrHisValGluAlaGlnGluLysGlnProGluProGluGlu 226  
DB 706 CAGAAATCCAGAGAGAGAGCCCATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 765  
QY 227 GlnThrGluGluProThrThrLeuAspTlPAspAspGluLeuGluArgGluAspTlPArg 246  
DB 766 GAGACCGAGACACCGGCACTGAGCTTCAATGACAGATGAGAGGAGGAGGAGGAGGAGG 825  
QY 247 PheGluTlPLeuArgGluLysGluProArgProProProSerArgArgArgArgPro 266

Db 826 TTGAGTACATTGGCCGCCAGAGAACCCAGGCCACCCCAAGCAGAGAGAGAGGCC 885  
Qy 267 GUAAGYValTTPProGluProProGluGluValAProAlaProGluGluArg 286  
Db 886 GAGCGGGTCTGGCGAGAGCCCCCTGAGAGAGAGAGCCCCCGCCAGGCCCGGAGAGAGG 945  
Qy 287 ILGLuProProVallyspProLeuLeuProProLeuProProAspTyrGlyAspGlyTyr 306  
Db 946 ATTGAGCTCTGTAAGGCTCTGTGCTGCCCCGCTGCCCCCTGACTATGATGATGTTAC 1005  
Qy 307 ValILeProAntyTyrAspAspMetAspTyrTyrPheGlyProProProGluNlyPro 326  
Db 1006 GTGATCCCCCAACTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065  
Qy 327 AspAlaGluArgGluThrAspGluGluGluGluGluGluGluGluGluGluGluGluGlu 346  
Db 1066 GATGCTGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125  
Qy 347 SerSerProlyArgGluGluThrAspLysTrpAlaValGluGluGluGluGluGluGlu 366  
Db 1126 AGCAGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1185  
Qy 367 ProArgLysGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 386  
Db 1186 CCCCAGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1245  
Qy 387 ProILeGlyMetGluSerHisArgGlyLeuAspAspAspGluLeuArgAlaSerSerMetLeu 406  
Db 1246 CCATTTGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305  
Qy 407 ArgHisGlyLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 426  
Db 1306 CGCAGCGGCTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365  
Qy 427 AspTyrTyrAspGlyAlaTyrCySAIAspAspAlaArgThrGlnTyrILeGluVal 446  
Db 1366 GACTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1425  
Qy 447 AspThrArgArgThrThrArgPheThrGlyValILeThrGlnGlyArgAspSerSerIle 466  
Db 1426 GACACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485  
Qy 467 HisAspAspPheValThrThrPhePheValGlyPheSerAspAspSerGlnThrTrpVal 486  
Db 1486 CATGACGATTTTGTGACACCTTCTGTGGCTTACGACATGACAGCCAGACATGGGTG 1545  
Qy 487 MetTyrThrAspGlyTyrGluGluMetThrPheHisGlyAsnValAspLysAspThrPro 506  
Db 1546 ATGTACACCAACGCGCTATGAGAAATGACCTTTCAATGGAACTGGACAAAGACACACC 1605  
Qy 507 ValLeuSerGluLeuProGluProValValAlaArgPheILeArgIleTyrProLeuThr 526  
Db 1606 GTGCTAGTGAAGCTCCACAGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1665  
Qy 527 TrpAspGlySerLeuCyMetArgLeuGluValLeuGlyCySerSerValAlaProValTyr 546  
Db 1666 TGGAAATGGCAGCTGTGATGCTGCTGAGAGTCTGGGGTGTCTGTGGCCCTGTCTAC 1725  
Qy 547 SerTyrTyrAlaGlnAsnGluValAlaAlaThrAspAspLeuAspPheArgHisIleSer 566  
Db 1726 AGCTACTACGACAGATGAGTGTGTGGCCACCGATGACTGGATTTCCGGCACCCAGC 1785  
Qy 567 TyrLysAspMetArgGluLeuMetLysValValAsnGluGluCyAspProThrIleThrArg 586  
Db 1786 TACAAAGACATGCGCAGCTCATGAAGTGTGAACGAGAGTGCCCAACATCACCCGC 1845  
Qy 587 ThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAsp 606  
Db 1846 ACTTACAGCTGGGCAAGAGCTCACAGGCTCAAGATCTATGCTATGAGACTTCAGAC 1905  
Qy 607 AsnProGlyGluHisGluGluGluProGluPheArgTyrThrAlaGlyIleHisGly 626  
Db 1906 AACCTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1965  
Qy 627 AsnGluValLeuGlyValArgGluLeuLeuLeuLeuMetGlnTyrLeuCyArgGlyTyr 646  
Db 1966 AACGAGTGTGGCGAGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2025  
Qy 647 ArgAspGlyAspProArgValArgSerLeuValGlnAspThrArgIleHisLeuValPro 666  
Db 2026 CGCGATGGAAACCAAGTGTGGCAGCTGTGTGACAGACACAGCATCCACTGTGTGCC 2085  
Qy 667 SerLeuAspProAspGlyTyrGluValAlaAlaGlnMetGlySerGluPheGlyAsnTyr 686  
Db 2086 TCACTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2145  
Qy 687 AlaLeuGlyLeuTyrThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsn 706  
Db 2146 GCGCTGGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2205  
Qy 707 SerValLeuTrpGlyValGluGluGluGluGluGluGluGluGluGluGluGluGlu 726  
Db 2206 TGTGTCTGTGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2265  
Qy 727 LeuProILeProGluArgTyrLeuSerProAspAlaThrValSerThrGluValArgAla 746  
Db 2266 TTGCCATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2325  
Qy 747 IleIleAlaTyrMetGluLysAsnProPheValLeuGlyValAsnLeuAsnGlyGly 766  
Db 2326 ATCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2385  
Qy 767 ArgLeuValSerTyrProTyrAspMetAlaArgThrProThrGlnGluGluLeuValAla 786  
Db 2386 CGGCTAGTATCCATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2445  
Qy 787 AlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluValSerGluAlaGlnGluThr 806  
Db 2446 GCAGCATGGCAGACCCCGGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2505  
Qy 807 ProAspHisAlaIlePheArgTyrLeuAlaIleSerPheAlaSerAlaHisLeuThrLeu 826  
Db 2506 CCAGACCAAGCATCTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2565  
Qy 827 ThrGluProTyrArgGlyGlyCySerGlnAlaGlnAspTyrThrGlyGlyMetGlyIleVal 846  
Db 2566 ACCGAGCTTACCGCGGAGGCTGCCAAGCCAGAGATTAACCGGCGCATGGGCTATGCT 2625  
Qy 847 AsnGlyAlaLysTrpAspProArgThrGlyTyrIleAsnAspPheSerTyrLeuHisThr 866  
Db 2626 AACGGGCGCAATGGAACCCCGGAGCCGGGACTATCAATGACTTCACTGATACCTGATAC 2685  
Qy 867 AsnCyLeuGluLeuSerPheTyrLeuGlyCyAspLysPheProHisGluSerGluLeu 886  
Db 2686 AACTGCTGAGACTCTCTTCACTGAGGCTGTGACAAATTCCTCATGAGAGTGAGCTG 2745  
Qy 887 ProArgGluTrpGluAspAsnLysGluAlaLeuLeuThrPheMetGluGlnValHisArg 906  
Db 2746 CCGCGAGATGGAGAAACAAGAGGCGCTGCATCCTTAAGGAGAGAGGCGACCCG 2805  
Qy 907 GlyIleLysGlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSer 926  
Db 2806 GGCATTAAAGGGGTGTGACGAGACAGACAGACATCCCATTTGCCAACCCACATCTCT 2865  
Qy 927 ValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeu 946  
Db 2866 GTGAGTGGCATTAATCAACGCGCTGAAGACAGCGAGTGTGTGATTAATCGGGAATCTTG 2925  
Qy 947 AsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLysThr 966  
Db 2926 AACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2985  
Qy 967 CyAsnValAspTyrAspIleGlyAlaThrGlnCyAspAspPheIleLeuAlaArgSerAsn 986  
Db 2986 TGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3045



QY 21 ProG1yG1yArpProG1nThrValleuThraAspaSg1u1leg1uG1uBheleuG1uG1y 40  
|  
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Db 179 CTTgAGAGGCGCCGCGAGAGGTGCTGAGCCAGACAGATCGAGAGGTTCTCGAGGCG 238  
QY 41 PheleuSerG1uBheleuG1uProG1uProArG1uAspaSg1u1a1aProProProPro 60  
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Db 239 TTCTGTGACAGAGTGAAGCTGAGGCCCGGAGAGACACTGAGAGGCCCGCGCTCCC 238  
QY 61 GluProThraProArG1uArG1uSg1uSg1uSg1uSg1uSg1uSg1uSg1uSg1uSg1u 80  
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|  
Db 299 GAGCCCAAGCCCGCGGCTCCAGAAAGCCAGCGGCGGCGCAAGCCAGGAGAGCGGCGCAAG 358  
QY 81 ThrAla1aG1uVal1aProProG1uSg1uSg1uSg1uSg1uSg1uSg1uSg1uSg1uSg1u 100  
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|  
Db 359 ACCGCGCGAGAGTGTCTCGGAGAAAGACCAAGAGCAAGAGAGAGAGAGAGAGAGAGAG 418  
QY 101 LySg1uProLySg1uProLySg1uSerLeuG1uG1ySerProArG1uProProLySg1u 120  
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Db 419 AAGGCGCCCAAGGTGCGCAAGAGTCTTGAGAGGCTCCCGAGCGCGCCCAAGAGAGG 478  
QY 121 LySg1uLySg1uProProLySg1uArG1uLySg1uProLySg1uProLySg1uArG1u 140  
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|  
Db 479 AAGGAGAGGCAAGCCCAAGGCGCAAGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAG 538  
QY 141 LySg1uProLySg1uProProLySg1uArG1uLySg1uProLySg1uProLySg1uArG1u 160  
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|  
Db 539 AAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598  
QY 161 ThrLySg1uProProSerG1uLySg1uArG1uProPro1e1u1a1aProSerG1uThraeG1u 180  
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|  
Db 599 ACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658  
QY 181 TrpProLeuProProProProProSerProG1yProG1uG1uBheleuProG1uG1yAla 200  
|  
|  
|  
Db 659 TGGCCACTGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718  
QY 201 ProLeuSerArSg1uArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1u 220  
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Db 719 CCCCTCTCAAAATTAATCGGAGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778  
QY 221 G1uProG1uProG1uG1uG1uThraG1uG1uProThrae1u1a1aProG1uG1uG1uG1u 240  
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Db 779 CGGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 838  
QY 241 ArG1uAspTyTc1uAspPheG1uTyT1eArG1uArG1uLySg1uProArG1uProPro 260  
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Db 839 AGGAGAGAGTATGAGAGACTTGTGATCATTCGCGCGAGAGAGAGAGAGAGAGAGAGAG 898  
QY 261 SerArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1uArG1u 280  
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Db 899 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 958  
QY 281 ProAlaProG1uG1uArG1uG1uProProVal1ySg1uProLeuBheleuProProPro 300  
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Db 959 CCAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018  
QY 301 AspTyTc1uAspG1yTyTVal11eProAsnTyTAspAspMetAspTyTc1uPheG1uPro 320  
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Db 1019 GACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078  
QY 321 ProProProG1uLySg1uProAspAlaG1uArG1uThraSg1uG1uLySg1uG1uLeuLy 340  
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Db 1079 CCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138  
QY 341 LySg1uProLySg1uAspSerSerProLySg1uG1uThraSg1uArG1uArG1uArG1u 360  
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Db 1139 AAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198  
QY 361 G1yLySg1uAspPhe1uLySg1uProArG1uG1uG1uG1uG1uG1uG1uG1uG1uG1u 380  
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Db 1199 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258

QY 381 GluLySg1uVal1ySg1uProProG1uG1uMetG1uSerHisArG1u1leg1uAspaSg1u1e 400  
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QY 401 ArgAlaSerSerMetLeuArG1uSg1uLySg1uVal1a1aArgG1yArG1uAspMetG1u 420  
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Db 1319 CGAGCTCTCTCATGCTGCGCCAGCGCTGGGGGACAGCGCGCGCGCTCAACATGACAG 1378  
QY 421 ThrG1yAla1aThraG1uAspArG1yTyTAspG1yAla1aTrpCysAlaG1uAspaAlaArG 440  
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Db 1379 ACCGATGCACTAGAGAGACACTACTATGATGGTGGCTGGTGGTCCGAGAGAGATGCCAG 1438  
QY 441 ThrG1uThraG1uVal1a1aAspThraArG1uArG1uThraArG1uPheThraG1yAla1a1eThraG1n 460  
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Db 1439 ACCAGATGATAGAGTGAACACAGAGAGAGTACCCGGTTCACAGCGCTCATCACCCAG 1498  
QY 461 GlyArG1uAspSerSer1eHisAspArPheVal1aThraPhePheVal1aG1yPheSerAr 480  
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Db 1499 GCGAGAGACTCCAGATCCATGACATTTTGACACACTTCTTGCGGGCTTCAGCAAT 1558  
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Db 1559 GACAGCAGACATGGGTGATGATACCAACGCTATGAGAGAAATGGTGGCACATGCC 1618  
QY 495 ----- 495  
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Db 1619 AGGCTTGAGCTCTGCTCCATTGCTGAGGAGAGGGTGGCTTCAGAGGGCTGGCAG 1678  
QY 496 -----ThraPhe1aG1yAsnVal1aAspLySg1uArG1uThraP 506  
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QY 506 ovalleuSerG1uLeuProG1uProVal1aArG1uPhe1aArG1uTyTc1uProLeuTh 526  
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Db 1739 CGGTGATGATGAGCTCCAGAGCGGTGGTGGCTGCTTCATCCGATCAACCACTCAC 1798  
QY 526 rTrpAsnG1ySerLeuCysMetArG1uG1uVal1a1eG1yCysSerVal1a1aProVal1y 546  
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Db 1799 CTGGAATGGACCTGTGTGATGCGCTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGT 1858  
QY 546 rSerTyTc1uVal1aG1uAsnG1uVal1a1aThraAspArPheAspPheArG1uHisS 566  
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QY 566 rTyTc1uAspMetArG1uLeuMetLySg1uVal1a1eG1uG1uCysProThra1eThra 586  
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Db 1919 CTACAAAGAGATGGCGCAGCTCATGAAAGTGGTGAACGAGAGTGGCCACCATCACCG 1978  
QY 586 gThraTyTc1uG1uLySg1uSerSerArG1uG1uLySg1uTyTc1uArG1u1eSerAr 606  
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Db 1979 CACTTACAGCTGGGCGAAGAGCTCACAGAGCTTCAAGATCTATGCCATGAGATCTCA 2038  
QY 606 pAsnProG1yG1uH1aG1uG1uG1uG1uProG1uPheArG1yTyTThraAlaG1y11eHisG1 626  
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Db 2039 CAACCTGGGAGACATGAATGGGGAGGCCAGATTCCTGCTACAGCTCGGATCCATG 2098  
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Db 2159 CCGCAGTGGAGAACCAACGCTGCGAGAGCTGTGTGACAGACACACGATCACCTGTGTC 2218  
QY 666 oSerLeuAsnProAspG1yTyTc1uVal1a1a1aG1uMetG1ySerG1uPheG1yAsnTr 686  
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Db 2219 CTACATGAACCTGTATGCTGATGAGGTGGACGACGATGGCTCAAGATTTGGAGACTG 2278  
QY 686 pAlaLeuG1yLeuTyTThraG1uG1uG1uG1uG1uPheAsp11ePheG1uAspPheProAspLeuAs 706  
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Db 2279 GCGCTGGGAGCTGTGAGACTGAGAGAGGCTTTGACATCTTTGAAGATTTCCCGAGATCTCA 2338  
QY 706 nSerVal1eThraG1yAlaG1uG1uArG1uLySg1uTyTc1uProTyTc1uArG1uProAsnAsnAs 726

Db 2339 CTCTGTGCTCTGGAGAGCTGAGAGAAATGGCTCCCTACCGGGTCCCAACAATTA 2398  
 Qy 726 mNeuPro1LeProGluArgTyrLeuSerProAspAlaThrVal1SerThrGluValArgAl 746  
 Db 2399 CTGGCCCATCCCTGAACGCTTACTTTCGCGAGATGCGATATCCAGGAGGTCCGGGC 2458  
 Qy 746 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 766  
 Db 2459 CATCATTTGCTGATGAGAGAAACCTTCTGCTGGAGCAAAATCTGAACGGCGGCGA 2518  
 Qy 766 uArgLeuVal1SerTyrProTyrAspMetAlaArgThrProThrGlnGlnGln1LeuVal1 786  
 Db 2519 GGGGCTAGATCTCTACCTTACGATATGCGCCGACGCTTACCCAGAGAGACGTCTGGC 2578  
 Qy 786 aAlaAlaMetAlaAlaAlaArgGlyGluuAspGluAspGluVal1SerGluVal1GlnGlu 806  
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 Qy 806 rProAspAlaAlaAlaLePheArgTyrLeuAla1LeSerPheAla1SerAla1LeuThrLe 826  
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 Qy 826 uThrGluProTyrArgGlyGlyCyseGlnAlaGlnAspTyrThrGlyGlyMetGlyTLeva 846  
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 Db 2879 GCGCCCGAGTGGGAGAAACAACAAGAGGCGCTGCTCACTTCAATGAGACAGGTGACCG 2938  
 Qy 906 gGly1LeuGlyVal1Val1ThrAspGlnGlnGly1LePro1LeaAlaAsnAlaThr1LeSe 926  
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 Qy 926 rVal1SerGly1LeaAsnHisGlyVal1LeuThrAlaSerGlyGlyAspTyrThrArg1Le 946  
 Db 2999 TGTGATGGCATTAATCAGCGCGCTGAAGACAGCAGGTGGTGGATTACTGGGAAATCTT 3058  
 Qy 946 uAenProGlyGluTyrArgVal1ThrAlaHisAlaGlnGlyTyrThrProSerAla1LeS 966  
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 Qy 966 rCyAsnVal1AspTyrAsp1LeGlyAlaThrGlnCyAsnPhe1LeuVal1ArgSerAs 986  
 Db 3119 CTGCAATGTTGACTATGACATCGGGGCACTCAGTCACTTATCTGCTGCTGCTCA 3178  
 Qy 986 nTPrLysArg1LeArgGln1LeMetAlaMetAsnGlyAsnArgPro1LeProHis1LeAs 1006  
 Db 3179 CTGGAGCGCATCCGGAGATCTAGGCGCATGAACGGGACCGGCTATCCACACATAGA 3238  
 Qy 1006 pProSerArgProMetThrProGln1ArgArgLeuGlnGln1ArgArgLeuGlnHisr 1026  
 Db 3239 CCGATGGCGGCTATGACCCGCCAACAAGGAGCGCTGAGACGACGCTTACACACCG 3298  
 Qy 1026 gLeuAlaGluLeuArgAlaGlnMeCarGluArgLeuAlaGluAsnAla1ThrThr1LeuGlyPr 1046  
 Db 3299 CCTGGCGCTTCCGGGCAAGATGCGGCTGCGCGCTTCAACGCCACACACCTTAAGGCC 3358  
 Qy 1046 oHisThrVal1ProProThrLeuProProAlaProAla1ThrThr1LeuSerThrThr1LeG 1066  
 Db 3359 CCAACATGAGCTTCCACAGGCTGCGCCCTGCGCCACCACTTGACCTTCCATAGA 3418  
 Qy 1066 uProTyrGlyLeu1LeProProThrThrAlaGlyTyrGlnGln1LeuSerGluThrGlnThr 1086

Db 3419 GCCCTGGGCGCTCATACCGCCACCAAGCGCTGGAGGAGTGCAGACTGAGACCTTA 3478  
 Qy 1086 rThrGluVal1Val1ThrGluPheGlyTThrGluVal1GluProGluPheGlyTThrVal1G 1106  
 Db 3479 CACAGAGGTGGTGAACAGATTGGAGCCGAGGTGAGCCGAGATTGGAGCAACAGGTGA 3538  
 Qy 1106 uProGluPheGluThrGlnLeuGluProGluPheGluThrGlnLeuGluProGluPheG 1126  
 Db 3539 GCCCAGTTTGAAGACCCAGTTTGAAGCTTGAAGTTCAGACCTGGAACCCGAGATTGA 3598  
 Qy 1126 uGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluG 1146  
 Db 3599 GGAAGAGGAGGAGGAGAGAAAGAGAGAGATACCACTGGCCAGGATTCCTCTTAC 3658  
 Qy 1146 rThrVal1GluThrTyrThrThrVal1AsnPheGlyAspPhe 1158  
 Db 3659 AACAGTGAAGACTTACACAGTGAACCTTGGGAGCTTC 3695  
 RESULT 11  
 ADE79063  
 ID ADE79063 standard; DNA, 3872 BP.  
 AC ADE79063;  
 XX 29-JAN-2004 (first entry)  
 DE Human protein modification and maintenance molecule (PMM) -43 gene.  
 KW protein modification and maintenance molecule; PMM;  
 KW protein modification; protein maintenance; protein function;  
 KW protein conformation; protein stabilization; protein degradation; kinase;  
 KW phosphatase; protease; protease inhibitor; isomerase; transferase;  
 KW molecular chaperone; anti-HIV; antileukic; antiinflammatory;  
 KW antianemic; antiparkinsonian; nootropic; anticonvulsant;  
 KW antidiabetic; antistomatitic; antistomatitic; immunosuppressive; antichyroid;  
 KW cytosolic; hepatocytic; dermatological; antidiabetic; nephrotropic;  
 KW antitumor; thymic; neuroprotective; osteopathic; antidiabetic;  
 KW antiparasitic; antihelminthic; antiparasitic; uropathic; ophthalmological;  
 KW antirheumatic; hemostatic; antibacterial; vincine; protozoic;  
 KW fungicide; gene therapy; cell proliferative disorder; arteriosclerosis;  
 KW hepatitis; polycythaemia vera; psoriasis; primary thrombocytopaenia;  
 KW cancer; developmental disorder; anaemia; mental retardation;  
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;  
 KW epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergies;  
 KW asthma; autoimmune thyroiditis; Crohn's disease; diabetes mellitus;  
 KW glomerulonephritis; Goodpasture's syndrome; multiple sclerosis;  
 KW arthritis; osteoporosis; pancreatitis; Sjogren's syndrome;  
 KW microbial infection; human; gene; ds.  
 KW Homo sapiens.  
 OS  
 XX  
 PN WO2003063688-A2.  
 PD 07-AUG-2003.  
 XX  
 PF 23-JAN-2003; 2003WO-US002500.  
 XX  
 PR 25-JAN-2002; 2002US-0351928P.  
 PR 25-FEB-2002; 2002US-0359903P.  
 PR 21-MAR-2002; 2002US-0366837P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Hafalia AUA, Li JX, Gorvad AE, Chawla NK, Sprague MW, Lee SY;  
 PI Chang H, Elliott VS, Ramkumar J, Khare R, Emerling BM, Kable AE;  
 PI Tang YT, Yue H, Glezen KJ, Lee S, Swarnakar A, Baughn MK;  
 PI Wilson AD, Jin P, Chien D, Hawkins PR, Jiang X, Jackson AA;  
 PI Bhacca U, Burtill JD, Blake JJ, Ho A, Zhang W, Ison CH, Margulis JP;  
 PI Tran UK, Lal PG, Warren BA, Xu Y, Honchell CD, Becha SD;  
 PI Lehr-Mason PM;  
 XX  
 PI WPI; 2003-636761/60.  
 DR P-PSDB; ADE79005.





QY 481 AASPserGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500  
 DB 1458 GACAGCACAATGGGTGATGTACACCAACGGCTAAGAGAAATGACCTTTATGGGAAC 1517  
 QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaIleArgPheIle 520  
 DB 1518 GTGGACAAAGACACCCGCTGCTGAGTGAAGCTCCAGACCCGGTGGTGGCTGTTTCAAC 1577  
 QY 521 ArgIleTyrProIleuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540  
 DB 1578 CGCATCTACCACTCACTGGAATGGCAGCCTGTGATGCGCTGGAGGTGGCTGGGGTGC 1637  
 QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaIleThrAspAspLeu 560  
 DB 1638 TCTGTGGCCCTGTCTACAGCTACTACGACAAAGAGAGTGTGGCCACCGATGACCTG 1697  
 QY 561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValAlaAsnGluGlu 580  
 DB 1698 GATTTCCGGACCAACAGCTACAGAGACATGCGCCACTCATGAAAGTGTGAACAGAGAG 1757  
 QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600  
 DB 1758 TGGCCACCATCAACCCGCACTTACAGCTGGGCAAGAGCTCAAGAGGCTCAAGATCTAT 1817  
 QY 601 AlaMetGluIleSerAspAsnProGluGluHisGluLeuGlyGluProGluPheArgTyr 620  
 DB 1818 GCCATGAAGATCTCAACAACCTGGGGAGCATGAATCTGGGGAGGCCAGATTCCTGCTAC 1877  
 QY 621 ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640  
 DB 1878 ACTGCTGGGATCATGGCAACAGAGTGTGGGCCGAGCTGTGTGCTGCTCAGCGAG 1937  
 QY 641 TyrLeuCysArgGlyLutyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660  
 DB 1938 TACCTTGCCGAGAGATACCGCGATGGGAAACCCAGTGTGGCAGCTGTGGCAGGACACA 1997  
 QY 661 ArgIleHisIleuValProSerLeuAsnProAspGlyTyrGluValAlaIleAsnMetGly 680  
 DB 1998 CGCATCACTGGTGGCTTACTGAAACCTGATGGCTACAGAGTGGCAGAGGATGGAG 2057  
 QY 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700  
 DB 2058 TCAGAGTTTGGGAACGTGGGGCTGGGACTGTGACTGAGAGAGGCTTTGACATCTTGA 2117  
 QY 701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluLysArgLysTrpValProTyr 720  
 DB 2118 GATTTCCCGGATCTCAACTGTGTCTGTGGGAGCTGAGGAGAGAAATGGGTCCCTTAC 2177  
 QY 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740  
 DB 2178 CGGGTCCCAACAATACCTTGGCCATCTGAAAGCTACCTTTCGCAAGATGGCACAGGA 2237  
 QY 741 SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla 760  
 DB 2238 TCACAGGAGGTCCGGGCATCATTTGGCTGATGAGAGAGAACCCCTTCGTGGTGGAGCA 2297  
 QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780  
 DB 2298 AATCTGAACGGCGGCGAGCGGCTAGTACTTACCCCTACGATATGGCCCGCACGCTTACC 2357  
 QY 781 GlnGluGlnLeuLeuAlaIleAlaMetAlaAlaAlaArgGlyGluLysAspGluValAla 800  
 DB 2358 CAGAGAGAGTGTGGCGGAGCGACATGGCAGACCCGGGGGAGAGATGGAGCAGAGTCC 2417  
 QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 820  
 DB 2418 TCCGAGGCCCAAGAGACTCAAGACAGCATCTTCGGGTGGCTTGGCATCTCTTCGCC 2477  
 QY 821 SerAlaHisIleuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840  
 DB 2478 TCCGACACCTCACTTGAACGAGCCTTACCGCGAGGCTGCACAAAGCCCAAGACTACACC 2537

QY 841 GlyGlyMetGlyIleValAsnGlyValAlaSerTrpAsnProArgThrGlyThrIleAsnAsp 860  
 DB 2538 GCGGCGATGGGACTGTCTACACGGGGCCAAAGTGAACCCCGGACCGGAGACTATCATGAC 2597  
 QY 861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880  
 DB 2598 TTCAGTTACTTCGATACCAACTGCTGGAGCTCTCTTCACTGCGGCTGTGACAAAGTTC 2657  
 QY 881 ProHisGluSerGluLeuProArgGluLutrpGluAsnAsnLysGluAlaLeuLeuThrPhe 900  
 DB 2658 CCTCATGAGAGTGAAGTCCCGCGAGTGGAGAAACAAGAGAGCCGTGCTCACTTC 2717  
 QY 901 MetGluGlnValHisArgGlyIleLysGlyValAlaThrAspGluGlnGlyIleProIle 920  
 DB 2718 ATGGAGCAGGTCCACCGT----- 2735  
 QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGly 940  
 DB 2736 -----GGCATTTAATCAGGCGCTGAGACAGACCCAGTGTGCT 2771  
 QY 941 AspTyrTrpArgIleLeuAsnProGluGluLutyrArgValAlaThrAlaHisAlaGluGlyTyr 960  
 DB 2772 GATTACTGGCGAATCTTGAACCGGCTGAGTACCGGTGACAGCCCGGAGGAGCTTAC 2831  
 QY 961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980  
 DB 2832 ACCCGAGCGCCAAACACTGGCATTTGACTATGACATCGGGGCCACTCAGTGCACATTC 2891  
 QY 981 IleuValArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000  
 DB 2892 ATCTGTGCTCGCTCCACATGGAAAGCGCATCCGGGAGATCATGGCCATGAACGGGAACCG 2951  
 QY 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLeuGlnGln 1020  
 DB 2952 CCTATCCACATAGACCATCGCCCTATGACCCGCCAACAGACGACCTGCAAGAG 3011  
 QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgLeuAsnAla 1040  
 DB 3012 CGAGCCTTACAAACACCGCTGGGCTGGGGCAGAGATGGCGCTGGGCGCTCAACCGCC 3071  
 QY 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060  
 DB 3072 ACCACACCCCTAGGCCCCACACACTGTGCTCCACAGCTGCCCGCCCTGCCACACCC 3131  
 QY 1061 LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu 1080  
 DB 3132 CTGAGCACTACCATAGAGCCTGGGGCTCATACCGCAACCGCTGGAGAGAG 3191  
 QY 1081 SerGluThrGluThrTyrThrGluValAlaThrGluPheGlyThrGluValGluProGlu 1100  
 DB 3192 TCGGAGACTGAGACTTACACAGAGGTGTGACAGAGTTTGGAGCGAGGTGGAGCCGAG 3251  
 QY 1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120  
 DB 3252 TTTGGGACCAAGTGAAGCCGAGTTTGAAGCCAGTTTGAAGCTTGAAGACCCAG 3311  
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140  
 DB 3312 CTGAAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3371  
 QY 1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158  
 DB 3372 CAGGACTTCCTTCAACAAGTATGAGACTTACAGAGTGAATCTTGGGAGCTTC 3425  
 DB  
 RESULT 12  
 ABQ54610  
 ID ABQ54610 standard; cDNA; 3523 BP.  
 XX  
 AC ABQ54610;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HNTAK22 cDNA, SEQ ID NO:490.



XX Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KM inflammatory condition; immune disorder; blood disorder;  
 KM cardiovascular disorder; respiratory disorder; neurological disorder;  
 KM gastrointestinal disorder; urinary system disorder; drug screening;  
 KM gene therapy; chromosome mapping; forensic analysis;  
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KM antiinflammatory; gynaecological; reproductive; chromosome 7; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN MO20020677-11.  
 PD 03-JAN-2002.  
 PF 07-JUN-2001; 2001MO-US018569.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Birse CE, Rosen CA;  
 XX WPI, 2002-147878/19.  
 DR P-PSDB; ABP41533.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 cancer), immune disorders, cardiovascular disorders and neurological  
 diseases.  
 PT  
 PS Claim 1; SEQ ID NO 490; 2922pp; English.  
 XX  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP4228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis), systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a cDNA encoding a human ovarian antigen of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 SQ Sequence 3523 BP; 862 A; 1069 C; 1054 G; 535 T; 0 U; 3 Other;

## Alignment Scores:

Pred. No.: 2,1e-264  
 Score: 5725.00  
 Percent Similarity: 99.8%  
 Best Local Similarity: 99.6%

Length: 3523  
 Matches: 1054  
 Conservative: 2  
 Mismatches: 2

Query Match:	91.3%	Indels:	0
DB:	6	Gaps:	0
US-10-642-946-3 (1-1158) x ABQ54610 (1-3523)			
Qy 101	LYSG1LysPProLyVal1ProLySG1SerLeuG1SerProArpProProLySG1Y	120	
Db 2	AAAGGCCCAAGGTGCCCAGAGTCTTGAGAGGGTCCCCAGGCGCCCAAGAGGGG	61	
Qy 121	LYSG1LysPProProLySa1aThLyLysPProLyG1LysPProProLySa1aThLyLys	140	
Db 62	AAAGGAGAGCCACCAAGGCCACCAAGAGGCCCAAGAGAGGACCTTAAGGCCCAAG	121	
Qy 141	LysPProLySG1LysPProProLySa1aThLyLysPProLySG1LysPProProLySa1a	160	
Db 122	AAAGCCCAAGAGAGAGCCACCAAGGCCACCAAGAGAGGCCCAAGAGAGGCCCAAG	181	
Qy 161	ThLyLysPProProSerG1LysPProProLySa1aThLyLysPProProLySa1aThLyLys	180	
Db 182	ACCAAGAGAGCCCGTCAAGAGAGAGAGGCCCGCCATTCCTGCTCCCAAGAACCTGAG	241	
Qy 181	TrpProLeuProProProProSerProG1YProG1LysPProG1LysPProG1LysPPro	200	
Db 242	TGGCCACTGCCCCCAGCCCCCAGCCCTGGCCCGAGAGACTACCCAGAGAGGAGGGG	301	
Qy 201	ProLeuSerArSa1aThLyLysPProG1YLysPProG1YLysPProG1YLysPProG1Y	220	
Db 302	CCCTCTCAATTAACCTGAGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	361	
Qy 221	G1nPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	240	
Db 362	CAGCTTACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	421	
Qy 241	ArgG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPPro	260	
Db 422	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	481	
Qy 261	SerArG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	280	
Db 482	AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	541	
Qy 281	ProAlaPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	300	
Db 542	CCAGCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	601	
Qy 301	AspTyG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	320	
Db 602	GACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	661	
Qy 321	ProProProG1LysPProProArSa1aThLyLysPProG1LysPProG1LysPProG1LysP	340	
Db 662	CTCCGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	721	
Qy 341	LysPProLyLysG1LysPProSerProLySG1LysPProG1LysPProG1LysPProG1LysP	360	
Db 722	AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	781	
Qy 361	G1LYLysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	380	
Db 782	GCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	841	
Qy 381	G1LYLysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	400	
Db 842	GAGAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	901	
Qy 401	ArgAlaSerSerMetLeuArG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	420	
Db 902	CAAGCTCTCTCATGCTGCGCAAGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	961	
Qy 421	ThLyLysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysPProG1LysP	440	
Db 962	ACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1021	

QY	441	ThgIntPrp1IegluValAspThrArgArgThrThrArgPheThrGluValIleThgIn	460
Db	1022	ACCCAGTGGATGAGAGTGGAGACCAACGAGGACTACCCCGATTACAGGGGTATACCCAG	1081
QY	461	GLyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn	480
Db	1082	GCGAGAGCTCCAGATCATGACGATTTTGTGACCACTCTTCGTGGGCTTCAGCAAT	1141
QY	481	AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn	500
Db	1142	GACAGCCAGACATGGGTGATGTACACCAACGGCTATGAGAAATGACTTTCATGGGAAC	1201
QY	501	ValAspIlyAspThrProValLeuSerGluLeuProGluProValAlaArgPheIle	520
Db	1202	GTGGACAAAGACACACCGGTGTGTAGCTCCAGACGGGTGGTGGCTTCGTTCAATC	1261
QY	521	ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValIleGlyCys	540
Db	1262	CGCATCTACCACTACCTGGAAATGGACGCTGTGCATGCCCTGGAGGTGCTGGGGTGC	1321
QY	541	SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaIleThrAspAspLeu	560
Db	1322	TCTGTGGCCCTGTCTACAGCTACTACGACAGATGAGTGGTGGCCACCGATGACTTG	1381
QY	561	AspPheArgHisHisSerTyrIlyAspMetArgGlnLeuMetIlyValIleAsnGluGlu	580
Db	1382	GATTTTCCGGCACACACGCTACCAAGACATGCCCGCTCATAGAAAGTGGTAAACAGAG	1441
QY	581	CysProThrIleThrArgThrTyrSerLeuGlyIlySerSerArgGlyPheIlySerIleTyr	600
Db	1442	TGCCCCACCATACCCCGCACTTACAGCTTGGGCAAGAGCTCAGAGGCTCTCAAGATCAT	1501
QY	601	AlaMetGluIleSerAspAsnProGlyGlnHisGluGlyGluProGluPheArgTyr	620
Db	1502	GCCATGGAGATCTCAGACACCTCGGGGAGCATGAATCGGGGAGACCCGAGTCCGGTAC	1561
QY	621	ThrAlaGlyIleHisGlyAsnGluValLeuGlyIlyArgGluLeuLeuLeuLeuMetGln	640
Db	1562	ACTGTGGGATTCATCAGGACACGAGGTGTGGGCGCAGAGCTGTGCTCTGTCTCATTCAG	1621
QY	641	TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr	660
Db	1622	TACCTGTGCGAGATACCGCATGGAAACCATGTGTGCCAGGCTGGTGCAGACACAA	1681
QY	661	ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly	680
Db	1682	CGCATCCACACTGTGTCCTCTCACTGAACCTGATGGCTACAGAGTGGACGCGAGATGGGC	1741
QY	681	SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	1742	TCAGAGTTTGGGAACTGGGGCGCTGGAGACTGTGAGCTGAGAGGGCTTTGACATCTTTGAA	1801
QY	701	AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgIlyLeuTrpValProTyr	720
Db	1802	GATTTCCCGGATCTCAACTCTGTGCTCTGGGGAGCTGAGAGAGGAAATGGGTCCCCTAC	1861
QY	721	ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal	740
Db	1862	CGGGTCCCAACAATPACTTGCCCATCCCTGAACGCTACTTTGCCAGATGCCACGGTA	1921
QY	741	SerThrGluValArgAlaIleIleAlaTrpMetGluIlyAsnProPheValLeuGlyAla	760
Db	1922	TCCAGCGAGGTCCGGGCGCATTCATTCCTGGATGGAGAAAGAACCCCTTGCTGCTGGAGACA	1981
QY	761	AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr	780
Db	1982	AATCTGAAGGGCGGAGCGGTAGATCTTACCCCTACGATATGACCCGCGCATCC	2041
QY	781	GlnGluGlnLeuLeuAlaIleAlaMetAlaAlaIleArgGlyGluAspGluAspIlyVal	800
Db	2042	CAGAGACAGCTGTGGCCGCGACCATGCGACAGACCCGGGGGGAAGATGAGGACAGAGTTC	2101
QY	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla	820

Db	2102	TCGAGAGCCCAAGAGACTCCAGACACAGCCATCTTCGGAGGCTTGCCATCTCTCTGGCC	2161
OY	821	SeRlAaHlsLeuThrLeuThrGluProTyArgGlyGlyCysGlnAlaGlnAspTyThr	840
Db	2162	TCGCAACACCTCACTTGACCTGACCGAGCCCTTACCGGGAGAGCTGCCAAGCCCAAGACTACAC	2221
OY	841	GlyGlyMetGlyIleValaAnGlyValaIleTyTrpAsnProArgThrGlyYThrIleAsnAsp	860
Db	2222	GGCGGCATGGGCATCGCAACGGGGCCCAAGTGAACCCCGGAGCCGGGACTATCAAGAC	2281
OY	861	PheserTyTrpLeuHsThranGlySLeuGlyLeuSerPheTyTrpLeuGlyCysAspLysPhe	880
Db	2282	TTGCGTTAAGCTGCATACCAACTGCTGAGACTCTCTCTTAAGCTGGGCTGTGACAACTTC	2341
OY	881	ProHsGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPhe	900
Db	2342	CCTCATGAGAGTAGTGCTGCCCGCGAGTGGAGAACAAACAAGAGGGCGGTCTCACTTC	2401
OY	901	MetGluGlnValHsIleArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIle	920
Db	2402	ATGAGAGAGGGGCGACCCCGGCATTAAAGGGGGGTGTGCGAGCAGCAAGGCAATCCCATT	2461
OY	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHsGlyValLysThrAlaSerGlyGly	940
Db	2462	GCCAAAGCCCACTCTGTGTGAGTGGCATTAATACGGCTGAAGACAGCCAGTGGTGT	2521
OY	941	AspTyTrpArgIleLeuAsnProGlyGlyLysTyArgValThrAlaHsIleAlaGluGlyTy	960
Db	2522	GATTACTGGGAAATCTTGAAACCGGGGTGAGNACCGCGTAGACGCCAGCGSAGGGCTAC	2581
OY	961	ThrProSerAlaLysThrTyIleAsnValAspTyTrpAspIleGlyAlaThrGlnCysAsnPhe	980
Db	2582	ACCCCGAGCGCAAGACCTCGCAAGTTGACTATGACTGCGGGGCACTCGATCGATGCACTTC	2641
OY	981	IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg	1000
Db	2642	ATCTGGCTGCTTCAACTGGAAACCGATCGGGAGATCATGGCCATGAAGGGAAACCGG	2701
OY	1001	ProIleProHsIleAspProSerArgProMetThrProGlnGlnArgLeuGlnGln	1020
Db	2702	CCTATCCCAACATAGAACCATGCGCGCCCTATAGACCCCAACAGCCAGCCTGCACAG	2761
OY	1021	ArgArgLeuGlnHsIleArgLeuArgLeuArgIleGlnMetArgLeuArgArgLeuAsnAla	1040
Db	2762	CGAGCGCTACAAACACCGCCTGGCGCTTCGGGCAACGATGGCGCTGCGCGCTTCMAACGCC	2821
OY	1041	ThrThrThrLeuGlyProHsIleThValProProThrIleuProProAlaProAlaThrThr	1060
Db	2822	ACCAACCAACCTCAAGGCCCCCAACAGTGCCTTCCACAGCGTGGCCCTGCCCCCTGCCAACCC	2881
OY	1061	LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu	1080
Db	2882	CTGAGCACTACATAGAGCCCTGGGGCTCATACCGCAACCAACCGCTGCTGGGAGGAG	2941
OY	1081	SerGluThrGluThrTyThrGluValValThrGluPheGlyThrGluValGluProGlu	1100
Db	2942	TCGAGAGACTGAGACTACACAGAGGTGTGACAAAGTTTGGGACCGAGGTGAGACCCGAG	3001
OY	1101	PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln	1120
Db	3002	TTTGGGACCAAGGTGGAGCCCGAATTGAGACCAAGTTGAGCGCTGAGTTTGAACCCAG	3061
OY	1121	LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	1140
Db	3062	CTGGAACCCCGAGTTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGATAGCCACTGGC	3121
OY	1141	GlnAlaPheProPheThrThrValGluThrTyThrValAsnPheGlyAspPhe	1158
Db	3122	CAGGCAATCCCTTCAACAACAGTAGAGCTTACACAGTGAACCTTTGGGGAACTTC	3175

RESULT 13  
AAT97611

ID AAT97611 standard; cDNA; 3633 BP.  
 XX AAT97611;  
 AC AAT97611;  
 XX 27-MAR-1998 (first entry)  
 XX  
 XX Mouse E2A-binding protein cDNA.  
 DE  
 XX E2A-binding protein; E2A-BP; mouse; vascular smooth muscle cell;  
 KM wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.  
 XX  
 XX Mus musculus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 46..3432  
 FT /\*tag= a  
 XX  
 XX MO9733900-A1.  
 XX  
 XX 18-SEP-1997.  
 XX  
 XX 14-MAR-1997; 97MO-US004117.  
 XX  
 XX 15-MAR-1996; 96US-0013439P.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX  
 XX Lee M, Haber E, Endege WO, Layne MD;  
 PI MPI; 1997-470808/43.  
 XX P-PSDB; AAW36817.  
 XX  
 XX DNA encoding human and mouse E2A binding proteins - useful for inhibiting  
 PT or stimulating growth of rheumatoid arthritis or retinopathic diabetes.  
 PT healing or treatment of rheumatoid arthritis or retinopathic diabetes.  
 XX  
 XX Claim 13; Page 62-68; 90pp; English.  
 XX  
 XX This sequence represents a full-length nucleotide sequence that codes for  
 CC mouse E2A binding protein (E2A-BP, see AAW36817). It was isolated using  
 CC 5'RACE with primers designed from mouse AEBP cDNA. E2A-BP is expressed in  
 CC vascular smooth muscle cells; mRNA is preferentially expressed in the  
 CC aorta. E2A-BP interacts with E2A proteins in vivo, binds to both E12 and  
 CC E47 and inhibits binding of E47 homodimer to an E-box probe (see  
 CC AAT97606). Human (see AAT97609-10) and rat (see AAT97612-13) E2A-BP  
 CC sequences have also been isolated. E2A-BP nucleic acids may be used in  
 CC gene therapy and antisense methods for treating vascular diseases such as  
 CC arteriosclerosis, to produce transgenic or knock-out animals, as well as  
 CC in methods of producing E2A-BP polypeptides that can be used  
 CC therapeutically to promote vascular smooth muscle cell growth e.g. for  
 CC wound healing, or to screen for modulator compounds useful e.g. for the  
 CC treatment of arteriosclerosis and angiogenesis. The E2A-BP gene promoter  
 CC can be used in gene therapy methods to direct vascular smooth muscle cell  
 CC -specific expression of the E2A-BP gene, antisense sequences or  
 CC heterologous genes  
 XX  
 XX Sequence 3633 BP; 927 A; 1065 C; 1043 G; 598 T; 0 U; 0 Other;  
 XX  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 1..9e-233 Length: 3633  
 XX Score: 5077.00 Matches: 960  
 XX Percent Similarity: 87.3% Conservative: 54  
 XX Best Local Similarity: 82.6% Mismatches: 110  
 XX Query Match: 80.9% Indels: 38  
 XX DB: 2 Gaps: 9  
 XX  
 XX US-10-642-946-3 (1-1158) x AAT97611 (1-3633)  
 XX  
 XX 1 MetAlaAlaValAlaArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20  
 XX Db 46 ATGGCTCCAGTGGACCGGACCTGCTGCGGCGCTCGGACACTGCGACGCTGTC 105  
 XX 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluLeuGluGluPheLeuGluGly 40

Db 106 CTTGAGGGGAAACCAACAGCGTCTGACGACGACGAGTTCAGAGGCTTCTCCAGAGGC 165  
 Qy 41 PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro 58  
 Db 166 TTCCTTCCGAGATTGAGAGACCAAGTCCCGCCCGGAGAGAGACGACTGGAAATGCCAGCCG 225  
 Qy 59 ProProGluProThrProArgValArgGlyValAlaGlnAlaGlyGlyLysProGlyLysArg 78  
 Db 226 CTTCCCGAACCACCCAGCGGTCCCGCAATCCAGGCGAGGGGGCAAG----- 273  
 Qy 79 ProGlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLys 98  
 Db 274 CAGCGGGCAGATTTAGAGTCTCTCCAGAAAAAACAAGACAAAGAGAAAGAAAGAG 333  
 Qy 99 LysAspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLys 118  
 Db 334 AAGGACAAAGGGCCCAAGGCAACAAA-----CCCTGGAGGGGCTTACAGGCCACCAAG 390  
 Qy 119 LysGlyLysGluLysProProLysValAlaThrLysLysProLysGluLysProProLysAla 138  
 Db 391 AAACCAAGAGAGAGACCCAGGCGACCAAGGACCAAGAGAAACCAACCAAGAGCC 450  
 Qy 139 ThrLysLysProLysGluGluProProLysValAlaThrLysLysProLysGluLysProPro 158  
 Db 451 ACCAAGAGCCCAAGAGAGAGCCCAAGGCGACCAAGAGCTTAAGAGAGAGAGAGAGCC 510  
 Qy 159 LysAlaThrLysLysProProSerGlyLysArgProProLeuLeuAlaProSerGluThr 178  
 Db 511 AAGGCCACTAAGAGGCGCTCGGAGAGAAAGATTCTCAAGCTGAGCCCTTGGAAAG 570  
 Qy 179 LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGly 198  
 Db 571 CTGGATCGGTACTCCCTCCACCTCCCAACCCAGGCGCCAGAGCTACCGCGAGAGAGA 630  
 Qy 199 GlyAlaProLeuSerAsnAsnTrpGluAsnProGluGluGluThrIstValGluAlaGln 218  
 Db 631 GACACACCTTCCCAATGCTGCGCAAGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 690  
 Qy 219 GluHisGlnProGluProGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 238  
 Db 691 GAGCCCGGCGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750  
 Qy 239 IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGluLysGlnProArgPro 258  
 Db 751 ATGAGAGAGAGATTACAGAGATTGAGTATCATCTGCGCAGAGAGAGAGAGAGAGAGAG 810  
 Qy 259 ProProSerArgArgArgArgProGluArgValTrpProGluProGluGluGluGluGlu 278  
 Db 811 ACACCCAGAGAGG-----AGGCTCTGCGCAGAGGCGCTTGAAGAGAGAGACT 858  
 Qy 279 ProAlaProAlaProGluGluArgGluGluGluGluGluGluGluGluGluGluGluGlu 298  
 Db 859 GAAAGACCAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909  
 Qy 299 ProProAspTyrGlyLysGlyTyrValIleProAsnTyrAspAspMetCysPheTyrPhe 318  
 Db 910 CTTCCGAGACTAGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 969  
 Qy 319 GlyProProProProGluProProProProAlaGluArgGluThrAspGluGluGluGlu 338  
 Db 970 CCCACCTCTCCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029  
 Qy 339 LeuLysLysProLysLysGluAspSerSerProLysGluGluThr---AspLysTrpAla 357  
 Db 1030 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1089  
 Qy 358 ValGluLysGlyLysAspHisLysGluProAlaGlyLysGluGluGluGluGluGluGlu 377  
 Db 1090 GTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
 Qy 378 ThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAsp 397

Db 1150 GGGCCAGTGGAGAAATCAAGTGGCCACCTATTGGGATGGAGTACACCGCATTTGAGGAC 1209  
QY AaenGlnIleArgAlaSerSerMetLeuAghIleGlyLeuGlyAlaGlnArgGlyArgLeu 417  
Db 1210 AACCAATCCGGCCCTCCCTCCATGCTGCGCCACCGGCTCGGAGCCGAGGGGCGGCTC 1269  
QY AaenMetGlnThrGlyValaThrGluAaPaspArgTyrTyrAspGlyValaTyrPysAlaGluAaP 437  
Db 1270 AACATCAAGGCTGTGTCCCAATGAAATGACTACTATGACGGGGCATGTGTCTGAGAGC 1329  
QY AaPAlaArgThrGlnTyrIleGlyValaAaPThrArgArgThrThrArgPheThrGlyVal 457  
Db 1330 GAGTCGACAGCCCAAGTGAATGAGTGAACACCCGAAGACAACCTGGTTACGAGGCGTC 1389  
QY 11eThGlnGlyArgArgSerSerIleHisAaPAspPheValThrThrPhePheValGly 477  
Db 1390 ATCACTCAGAGGCGGTACTCCAGCATCCATGACGACTTCGTGATCACTCTTTGGGGC 1449  
QY PheSerAsnAaPserGlnThrTyrPValMetTyrThrAsnGlyTyrGlnGluMetThrPhe 497  
Db 1450 TTCAGCAATGACAGCCAGACTGGGTGATGTACCAATGGCTACGAGAAATGACTTC 1509  
QY H1sGlyAaPValAaPlyAaPThrProValLeuSerGluLeuProGluProValValAla 517  
Db 1510 TATGAAATGTGGACAAGGACACACTGTGTGAGGAGCTCCCTGAGCCAGTTGTGGCC 1569  
QY ArgPheIleArgIleTyrProLeuThrTyrPAsnGlySerLeuGlyMetArgLeuGlyVal 537  
Db 1570 CGTTTATCCGACTTCATCACTCACTGACCTGGAAAGGAGCTGTGATGGCTGGAGGGT 1629  
QY LeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGlyValValaIleThr 557  
Db 1630 CTAGGCTGCCCTGACCCCTGACCTGTCTACGCTACTAGCAGCAAGATAGGTGCTACT 1689  
QY AaPAspLeuAaPAspPheArgHisSerTyrTyrAaPAspMetArgGluLeuMetLysValVal 577  
Db 1690 GACAGCTGGACTTCGGGACACACACTCAAGATGAGATGGCGAGCTGATGAAGGCTGTC 1749  
QY AaenGlnGluAaPProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLys 597  
Db 1750 AATGAGAGAGTCCCAACATCACTCGACATACAGCTGGGCAAGGTTTCAAGAGGCTC 1809  
QY LysIleTyrAlaMetGluIleSerAaPAspProGlyGluHisGlyLeuGlyGluProGlu 617  
Db 1810 AATATCTACCATGGAATCTCAAGCAACCTGGGGATCATGAATCGGGGAGGCCGAG 1869  
QY PheArgTyrThrAlaGlyIleHisGlyAaenGluValLeuGlyValArgGluLeuLeuLeu 637  
Db 1870 TTCGGTACACAGCCGGGATCCAGGCAATGAGGTGCTAGGGCCGAGAGCTCTGCTCTG 1929  
QY LeuMetGlnTyrLeuGlyAaArgGlyTyrArgAaPAspGlyAaPProArgValArgSerLeuVal 657  
Db 1930 CTATGCAATACCTATGCGAGTACCGGAGTACCGGATGGGAACCGAGAGTGGCAACTGGT 1989  
QY GlnAaPThrArgIleHisLeuValProSerLeuAaPProAaPAspGlyTyrGluValAlaAla 677  
Db 1990 CAGGACACAGCATCCACTGTGTGCTCTGCTGTAACCTGATAGGCTATAGAGTGGCAGG 2049  
QY GlnMetGlySerGluPheGlyAaPThrPAlaLeuGlyLeuTyrThrGlnGluGlyPheAaP 697  
Db 2050 CAATGGGCTCAAGATTGGGAAGTGGGCACTGGGGCTGTGAGCTAGAGGAGGCTTTGAC 2109  
QY 11ePheGluAaPAspPheProAaPLeuAaPValLeuTyrGlyAlaGluGluAaGlySerP 717  
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QY ValProTyrArgValProAaPAsnAaPLeuProIleProGluArgTyrLeuSerProAaP 737  
Db 2170 GTCCCTCAAGGCTCCAAACATTAATCTGCAATCCCTGAAAGCTTACCTGTCCCAAGT 2229  
QY AlaThrValSerThrGluValAlaGlyAlaIleIleAlaTyrMetGluLysAaPProPheVal 757  
Db 2230 GCCACGGTCTCCACAGAAATCCGGGCAATTAATTTCTGATGAGAGAAACCCCTTTGTG 2289

QY LeuGlyAlaAaPLeuAaPAspGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArg 777  
Db 2290 CTGGGTGCAATCTGAACGGTGTGAGGCGGCTGTGTCTTATCCCTATGACATGGCCGG 2349  
QY ThrProThrGlnGlnGlnLeuAlaAlaMetAlaAlaAlaArgGlyGluAaPAspGlu 797  
Db 2350 AACCTAGCCAGAGCACTGTGGCCGAGCACTGGCAGCTGCCCGGAGAAATGATAT 2409  
QY AaPAlaValSerGluAlaGlnGluThrProAaPHisAlaIlePheArgTyrPheAlaIle 817  
Db 2410 GACGGGTGTGAGGCCAGAGAGCTCAAGATCAAGCTATTCTCCGTGCTGACATC 2469  
QY SerPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGln 837  
Db 2470 TCATTTGCTCCGCCATCTCACTCACTGACGAGGCTTACGGGAGGAGGCTCCAGGCC 2529  
QY AaPThrArgGlyMetGlyTyrLeuAlaAaPValAaPArgGluLeuSerPheTyrLeuGlyCys 857  
Db 2530 GACTACACAGCGCATGGGCTGTGCAACGGGGCCAAAGTGAATCTGTCTGGGACT 2589  
QY 11eAaPAspPheSerTyrLeuHisThrArgCysLeuGluLeuSerPheTyrLeuGlyCys 877  
Db 2590 TTCAATGACTTATGCTTACCTGACACAACTGTGTGAGCTCTCGTATACCTGGGCTGT 2649  
QY AaPlyPAspProHisGlySerGluLeuProArgGluTyrPAspAsnLysGluAlaLeu 897  
Db 2650 GACAACTTCCCAAGAGTGAAGTACCTCCAGAAATGGAGAAACAACAAGAACGCTG 2709  
QY LeuThrPheMetGluGlnValHisArgGlyIleLysGlyValValThrAaPAspGlnGly 917  
Db 2710 CTCACCTTCATGACAGAGTGACCGGTGCAATTAAGGTGTGTGATGACATGAGCAAGGC 2769  
QY 11eProIleAlaAaPAlaThrIleSerValSerGlyIleAaPHisGlyValIleThrAla 937  
Db 2770 ATCCCATTTGCCAAAGCCACCACTCTGTGAGTGCATCAACCAATGAGTGAAGCAAGA 2829  
QY SerGlyGlyAaPThrArgIleLeuAaPProGlyGluTyrArgValThrAlaHisAla 957  
Db 2830 AGTGAAGTGAATCTGCGCATTTGAAACCGGGTGAAGTCCGATGACACTCAGCA 2889  
QY GlnGlyTyrThrProSerAlaLysThrCysAaPValAaPThrArgPAspIleGlyAlaThrGln 977  
Db 2890 GAGGCTACACTCAAGTCCAAAGATCTGCATGTGACTACAGATATGGGGCCACTCAG 2949  
QY CysAaPAspPheIleLeuAlaArgSerAaPThrPlyAaGlyIleArgGluIleMetAlaMetAaP 997  
Db 2950 TCCAACTTCATCTGAGTGCATCACTGAAAGCGCATTCGGAGATCTTGCTATGAAC 3009  
QY GlnAaPAspProIleProHisIleAaPProSerArgProMetThrProGlnGlnArgArg 1017  
Db 3010 GGGAAACGCCCATCTCGAATTCGACCTCAACACCACTAACCCCAAGCAGGGCGGC 3069  
QY LeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArg 1037  
Db 3070 ATGCAAGCAGCGCGCTACAGTACAGGAGTCCCAATGAGGAAACAGATGAGTGCCTCC 3129  
QY LeuAaPAlaThrThrThrLeuGlyProHisIleThrValPro--ProThrLeuProProAla 1056  
Db 3130 CTCATTTCAACGCA-----GGCCCTGCACAAAGCCCACTGCTGCTTATGCTCC 3183  
QY ProAlaThrThrLeuSerThrThrIleGluProTyrPAspGlyLeuIleProProThrThrAla 1076  
Db 3184 CTTCCCTCAACACAGCATTTACTGTAGAGCCCTGGAAAGTCTTACCACTACCACTGCA 3243  
QY GlnTyrPAspGluSerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGlu 1096  
Db 3244 GCTGGAGAGATCAGAGCTGAGACTATATACAGAAATGATGACAGAGTTT----- 3294  
QY ValGluProGluPheGlyThrThrValGluProGluPheGluThrGlnLeuGluProGlu 1116  
Db 3295 -----GAGACAGAG 3303

Qy	1117	PheGIGurInLueGIuPProdiuPhegiugIugiugluYegIuglu 1136 :::
Dp	3304	TATGGACCTGACTTGAGGTGAAGAAGATTAGAGCAGCAGAGGAGAGGAGAGAG 3353 
Qy	1137	IleaIattnrGLyGlAlaAPheProBheThrThrValIguthrTYrThrValAsnPhelY 1156 :::
Dp	3364	ATGACACAGCGCTTACATTTCCTCACTCACACAGTAGAGACTTACACAGTGAACTTTGGG 3423 
Qy	1157	AepPhe 1158 
Dp	3424	GACTTC 3429 
<b>RESULT 14</b>		
ID	AAOS8708	standard; cDNA to mRNA; 3728 BP.
XX	AAOS8708;	
AC	AAOS8708;	
XX	16-OCT-2003 (revised)	
DT	25-MAR-2003 (revised)	
DT	23-SEP-1994 (first entry)	
XX	Mouse OSF-5 coding sequence.	
DE		
XX	Mouse OSF-5; bone-related carboxypeptidase-like protein; growth factor; adhesion molecule; osteogenesis; bone induction; ds.	
KW		
KM		
XX	Mus musculus; (osteoblastic cell line MC3T3E1).	
OS		
XX	Key Location/Qualifiers	
FH	CDS 69..345	
FT	/*tag= "a"	
FT	/product= "OSF-5"	
PN	EP588118-A2.	
PD	23-MAR-1994.	
XX		
PF	25-AUG-1993; 93EP-00113604.	
PR	28-AUG-1992; 92JP-00230029.	
PR	03-DEC-1992; 92JP-00324033.	
XX	(PARH ) HOECHST JAPAN LTD. (HMRI ) HOECHST MARION ROUSSELL LTD.	
PA		
XX	Kawai S, Takeshita S, Okazaki M, Amann E;	
DR	WPI; 1994-093794/12.	
DR	P-PSDB; AAR49994.	
PT	New bone-related carboxypeptidase OSF-5 - used to obtain prodn. for the diagnosis and treatment of bone metabolic diseases, e.g. osteoporosis, or Paget's disease.	
XX	Claim 1; Page 13-19; 26pp; English.	
XX	The cDNA of mouse OSF-5 was isolated from a mouse osteoblastic cell line MC3T3-E1 cDNA library constructed by a combination of PCR and the subtraction cloning method, followed by cloning using the differential screening technique. OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion molecule or growth factor; it takes part in osteogenesis at the site of bone induction. OSF-5 can be used to treat bone metabolic diseases, e.g. osteoporosis, Paget's disease, osteomalacia, hyperostosis or osteopetrosis. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 16-OCT-2003 to standardize OS field)	
CC		
CC	Sequence 3728 BP; 966 A; 1091 C; 1059 G; 612 T; 0 U; 0 Other;	
<b>Alignment Scores:</b>		
Pred. No.:	4.23e-232	Length: 3728
Score:	5049.00	Matches: 956

	Percent Similarity:	87.0%	Conservative:	55
	Best Local Similarity:	82.3%	Mismatches:	113
	Query Match:	80.5%	Indels:	38
DB:		2	Gaps:	9
US-10-642-946-3 (1-1158) x MA058708 (1-3728)				
OY	1 MetAlaLaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys	20		
Db	69 ATGGCTCAGTGGCGACCGCATTCCTGCTCTGGCGCTCTGGCACTGCTACCGTGGC	128		
OY	21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40		
Db	129 CCTGAGGGGAACCCACAGACGGGTGTGACGACGACGATCGAGAGTTCTCTGAAGGC	188		
OY	41 PheLeuSerGluLeuGluProGlu-----ProIleGluAspAspValGluAlaProPro	58		
Db	189 TTCCTTTCCGAGTTGAGAGCCAGTCCCGCCCGGGAAGACGAGTGGAAAGTCCAGCCG	248		
OY	59 ProProGluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArg	78		
Db	249 CTTCCGGAACCCACCGACGCTCCCGCAATCCAAAGCAGGGGGCAG-----	296		
OY	79 ProGlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysGlyLys	98		
Db	297 CAGCGGCGAGATGTAAAGTCCCTCCAGAAAAAACAAGCAAAAGAGAAAGAAAG	356		
OY	99 LysAspLysGlyProLysValProLysGluSerIleGluGlyLysArgProArgProProLys	118		
Db	357 AAGACAAAGGCCCCCAAGCCCAAAA-----CCCTGGAGGGCTCTACAGGCCCAAG	413		
OY	119 LysGlyLysGlyLysProLysAlaThrLysLysProLysGlyLysProProLysAla	138		
Db	414 AAACCAAGAGAAAGCCACCAAGGCGACCAAGAGGCCCAAGAGAAACCAACCAAGGCC	473		
OY	139 ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGlyLysProPro	158		
Db	474 ACCAAGAAAGCCCAAGAGAAACACCAAGGCGACCAAGAGCCTTAAGAGAAACCCACC	533		
OY	159 LysAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr	178		
Db	534 AAGGCCACTAAGAGGCCCTCCGCGAAGAAAGATTCTCACTGTGGCCCCCTTGGAAAG	593		
OY	179 LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGluGly	198		
Db	594 CTGAGATCGGTACTCCCTCACCTCCCAACCCCAAGCGCCGAGAGCTACCGCAAGAGA	653		
OY	199 GlyAlaProLeuSerAspAspThrGlnAsnProGlyGluGluThrHisValGluAlaGln	218		
Db	654 GACACACCCCTCCCAATACCTCGGAAAGGTCAAGAGAAAGAGCCCAAGTGAAGCCAG	713		
OY	219 GluHisGlnProGluProGluGluGluThrGluGluProThrLeuAspLysAspGln	238		
Db	714 CAGCCCGGCGAGAGCCAGAGAGAGACTGAGATGCCCACTCGAGACTCAATGACAG	773		
OY	239 IleGluLysGluAspLysArgLysAspPheGluLysTrpIleArgArgGlnLysGlnProArgPro	258		
Db	774 ATGAGAAAGAGATTACAGAGATTTTAAGTACATCTTTGCCAAGAGACGCCAGGCCA	833		
OY	259 ProProSerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAla	278		
Db	834 ACACCCAGCAGAG-----AGGCTGTGGCCAGAGCGCCCTTGAGAGAGAGACT	881		
OY	279 ProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeu	298		
Db	882 GAAGAGCCAGAGAAAGAAAGAAATCCAGCCACTGTGAAGCCCTCG-----CTG	932		
OY	299 ProProAspLysGlyAspGlyThrAlaIleProAsnLysAspAspMetAspLysTrpPhe	318		
Db	933 CTTCCGACTATGGGATAGCTACGTGATCCCAACTGATGAGCTTGAAGCTATATATTC	992		
OY	319 GlyProProProGluLysProAspAlaGluArgGlnThrAspGluGluLysGluGlu	338		

Db CCCCACTCCACCGAGAGCCTGATGTTGGACAAGAGTGATGAGAAAAAGAGAGC 1052  
QY LeuLYbLYsProLYaLYeGLuAsPseSerProLYeGLuThr--AsPlySTrPaLa 357  
Db ATGAAAGAACCCAAAAGAGAGGTAGTACCCCAAGAGAGACACAGAGACAAGTGAGACC 1112  
QY ValGLuLYeGLyLYaAsPbHsLYeGLuPProLYeGLyGLuGLuLeuGLuGLuGLuTP 377  
Db GTGGAGAAAAACAAGACCAAAAGGGCCCCGAGAGGTAGAGAGCTGGAGAGAGATGG 1172  
QY ThrProThrGLuLYeValLYeCYsPProLYeGLyMeGLuSeHsIAsrGLeGLuAsP 397  
Db GGGCCAGTGGAGAAATCAAGTGCCCACTATTGGATGAGTCAACCGCATTTGAGAGC 1232  
QY AAsnMeGLInThrGLyAlaThrGLuAsPAsPTrTYrTYrAsPGLyAlaTrpCYsaGLuAsP 437  
Db AACATCCAGGCTGTGTCCCAATGAAGATGACTACTATGACGGGCAATGTGTCTGAGAGC 1352  
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QY AsrPheIleAsrGLeLYrProLeuThrTrpAsnGLySerLeuCYmeCTrGLeGLuVal 537  
Db CGTTTCATCCGACTTCATCACTCACTGACCTGAGACGGTATGGCTGGAGGGTC 1652  
QY LeuGLyCYseSerValAlaProValTYrSeTYrTYrAlaGLInAsnGLuValAlaThr 557  
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QY AsPAsPLeuAsPHeAsrGLHsIAsSerTYrLYAsPMeCAsrGLInLeuMeLYsValVal 577  
Db GACAGCTGGACTTCCGGCACACAGCTACAGAGACATGGCCAGCTGATGAAGGCTGTC 1772  
QY AAsnGLuGLuCYsPProThrIleThrAsrGLThrTYrSeTYrGLySeSerAsrGLyLeu 597  
Db AATGAGAGAGTCCCCCAATCACTCCACATACATACAGCTGGGCAAGATTCAACAAGGCTC 1832  
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Db AAGATTTACGCATGGAATCTCAGACAACTCTGGGATCATGAATCGGGGAGAGCCGAG 1892  
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QY GlnMeGLySeGLuPheGLyAsnTrpAlaLeuGLyLeuTrpThrGLuGLuGLyPheAsP 697  
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QY IlePheGLuAsPHeProAsPLeuAsnSeValLeuTrpGLyAlaGLuGLuAsrGLySTrP 717  
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QY ValProTYrAsrGLValProAsnAsnAsnLeuProIleProGLyAsrGLyLeuSeProAsP 737  
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QY AlaThrValSeSerThrGLuValAsrGLaIleIleAlaTrpMeGLuLYeAsnProPheVal 757  
Db GCCACGTCTCCACAGAAAGTCCGGGCTTATTCTTCTGATGAGAAACAAACCCCTTTGG 2312  
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QY ThrProThrGLInGLuGLuLeuValAlaAlaMeCValAlaAlaAsrGLyGLuAsrGLu 797  
Db AACCTTACAGAGACACTGTGTGGCCGAGGCACTGGACGCTGCCCGGAGAAAGATAT 2432  
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Db GACGGGGTGTGAGGCCAGAGACTCCAGATCCAGTATTTTCCGTGGCTGGCCATC 2492  
QY SerPheAlaSeSerAlaHsIleuThrLeuThrGLuPProTYrAsrGLyGLyCYsGLInaGLIn 837  
Db TCATTTGCTCCGCCCATCTCACTGACGAGAGCTTACCGGGAGGGGTCCAGGCCAG 2552  
QY AsPTrpThrGLyGLyMeGLyIleValaAsnGLyAlaLYSTrPAsnProAsrGLThrGLyThr 857  
Db GACTACACAGCGGATGGAGCTGTGTCAACGGGGCCAAAGTGAATCTCGCTGGAGACT 2612  
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QY GlnGLyTYrThrProSeValAsrThrCYsAsnValAsPTrTYrAsrGLyAlaTrpGLIn 977  
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QY CYsAsnPheIleLeuAlaSeSerAsnTrpLYsAsrGLIleAsrGLuIleMeCAlaMeCAsn 997  
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QY LeuGLInaAsrGLyGLeGLInHsIleAsrGLeAsrGLeAsrGLaIleGlnMeCAsrGLeAsrGLy 1037  
Db ATGCAAGAGCGCGCTACAGTACAGGCGCTCCCAAGAGGGAACAGATGCAACTGCTCCG 3152  
QY LeuAsnAlaThrThrThrLeuGLyProHsIleThrValPro--ProThrLeuProProAla 1056  
Db CTCATTTTCAACGCA-----GGCCCTGCACAAAGCCCACTGCGCTTATGCTCC 3206





QY 421 hrg1y1a1aThrg1uabpAprrTyrrTyraSpGly1a1aTrpCy8a1aGlu1uabpApRa1aA9T 441  
 DB 647 CCGGGGCCACTGAGACGACTACTGATGAGTGGCGTGTGCACGAGGACGATGCCAGGA 706  
 QY 441 hrg1nTrp11eGluVala1aBpThrArGArGThrThxArpTherhrg1y1a11eThrGlnG 461  
 DB 707 CCCAGTGGATTAAAGGTGGACACACGAGGAGACTACCGGGTTCAACAGGCGTCATCACCCAGG 766  
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 DB 767 GCAGAGACTCCAGCATCCCATGACGATTTGTGACCACTTCTTCGGGGCTTCAGCAAGG 826  
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 DB 827 ACAGCCAGCATGGGTGATGATACACCAAGCGCTATGAGAAATGACCTTTCATGGGAGCG 886  
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 DB 887 TGGACAAAGGACACACCCGTGGTGAAGTCCCAAGCGGGTGGTGGCTTCGTTTCATCC 946  
 QY 521 rG11eTyrrProLeuThrTrpAsnGlySerLeuCy8eArGleuGluVal1LeuGlyCy8S 541  
 DB 947 GCATCAACCCACTCACTGGAATGGCAGCGCTGTGCATGGCGCTGGAGGTGCTGGGGTGTCT 1006  
 QY 541 eV1a1a1aProVal1TyrrSerTyrrTyrrAla1aSpGluVala1a1aThraBpApLeuA 561  
 DB 1007 CTGTGGCCCCCTGTCTACACTACTACGACACAGATAGGTGGTGGCCACCGATGACTTGG 1066  
 QY 561 BPpHeArGh1h1sSerTyrrTyrrSaBpMeArGglInLeuMeTyrrVala1aSpGluGluC 581  
 DB 1067 ATTTCCGGGACACACACTCAAGGACATGCGGACGCTCATGAAGGTGGTGAACGAGAGT 1126  
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 DB 1127 GCCCCACATCAACCCGACTTACAGCTGGGCAAGGCTCACAGAGGCTTCAAGATTTAGG 1186  
 QY 601 1aMeGlu1LeuSerAaBpAnProGlyGlu1h1sGluLeuGlyGluProGluPheArGTYrr 621  
 DB 1187 CCATGGAGATCTCAAGACCAACCTGGGGAGCATTAACCTGGGGAGCCCGAGTTCCGCTACA 1246  
 QY 621 hz1aG1y11eh1sGlyAaSpGluVal1LeuGlyArGgluLeuLeuLeuLeuMeG1nT 641  
 DB 1247 CTGGCTGGATCCATGGCAACGAGGTGCTGGGCGGAGCGTGTGGCTGCTCATCACTAGT 1306  
 QY 641 yrrLeuCy8ArGgluTyrrArGAspGly1y1aBpProArGVala1aArGSerLeuVal1GlnAspThra 661  
 DB 1307 ACCTGTGGCGAGGTACCGGAGTGGAAACCAAGTGTGGCGACGCTGGGACAGACAC 1366  
 QY 661 rG11eh1sLeuVal1ProSerLeuAaBpArG1yTyrrGluVala1a1aG1MeG1yS 681  
 DB 1367 GCATCAACCTGGTGGCTTCACTGAACCTGATGGCTTCAAGGTGGAGCCGACAGATGGGCT 1426  
 QY 681 eGrluPheGlyAaBpThra1aLeuGlyLeuTrpThrgluGluGlyPheAsp11ePheGluA 701  
 DB 1427 CAGAGTTTGGGAACCTGGGCGCTGGGACTGTGACTGGAGGAGGCTTTGACATCTTTGAAG 1486  
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 DB 1667 ATTTGAACCGGCGGAGGCTAGTATCTTAACCTTAAGATATAGGCCCGGACCCCTACCC 1726  
 QY 781 lng1uGlnLeuAa1a1a1aMeAla1a1a1aArGgl1yGluAaBpGluAaBpGluValS 801

DB 1727 AGAGACACTCTGGCGGACACCATGGAGGACGCCGGGGGAGGATGAGGACGAGTCT 1786  
 QY 801 eGrluAla1GlnGluThrProAspH1sa1a11ePheArGTYrrLeuAla1LeSerPheAlaS 821  
 DB 1787 CCGAGGCCAGAGACTCCACAGCACCGCACTTCCGGGTGGCTTGCATCTCTTCGGCT 1846  
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 DB 1847 CCGACACTCACTTGAACCAAGCCCTACCGGAGGCTGCCAAGCCCAAGACTACACCG 1906  
 QY 841 lYglYMeGly11eVala1aSpGly1a1y1aTrpAsnProArGThrg1yThr11eAaBp 861  
 DB 1907 GCGGCAATGGGATGCTCAACCGGAGCCAGTGGAAACCCCGGACCGGACTATCAATGACT 1966  
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 DB 1967 TCAGTTACTGTGATCAAACTGCTGGAGCTCTCTTCACTGGGCTGTGAACAAGTTCC 2026  
 QY 881 rOh1sGluSerGluLeuProArGgluTyrrGluAaBpAaBpGluAla1eLeuLeuThrPhe 901  
 DB 2027 CTCAAGAGATGAGCTGCCCGGAGTGGAGAAACAAGAGGCGCTGCTCACTTCA 2086  
 QY 901 eGluGlnVal1h1sArGgl1y1e1yGlyVala1ThraBpGluGlnGly11ePro11ea 921  
 DB 2087 TGGACAGGTGCACCGTGGCATTTAAGGGGTGTGACCGAGCAAGCAAGCATCCCATTTG 2146  
 QY 921 1aBpAla1aThr11eSerVal1SerGly11eAaBpGlyVala1y1eThra1aSerGlyGlyA 941  
 DB 2147 CCMAAGCCACCACTCTGTGAGTGGCAATTACAGAGGCTGAAGACAGCAAGTGGTGGTG 2206  
 QY 941 sPTyrrTrpArG11eLeuAaBpProGlyGluTyrrArGVala1Thra1a1a1aGluGlyTYrr 961  
 DB 2207 ATTTACTGGCAATCTTGAACCCGGGTGAAGTACCGGTGAACCCACCGGAGGGCTTACA 2266  
 QY 961 hPProSerAla1y1eThrcy8aBpVala1aBpTyrrAsp11eGlyAla1ThrglnCy8aBpHe 981  
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 QY 981 1eLeuAla1ArGSerArh1sArGgl1eArGglu11eMeV1aMeArh1sAaBpAaBpArG 1001  
 DB 2327 TCTGTGCTGCTCCAACTGGAAAGCGCATTCGGGAAATCATGGCCATGAACGGGAACCGG 2386  
 QY 1001 rO11eProH1s11eAspProSerArGpPomeThrProGlnGlnArGArGleuGlnGlnA 1021  
 DB 2387 CTATCCACACATTAACCATGCGCCCTATTAACCCCAACAGGACCGCTGCGAGCAC 2446  
 QY 1021 rGArGLeuGlnH1sArGleuArGleuArGAla1aGlnMeArGleuArGArGleuAaBpAlaT 1041  
 DB 2447 GACGCTTACAAACAGCGCTGCGGCTTGGGCAACAATGCGGCTGGGCGCTCAACGCCA 2506  
 QY 1041 hTrThThrLeuGlyProH1sThrVal1ProProThrLeuProProAla1aThrThrl 1061  
 DB 2507 CCACACCCCTTAAGCCCCCACTGTGCTCCACAGCTGCCCCCTGCGCCACACACC 2566  
 QY 1061 eUSeSerThrTr11eGluProTyrrGlyLeu11eProProThrThra1aGlyTyrrGluGluS 1081  
 DB 2567 TGAACATTAACATTAAGCCCTGGGGCTCATACCGCAACACACCGCTGGCTGGAGAGGT 2626  
 QY 1081 eGrluThrgluThrTyrrThrgluVala1ThrgluPheGlyThrgluVala1GluProGluP 1101  
 DB 2627 CGAGACTGAACCTTACACAGAGGTGTGAACAAGTTTGGGACCGGAGGTGGAGCCGAGT 2686  
 QY 1101 hGgl1yThrTyrrVala1GluProGluPheGluThrgluLeuGluPheGluThrglu 1121  
 DB 2687 TTGGAGCAAGGTGAGGCCGAGTTTGAGAACCAAGTTGAAGCTTGATTGAACCCAG 2746  
 QY 1121 eUgluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1141  
 DB 2747 TGGAACCGAGTTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCACCTGGCC 2806  
 QY 1141 1a1a1aBpProBpThrThrVala1GluThrTyrrThra1aBpPheGlyAaBpHe 1158



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Job time : 1662 secs

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REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
AUTHORS Hominiidae; Homo.  
TITLE  
JOURNAL

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ORIGIN

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Best Local Similarity 68.4%; Pred. No. 6.5e+05;  
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 21 TTTTGTACCTGGCTGGAGCTCCACCTCCCGAGCTG 58  
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RESULT 3  
AX517772/c 41 bp DNA linear PAT 05-OCT-2002  
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DEFINITION Sequence 3970 from Patent WO02052044.  
ACCESSION AX517772  
VERSION AX517772.1 GI:23566740  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 3970 04-JUL-2002;  
Riken (JP)

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Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 21 TTTTGTACCTGGCTGGAGCTCCACCTCCCGAGCTG 58  
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RESULT 4  
AX612102/c 45 bp DNA linear PAT 17-FEB-2003  
LOCUS  
DEFINITION Sequence 3127 from Patent WO02072882.  
ACCESSION AX612102  
VERSION AX612102.1 GI:28407531  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3127 19-SEP-2002;  
OGHAM GmbH (DE)

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Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 116 ACTAGCGCTTCCTTCATCTCTTTGAGCAGCTCTCAGCTG 157  
45 ACTGCGCTTCTTCTCATCTCCGCTTCAGAGGCTCCACAGG 4

RESULT 5  
AX612103/c 45 bp DNA linear PAT 17-FEB-2003  
LOCUS  
DEFINITION Sequence 3128 from Patent WO02072882.  
ACCESSION AX612103  
VERSION AX612103.1 GI:28407532  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3128 19-SEP-2002;  
OGHAM GmbH (DE)

FEATURES  
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RESULT 6  
AX612100/c 48 bp DNA linear PAT 17-FEB-2003  
LOCUS  
DEFINITION Sequence 3125 from Patent WO02072882.  
ACCESSION AX612100  
VERSION AX612100.1 GI:28407529  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3125 19-SEP-2002;  
OGHAM GmbH (DE)

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ORIGIN

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AX612100/c 48 bp DNA linear PAT 17-FEB-2003  
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DEFINITION Sequence 3125 from Patent WO02072882.  
ACCESSION AX612100  
VERSION AX612100.1 GI:28407529  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3125 19-SEP-2002;  
OGHAM GmbH (DE)

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45 ACTGCGCTTCTTCTCATCTCCGCTTCAGAGGCTCCACAGG 4

RESULT 6  
AX612100/c 48 bp DNA linear PAT 17-FEB-2003  
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DEFINITION Sequence 3125 from Patent WO02072882.  
ACCESSION AX612100  
VERSION AX612100.1 GI:28407529  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3125 19-SEP-2002;  
OGHAM GmbH (DE)

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ORIGIN

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Matches	28;	Conservative	0;	Mismatches 14; Indels 0; Gaps 0;
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RESULT 7				
AX612101/c				
LOCUS	AX612101	48 bp	DNA	linear
DEFINITION	Sequence 3126 from Patent WO02072882.			PAT 17-FEB-2003
ACCESSION	AX612101			
VERSION	AX612101.1	GI:28407530		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Cullen,P. and Seedorf,U.			
TITLE	Coronary chip			
JOURNAL	Patent: WO 02072882-A 3126 19-SEP-2002;			
FEATURES	OGHAM GmbH (DE)			
source	Location/Qualifiers			
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Matches	28;	Conservative	0;	Mismatches 14; Indels 0; Gaps 0;
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RESULT 8				
AR017890				
LOCUS	AR017890	50 bp	DNA	linear
DEFINITION	Sequence 37 from patent US 5780269.			PAT 05-DEC-1998
ACCESSION	AR017890			
VERSION	AR017890.1	GI:3973493		
KEYWORDS				
SOURCE				
ORGANISM	Unknown.			
	Unclassified.			
REFERENCE	1 (bases 1 to 50)			
AUTHORS	Inouye,S. and Inouye,M.			
TITLE	Hybrid molecules			
JOURNAL	Patent: US 5780269-A 37 14-JUN-1998;			
FEATURES	Location/Qualifiers			
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Db	41	GCTCCACTCCCGACGCTCTGCTCAGCTGCTTTTCCAACC	82	
	2	GATAAACCCTCCACCTGCGTGTCTCACCCTGCTGGACACC	43	
RESULT 9				
AR681730/c				

LOCUS	AR681730	50 bp	DNA	linear	PAT 12-SEP-2005
DEFINITION	Sequence 1159 from patent US 6905827.				
ACCESSION	AR681730				
VERSION	AR681730.1	GI:7463500			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 50)				
TITLE	Wohlgenuth, J., Fry, K., Woodward, R. and Ly, N.				
JOURNAL	Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases				
FEATURES	Patent: US 6905827-A 1159 14-JUN-2005; Expression Diagnostics, Inc./ So. San Francisco, CA				
source	Location/Qualifiers 1..50 /organism="unknown" /mol_type="genomic DNA"				
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Best Local Similarity	66.7%; Pred. No. 8.6e+05;				
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Qy	35 CTGGAGCTCCACCTCCGCCAGCTGCTGCTTTC 76				
Db	50 CTGTGCGCTTCCCTTTCAGATTACAGCCCGACCTCTTTC 9				
RESULT 10					
LOCUS	AR016521	39 bp	DNA	linear	PAT 05-DEC-1998
ACCESSION	AR016521				
DEFINITION	Sequence 35 from patent US 5776746.				
VERSION	AR016521				
KEYWORDS	AR016521.1 GI:3972798				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 39)				
TITLE	Denney, D.W. Jr.				
JOURNAL	Gene amplification methods				
FEATURES	Patent: US 5776746-A 35 07-JUL-1998; Location/Qualifiers 1..39 /organism="unknown" /mol_type="unassigned DNA"				
ORIGIN					
Query Match	7.9%; Score 19.2; DB 2; Length 39;				
Best Local Similarity	75.0%; Pred. No. 1.1e+06;				
Matches	24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;				
Oy	211 TGATCAGATPCCCACTAAATGATTCAC 242				
Db	37 TGAACAGATPCCCACTAAATGATTCAC 6				
RESULT 11					
LOCUS	AR096904	39 bp	DNA	linear	PAT 08-SEP-2000
ACCESSION	AR096904				
DEFINITION	Sequence 35 from patent US 5972334.				
VERSION	AR096904				
KEYWORDS	AR096904.1 GI:10009428				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 39)				
TITLE	Denney, D.W. Jr.				
JOURNAL	Vaccines for treatment of lymphoma and leukemia				
FEATURES	Patent: US 5972334-A 35 26-OCT-1999; Location/Qualifiers				



Mon Oct 2 13:05:56 2006

us-10-642-946-6\_copy\_1967\_2208.sz50.rge

Page 5

Db 13 CCACTCCCCAGCTGCTGC 31

Search completed: October 1, 2006, 01:33:49  
Job time : 2027.61 secs

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misc\_feature

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## ORIGIN

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Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 69 TGTAAACGTAACATTTGCGCCACTAGCGCTGTTCCATCTCT 138  
DB 1 TTTGACGGTAATTAATTTTCCCATCTCTCACCGTTACCACTCTT 50

## RESULT 2

AV960508 45 bp mRNA linear EST 26-MAY-2005  
LOCUS AV960508 Nori Satoh unpublished cDNA library, cleavage stage embryo  
DEFINITION Ciona intestinalis cDNA clone cici12n17 5', mRNA sequence.  
ACCESSION AV960508  
VERSION AV960508.1 GI:19448807  
KEYWORDS EST.

SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 45)  
Satoch, N., Satou, Y., Kohara, Y. and Shin-i, T.  
Expressed genes in Ciona intestinalis  
Unpublished (2000)

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-Ku, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoch@ascidian.zool.kyoto-u.ac.jp.

## FEATURES

source

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/organism="Ciona intestinalis"  
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Query Match 8.0%; Score 19.4; DB 7; Length 45;  
Best Local Similarity 70.3%; Pred. No. 8.5e+05;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCTGTTTCCAAACCCACCC 88  
DB 1 CCTGCAGCTGCCCAACAGCTGTACCAAGTCCAAACAC 37

## RESULT 3

DUS32846 47 bp mRNA linear GSS 06-OCT-2005  
LOCUS DUS32846 YHR292 BayGenomics Gene Trap Library pGTOLxf Mus musculus cDNA,  
DEFINITION mRNA sequence.  
ACCESSION DUS32846  
VERSION DUS32846.1 GI:77358565  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
1 (bases 1 to 47)  
BayGenomics.  
http://baygenomics.ucsf.edu/  
Unpublished (2001)  
Contact: BayGenomics  
Bay Area Functional Genomics Consortium (BayGenomics)  
Email: info@baygenomics.ucsf.edu  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACT&TYPE=  
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Class: Gene trap.

## FEATURES

source

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/note="Vector: pGTOLxf"

## ORIGIN

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Best Local Similarity 67.5%; Pred. No. 9.8e+05;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 38 GAGCTCACCTCCCGACCTGCTGCTCAGCTGCTTCC 77  
DB 1 GGGCTTCGGCGCGCGCTGCGCTCCCGGCTTCC 40

## RESULT 4

BM392535 42 bp mRNA linear EST 17-JAN-2002  
LOCUS BM392535 50071-2-10-A02.f.1 Chilcoal/turkewitz cDNA (small fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM392535  
VERSION BM392535.1 GI:18192573  
KEYWORDS EST.

SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 42)  
Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, J.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

source

1. .42  
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

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 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 25 GGTCACTGCTGGAGCTCCAGCTCCCGAGCTGC 59  
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Db 1 GGACACAAAGCTGGAGCTCCACCGCGTGGCGGC 35

RESULT 5  
 BM393595 42 bp mRNA linear EST 17-JAN-2002  
 LOCUS 50072-2-10-A02.f.1 Chilicoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM393595  
 VERSION BM393595.1 GI:18193648  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
 Hymenostomata; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
 1 (bases 1 to 42)  
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
 Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 CONTACT: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
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 preparation can be found in Chilicoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 7.9%; Score 19; DB 2; Length 42;  
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Db 1 GGACACAAAGCTGGAGCTCCACCGCGTGGCGGC 35

RESULT 6  
 CZ550492 49 bp DNA linear GSS 24-MAY-2005  
 LOCUS 02F0151-13C2-B12 UniformMu MutTail Library Zea mays genomic clone  
 DEFINITION 02F0151-13C2-B12, genomic survey sequence.  
 ACCESSION CZ550492  
 VERSION CZ550492.1 GI:66476962  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 49)  
 Lathaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.  
 Sequence tagged transposon insertions from the UniformMu maize  
 population

JOURNAL Unpublished (2003)  
 COMMENT Contact: Donald R. McCarty  
 Plant Molecular and Cellular Biology Program  
 University of Florida  
 PO 110690 Gainesville, FL 32611-0690, USA  
 Tel: 352-392-1928 x322  
 Email: drmc@ufl.edu  
 Sequence flanking probable Mu insertion site in UniformMu line:  
 02F0151-1  
 Class: transposon insertion site.  
 Location/Qualifiers  
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 /cultivar="UniformMu"  
 /db\_xref="taxon:4577"  
 /clone\_11b="UniformMu MutTail Library"  
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon  
 insertions in Mu inactive lines were extracted from the  
 UniformMu maize population by the thermo asymmetric  
 interlaced PCR (TAIL) protocol using primers specific for  
 the Mu terminal inverted repeat and a set of 16 arbitrary  
 primers. Amplicons were size enriched using Sepharose 400  
 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 7.9%; Score 19; DB 13; Length 49;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+06;  
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 125 GGTTCATCTCTTGGAGCAGCTCTCAGCTGAG 159  
 |||||  
 1 CGCCTCATTTCTCGAATCCCTTCGCGTGAG 35

Db 1 CGCCTCATTTCTCGAATCCCTTCGCGTGAG 35

RESULT 7  
 BH801643 44 bp DNA linear GSS 25-APR-2002  
 LOCUS 1008118610.1EL.X1 1008 - RescueMu Grid I Zea mays genomic, genomic  
 DEFINITION survey sequence.  
 ACCESSION BH801643  
 VERSION BH801643.1 GI:20314925  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 44)  
 Walbot, V.  
 Maize genomic sequences found using engineered RescueMu transposon  
 Unpublished (2001)  
 CONTACT: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Very probable ligation site of ends cut by single endonuclease.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1008118 row: 21  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..44  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"

/lab\_host="DH10B"  
/clone\_lib="1008 - RescuedMu Grid 1"  
/note="Organ: leaf; Vector: RescuedMu (engineered from  
blue-script backbone); Site\_1: BamHI; Site\_2: BglII;  
RescuedMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuedMu, go to the web  
site www.zmmb.iastate.edu and follow the links for  
'RescuedMu.' Grid 1 was grown at Berkeley in 2001. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

## ORIGIN

Query Match 7.8%; Score 18.8; DB 11; Length 44;  
Best Local Similarity 68.4%; Pred. No. 1.3e+06;  
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 45 CACCTCCGAGCTGCTCCTCACTGCTTTTCCAAAC 82  
1 CTCCTCCATCGTGGCGTCCCTCCCTTCCCTATCC 38

RESULT 8 45 bp mRNA linear EST 14-AUG-2003  
CF297420 30DGS--08-E12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--08-E12, mRNA  
sequence.

ACCESSION CF297420.1 GI:33666453  
VERSION CF297420.1  
KEYWORDS EST.

## SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP  
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 45)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## COMMENT

Location/Qualifiers

## FEATURES

1. 45  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="30DGS--08-E12"  
/cissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-T080, Site 1: EcoRI, mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

## ORIGIN

Query Match 7.7%; Score 18.6; DB 5; Length 45;  
Best Local Similarity 65.9%; Pred. No. 1.5e+06;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 28 CACCTGCTGGAGCTCCACCTCCGAGCTGCTGCTCAC 68  
1 CACCTGCTGGAGCTCCACCTCCGAGCTGCTGCTCAC 68

Db 5 CCCCTTCTGAACAGACACCCCTTCTGCTGATCTCC 45

RESULT 9 50 bp DNA linear GSS 06-JUL-2004  
CR249499/c CR249499/c  
LOCUS Reverse strand read from insert in 5'HPT insertion targeting and  
chromosome engineering clone MHPN350a08, genomic survey sequence.

ACCESSION CR249499.1 GI:50028352  
VERSION CR249499.1  
KEYWORDS GSS; genome survey sequence; MICR.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICR  
Location/Qualifiers

1. 50  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN350a08"  
/clone\_lib="MHPN"

## ORIGIN

Query Match 7.7%; Score 18.6; DB 14; Length 50;  
Best Local Similarity 65.9%; Pred. No. 1.5e+06;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TTCTCAGACACAGCACTGATTTGTGACCTGCTGGAG 41  
46 TCCCCACACCCCGACGATTTTGTGACATGCTGGAG 6

RESULT 10 46 bp DNA linear GSS 03-DEC-2003  
CG892412/c CG892412/c  
LOCUS 01S0720-08D1-C03 UniformMu MURAIL Library Zea mays genomic clone  
01S0720-08D1-C03, genomic survey sequence.

ACCESSION CG892412  
VERSION CG892412  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 46)

REFERENCE Labshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.  
Population tagged transposon insertions from the UniformMu maize  
population Unpublished (2003)  
Contact: Donald R. McCarty  
Plant Molecular and Cellular Biology Program  
University of Florida  
PO 110690 Gainesville, FL 32611-0690, USA  
Tel: 352-392-1928 x322  
Email: drmc@ufl.edu

Sequence flanking probable Mu insertion site in UniformMu line:  
01S0720-08, Primer set: D  
Class: transposon insertion site.  
Location/Qualifiers

1. 46  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="W22 (ACR, bz1-m9)"

/cultivar="UniformMu"  
/db\_xref="taxon:4577"  
/clone="01S0720-08D-C03"  
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon  
insertions in Mu inactive lines were extracted from the  
UniformMu maize population by the thermo asymmetric  
interlaced PCR (TAIL) protocol using primers specific for  
the Mu terminal inverted repeat and a set of 16 arbitrary  
primers. Amplicons were size enriched using Sepharose 400  
spin columns and cloned into the TOPO PCR4 vector."

## ORIGIN

Query Match 7.6%; Score 18.4; DB 12; Length 46;  
Best Local Similarity 63.6%; Pred. No. 1.7e+06;  
Matches 28; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 125 CGTTTCATCTCTTTGAGCAGCCTCTGACGTGAGTGAACAGA 168  
DB 46 CGCTCCATTTCTGCGAATCACCCTCTCTTGTGACAAACCAA 3

RESULT 11  
AUI05790  
LOCUS  
DEFINITION AUI05790 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
ACCESSION HRC09728. mRNA sequence.  
VERSION AUI05790.1 GI:13555311  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,  
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,  
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL PUBLISHED 11375929  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Tel: 81-3-5449-5343  
Fax: 81-3-5449-5416  
Email: yusuzuki@igc.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and  
Sugano,S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

## FEATURES

source  
1..50  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HRC09728"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 7.6%; Score 18.4; DB 1; Length 50;  
Best Local Similarity 63.6%; Pred. No. 1.7e+06;  
Matches 28; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 145 ACCTTCACGTGAGCTGAACAGACCTGTTAAGCCACCG 188  
DB 6 AACTGGGCGCTGCGGATGAACCAACCCGCGGTTAAGGCGCCG 49

RESULT 12

C2294180/c  
LOCUS C2294180 44 bp mRNA linear GSS 21-DEC-2005  
DEFINITION P063B09.GV09C05 Mus musculus cDNA clone P063B09, mRNA sequence.  
ACCESSION C2294180  
VERSION C2294180.1 GI:61681930  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE

AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,  
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.  
A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
12904583

## JOURNAL

## PUBLISHED

Contact: GGTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
rf1PROSAbetrago gene trap. Sequence tag generated by 5'RACE.  
Additional sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P063B09'. ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm1'.  
Inhouse Sequence Identifier: 24822  
Class: Gene Trap.

## FEATURES

source  
1..44  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="P063B09"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
/clone\_lib="GV09C05"  
/note="Vector: rf1PROSAbetrago"

## ORIGIN

Query Match 7.5%; Score 18.2; DB 13; Length 44;  
Best Local Similarity 74.2%; Pred. No. 1.9e+06;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 35 CTGGAGCTGCACCTCCCGAGCTGTCGCTC 65  
DB 32 CTGAGCCCGCGCTGCTCAAGCTGCTGCTC 2

RESULT 13  
A1719194/c  
LOCUS A1719194 46 bp mRNA linear EST 10-JUN-1999  
DEFINITION at06h08.x1 Barstead aorta HPRB6 Homo sapiens cDNA clone IMAGE:2354367.3, similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH  
PROTEIN RP15 PRECURSOR, contains MER22.b2 TARI repetitive element  
, mRNA sequence.

ACCESSION A1719194  
VERSION A1719194.1 GI:5036450  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
Kritzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,  
Martin,J., Moore,B., Schellenberg,K., Stepien,M., Tan,F.,  
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-NCI human EST Project



Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 165 CAGACGACCTGTTAAGCCCAACCGTGTCTGTTAGGTTG 203  
 Db 41 CAGAGCAGCCTGTGTGCTCCCTCCGCTCGAAGAGTTTG 3

Search completed: October 1, 2006, 06:42:19  
 Job time : 3612.75 secs

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CC The method comprises determining the expression of one or more families  
CC of transposable elements, and assigning the expression pattern obtained  
CC to the level of developmental potential of a cell. Also disclosed are a  
CC method of determining the developmental potential of a stem cell, a  
CC method of identifying a cellular differentiation induction factor, a  
CC method of identifying a factor that increases the developmental potential  
CC of a cell, a method of assigning a methylation pattern of transposable  
CC elements to the level of developmental potential of a cell, and a method  
CC of assigning a chromatin status pattern of transposable elements to the  
CC level of developmental potential of a cell. In assigning an expression  
CC pattern of transposable elements to the level of developmental potential  
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
CC cell, or a differentiated cell. The expression pattern is determined by  
CC microarray analysis. One or more of the families of transposable elements  
CC are retroelement families, or DNA element families. One or more of the  
CC families of retroelements is selected from the group consisting of  
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
CC elements (SINEs), and a family of long interspersed nuclear elements  
CC (LINEs). The expression of the transposable elements is measured by  
CC assaying for the mRNA transcribed from the genes or proteins translated  
CC from an mRNA transcribed from the genes. The expression of two or more  
CC families of transposable elements is determined and used to form the  
CC pattern of expression. The methylation of the transposable element genes  
CC is monitored by enzymatic means, microarray analysis, or methylation-  
CC specific PCR. The methylation pattern is determined by microarray  
CC analysis. The methods of the invention are useful for assigning an  
CC expression pattern of transposable elements to the level of developmental  
CC potential of a cell. This sequence represents an oligonucleotide  
CC identifier of a retroelement consensus sequence.  
SQ Sequence 50 BP; 10 A; 12 C; 12 G; 15 T; 0 U; 1 Other;

Query Match 13.8%; Score 32.6; DB 13; Length 50;  
Best Local Similarity 79.2%; Pred. No. 1.5;  
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 61 GTGAGTTACGTCGAGAGCTGTTGTTGAAGAGCCGCCCCCTCTC 108  
DB 2 GTTAGTTCACGCGAGATCTGTTGTTTAAAGAGTNTGACACTCCCC 49

RESULT 2  
ADU22514  
ID ADU22514 standard; DNA; 50 BP.  
AC ADU22514;  
XX  
XX  
XX 27-JAN-2005 (first entry)  
DE Human transposable element representative sequence, SEQ ID 518.  
XX  
XX Human; ss; transposable element; DNA methylation; chromatin; cancer;  
KW LINE; long interspersed nuclear element; SINE;  
KW short interspersed nuclear element; HERV; human endogenous retrovirus;  
KW microarray.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004096021-A2.  
PN  
XX  
XX 11-NOV-2004.  
PD  
XX  
XX 29-APR-2004; 2004WO-US013522.  
PF  
XX  
XX 29-APR-2003; 2003US-0466798P.  
PR  
XX  
XX (UYGB-) UNIV GEORGIA RES FOUND INC.  
PA  
XX  
XX McDonald JF;  
PI  
XX  
XX WPI; 2004-804560/79.  
DR  
XX  
XX Determining expression, methylation or chromatin status pattern of

PT families of transposable elements in a sample e.g. for diagnosing cancer,  
PT comprises determining the expression, methylation or chromatin status of  
PT the elements.  
XX  
XX Disclosure; SEQ ID NO 518; 68bp; English.  
XX  
XX The invention relates to determining expression, methylation or chromatin  
XX status pattern of one or more families of transposable elements in a  
XX sample comprising determining expression, methylation or chromatin status  
XX of one or more families of transposable elements. Also included are a  
XX method of assigning an expression pattern of transposable elements to a  
XX type of cancerous cell in a sample, a method of diagnosing cancer, a  
XX method of determining the effectiveness of an anti-cancer therapeutic in  
XX a subject, a method of assigning a methylation pattern of one or more  
XX families of transposable elements to a type of cancerous cell in a sample  
XX and a method of assigning a chromatin status pattern of transposable  
XX elements to a type of cancerous cell in a sample. The method is useful in  
XX determining an expression, methylation or chromatin status pattern of one  
XX or more families of transposable elements (e.g. LINE, long interspersed  
XX nuclear element, SINE, short interspersed nuclear element, or HERV, human  
XX endogenous retrovirus) in a sample for diagnosing cancer or determining  
XX the effectiveness of an anti-cancer therapeutic. The present sequence is  
XX a representative sequence for a human transposable element, used in a  
XX microarray to study the expression, methylation or chromatin status  
XX pattern of the transposable elements.  
SQ Sequence 50 BP; 10 A; 12 C; 12 G; 15 T; 0 U; 1 Other;

Query Match 13.8%; Score 32.6; DB 13; Length 50;  
Best Local Similarity 79.2%; Pred. No. 1.5;  
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 61 GTGAGTTACGTCGAGAGCTGTTGTTGAAGAGCCGCCCCCTCTC 108  
DB 2 GTTAGTTCACGCGAGATCTGTTGTTTAAAGAGTNTGACACTCCCC 49

RESULT 3  
ADU25299  
ID ADU25299 standard; DNA; 50 BP.  
AC ADU25299;  
XX  
XX  
XX 27-JAN-2005 (first entry)  
DE Retroelement consensus sequence identifier oligonucleotide #769.  
XX  
XX Expression pattern; transposable element; developmental potential;  
KW stem cell; cellular differentiation induction factor;  
KW methylation pattern; chromatin status pattern; endogenous retrovirus;  
KW ERV; short interspersed nuclear element; SINE;  
KW long interspersed nuclear element; LINE; retroelement; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO2004097005-A2.  
PN  
XX  
XX 11-NOV-2004.  
PD  
XX  
XX 29-APR-2004; 2004WO-US013667.  
PF  
XX  
XX 29-APR-2003; 2003US-0466801P.  
PR  
XX  
XX (UYGB-) UNIV GEORGIA RES FOUND INC.  
PA  
XX  
XX McDonald JF;  
PI  
XX  
XX WPI; 2004-804756/79.  
DR  
XX  
XX Assigning an expression pattern of transposable elements to the level of  
PT developmental potential of a cell comprises determining expression of one  
PT or more families of transposable elements, and assigning the expression  
PT pattern.

**SQ** Sequence 50 BP; 5 A; 15 C; 10 G; 20 T; 0 U; 0 Other;

Oy 139 CCTGCTCCCCCTTCCTTCTGCCATGATTTTTAAGATTCAGGGACTT 186  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 CTTGCTTCCCTTTGCCTTCTGCCATGATTGTAACTTCTCGAGGCT 50

AC	ADU22766;
XX	
DT	27-JAN-2005 (first entry)

KM Human, ss; transposable element; DNA methylation; chromatin; cancer;  
KM LINE; long interspersed nuclear element; SINE;  
KM short interspersed nuclear element; HHRV; human endogenous retrovirus  
KM microarray.

PN WO2004096021-A2

PF 29-APR-2004; 2004WO-US013522.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

DR WPI; 2004-804580/79.

PS Disclosure; SEQ ID NO 770; 68bp; English

**SQ** Sequence 50 BP; 5 A; 15 C; 10 G; 20 T; 0 U; 0 Other;

Oy 139 CCTGCTCCCCCTTCTCCTTTGCCATGATTTTAAGATTCCAGGACTT 186  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 CTTGCTTCCCCTTTGCCTTCGCCATGATTTGAAGTTTCCTGAGGCGCT 50

RESULT 5  
ADU24578  
ID ADU24578 standard; DNA; 50 BP

AC	ADU24578;
XX	
DT	27-JAN-2005 (first entry)

DE Retroelement consensus sequence identifier oligonucleotide #48.

**KW** Expression pattern; transposable element; developmental potential;

KM methylation pattern; chromatin status pattern; endogenous retrovirus;

**KW** long interspersed nuclear element; LINE; retroelement; ss.

OS Synthetic

PN WO2004097005-A2.

PD 11-NOV-2004

PF 29-APR-2004; 2004WO-US013667

PR 29-APR-2003; 2003US-0466801P

PA (UYGE-) UNIV GEORGIA RES FOUND INC

PI McDonald JF;

DR WPI; 2004-804756/79.

XX Assigning an expression pattern of transposable elements to the level of  
PT developmental potential of a cell comprises determining expression of one  
PT or more families of transposable elements, and assigning the expression  
PT pattern.  
XX  
PS Disclosure; SEQ ID NO 48; 50bp; English.  
XX  
CC The invention relates to a method of assigning an expression pattern of  
CC transposable elements to the level of developmental potential of a cell.  
CC The method comprises determining the expression of one or more families  
CC of transposable elements, and assigning the expression pattern obtained  
CC to the level of developmental potential of a cell. Also disclosed are a  
CC method of determining the developmental potential of a stem cell, a  
CC method of identifying a cellular differentiation induction factor, a  
CC method of identifying a factor that increases the developmental potential  
CC of a cell, a method of assigning a methylation pattern of transposable  
CC elements to the level of developmental potential of a cell, and a method  
CC of assigning a chromatin status pattern of transposable elements to the  
CC level of developmental potential of a cell. In assigning an expression  
CC pattern of transposable elements to the level of developmental potential  
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
CC cell, or a differentiated cell. The expression pattern is determined by  
CC microarray analysis. One or more of the families of transposable elements  
CC are retroelement families, or DNA element families. One or more of the  
CC families of retroelements is selected from the group consisting of  
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
CC elements (SINES) and a family of long interspersed nuclear elements  
CC (LINEs). The expression of the transposable elements is measured by  
CC assaying for the mRNA transcribed from the genes or proteins translated  
CC from an mRNA transcribed from the genes. The expression of two or more  
CC families of transposable elements is determined and used to form the  
CC pattern of expression. The methylation of the transposable element genes  
CC is monitored by enzymatic means, microarray analysis, or methylation-  
CC specific PCR. The methylation pattern is determined by microarray  
CC analysis. The methods of the invention are useful for assigning an  
CC expression pattern of transposable elements to the level of developmental  
CC potential of a cell. This sequence represents an oligonucleotide  
CC identifier of a retroelement consensus sequence.  
XX  
SQ Sequence 50 BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 12.3%; Score 29; DB 13; Length 50;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
XX  
QY 37 TTATGTCATCCCTTGTGATGATGAGTTCACGTGAGAGCTGG 81  
DB 6 TTGGTGTCTGCTCGTATGATGAGTTCCTCGTATGAGTCTGG 50  
XX  
RESULT 6  
ADU22045 ID ADU22045 standard; DNA; 50 BP.  
XX  
AC ADU22045;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Human transposable element representative sequence, SEQ ID 48.  
XX  
KW Human; ss; transposable element; DNA methylation; chromatin; cancer;  
KW LINE; long interspersed nuclear element; SINE;  
KW short interspersed nuclear element; HRRV; human endogenous retrovirus;  
KW microarray.  
XX  
OS Homo sapiens.  
XX  
PN WO2004096021-A2.  
XX  
PD 11-NOV-2004.  
XX  
PR 29-APR-2004; 2004WO-US013522.  
XX

XX  
PR 29-APR-2003; 2003US-0466798P.  
XX  
PA (UTGE-) UNIV GEORGIA RES FOUND INC.  
XX  
PI McDonald JF;  
XX  
DR WPI; 2004-804580/79.  
XX  
XX  
PT Determining expression, methylation or chromatin status pattern of  
PT families of transposable elements in a sample e.g. for diagnosing cancer,  
PT comprises determining the expression, methylation or chromatin status of  
PT the elements.  
XX  
PS Disclosure; SEQ ID NO 48; 68bp; English.  
XX  
CC The invention relates to determining expression, methylation or chromatin  
CC status pattern of one or more families of transposable elements in a  
CC sample comprises determining expression, methylation or chromatin status  
CC of one or more families of transposable elements. Also included are a  
CC method of assigning an expression pattern of transposable elements to a  
CC type of cancerous cell in a sample, a method of diagnosing cancer, a  
CC method of determining the effectiveness of an anti-cancer therapeutic in  
CC a subject, a method of assigning a methylation pattern of one or more  
CC families of transposable elements to a type of cancerous cell in a sample  
CC and a method of assigning a chromatin status pattern of transposable  
CC elements to a type of cancerous cell in a sample. The method is useful in  
CC determining an expression, methylation or chromatin status pattern of one  
CC or more families of transposable elements (e.g. LINE, long interspersed  
CC nuclear element, SINE, short interspersed nuclear element, or HRRV, human  
CC endogenous retrovirus) in a sample for diagnosing cancer or determining  
CC the effectiveness of an anti-cancer therapeutic. The present sequence is  
CC a representative sequence for a human transposable element, used in a  
CC microarray to study the expression, methylation or chromatin status  
CC pattern of the transposable elements.  
XX  
SQ Sequence 50 BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 12.3%; Score 29; DB 13; Length 50;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
XX  
QY 37 TTATGTCATCCCTTGTGATGATGAGTTCACGTGAGAGCTGG 81  
DB 6 TTGGTGTCTGCTCGTATGATGAGTTCCTCGTATGAGTCTGG 50  
XX  
RESULT 7  
ADU25274 ID ADU25274 standard; DNA; 50 BP.  
XX  
AC ADU25274;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Retroelement consensus sequence identifier oligonucleotide #744.  
XX  
KW Expression pattern; transposable element; developmental potential;  
KW stem cell; cellular differentiation induction factor;  
KW methylation pattern; chromatin status pattern; endogenous retrovirus;  
KW ERV; short interspersed nuclear element; SINE;  
KW long interspersed nuclear element; LINE; retroelement; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004097005-A2.  
XX  
PD 11-NOV-2004.  
XX  
PR 29-APR-2004; 2004WO-US013667.  
XX  
PR 29-APR-2003; 2003US-0466801P.  
XX

PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
PI McDonald JF;  
XX  
DR WPI; 2004-804756/79.  
XX  
PT Assigning an expression pattern of transposable elements to the level of  
PT developmental potential of a cell comprises determining expression of one  
PT or more families of transposable elements, and assigning the expression  
PT pattern.  
XX  
PS Disclosure; SEQ ID NO 745; 50bp; English.  
XX  
CC The invention relates to a method of assigning an expression pattern of  
CC transposable elements to the level of developmental potential of a cell.  
CC The method comprises determining the expression of one or more families  
CC of transposable elements, and assigning the expression pattern obtained  
CC to the level of developmental potential of a cell. Also disclosed are a  
CC method of determining the developmental potential of a stem cell, a  
CC method of identifying a cellular differentiation induction factor, a  
CC method of identifying a factor that increases the developmental potential  
CC of a cell, a method of assigning a methylation pattern of transposable  
CC elements to the level of developmental potential of a cell, and a method  
CC of assigning a chromatin status pattern of transposable elements to the  
CC level of developmental potential of a cell. In assigning an expression  
CC pattern of transposable elements to the level of developmental potential  
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
CC cell, or a differentiated cell. The expression pattern is determined by  
CC microarray analysis. One or more of the families of transposable elements  
CC are retroelement families, or DNA element families. One or more of the  
CC families of retroelements is selected from the group consisting of  
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
CC elements (SINES) and a family of long interspersed nuclear elements  
CC (LINES). The expression of the transposable elements is measured by  
CC assaying for the mRNA transcribed from the genes or proteins translated  
CC from an mRNA transcribed from the genes. The expression of two or more  
CC families of transposable elements is determined and used to form the  
CC pattern of expression. The methylation of the transposable element genes  
CC is monitored by enzymatic means, microarray analysis, or methylation-  
CC specific PCR. The methylation pattern is determined by microarray  
CC analysis. The methods of the invention are useful for assigning an  
CC expression pattern of transposable elements to the level of developmental  
CC potential of a cell. This sequence represents an oligonucleotide  
CC identifier of a retroelement consensus sequence.  
XX  
SQ Sequence 50 BP; 10 A; 11 C; 12 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 9.6%; Score 22.6; DB 13; Length 50;  
Best Local Similarity 86.2%; Pred. No. 2.9e+03;  
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 149 CTTCTCCTTCTGCCATGATTTAAGATTTC 177  
DB 22 CTTCCCTTCGCCCATGATTGTAAGTTTC 50  
XX  
RESULT 8  
ADU25263 ID ADU25263 standard; DNA; 50 BP.  
XX  
AC ADU25263;  
XX  
DT 27-JUN-2005 (first entry)  
XX  
DE Retroelement consensus sequence identifier oligonucleotide #733.  
XX  
KM Expression pattern; transposable element; developmental potential;  
KM stem cell; cellular differentiation induction factor;  
KM methylation pattern; chromatin status pattern; endogenous retrovirus;  
KM ERV; short interspersed nuclear element; SINE;  
KM long interspersed nuclear element; LINE; retroelement; ss.  
XX  
OS Synthetic.

XX  
PN W02004097005-A2.  
XX  
PD 11-NOV-2004.  
XX  
PF 29-APR-2004; 2004WO-US013667.  
XX  
PR 29-APR-2003; 2003US-0466801P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
PI McDonald JF;  
XX  
DR WPI; 2004-804756/79.  
XX  
PT Assigning an expression pattern of transposable elements to the level of  
PT developmental potential of a cell comprises determining expression of one  
PT or more families of transposable elements, and assigning the expression  
PT pattern.  
XX  
PS Disclosure; SEQ ID NO 734; 50bp; English.  
XX  
CC The invention relates to a method of assigning an expression pattern of  
CC transposable elements to the level of developmental potential of a cell.  
CC The method comprises determining the expression of one or more families  
CC of transposable elements, and assigning the expression pattern obtained  
CC to the level of developmental potential of a cell. Also disclosed are a  
CC method of determining the developmental potential of a stem cell, a  
CC method of identifying a cellular differentiation induction factor, a  
CC method of identifying a factor that increases the developmental potential  
CC of a cell, a method of assigning a methylation pattern of transposable  
CC elements to the level of developmental potential of a cell, and a method  
CC of assigning a chromatin status pattern of transposable elements to the  
CC level of developmental potential of a cell. In assigning an expression  
CC pattern of transposable elements to the level of developmental potential  
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
CC cell, or a differentiated cell. The expression pattern is determined by  
CC microarray analysis. One or more of the families of transposable elements  
CC are retroelement families, or DNA element families. One or more of the  
CC families of retroelements is selected from the group consisting of  
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
CC elements (SINES) and a family of long interspersed nuclear elements  
CC (LINES). The expression of the transposable elements is measured by  
CC assaying for the mRNA transcribed from the genes or proteins translated  
CC from an mRNA transcribed from the genes. The expression of two or more  
CC families of transposable elements is determined and used to form the  
CC pattern of expression. The methylation of the transposable element genes  
CC is monitored by enzymatic means, microarray analysis, or methylation-  
CC specific PCR. The methylation pattern is determined by microarray  
CC analysis. The methods of the invention are useful for assigning an  
CC expression pattern of transposable elements to the level of developmental  
CC potential of a cell. This sequence represents an oligonucleotide  
CC identifier of a retroelement consensus sequence.  
XX  
SQ Sequence 50 BP; 14 A; 13 C; 10 G; 12 T; 0 U; 1 Other;  
XX  
Query Match 9.6%; Score 22.6; DB 13; Length 50;  
Best Local Similarity 71.8%; Pred. No. 2.9e+03;  
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
XX  
QY 197 AATGCTAACGCCATGCTTTGTTGTCTGCAAACT 235  
DB 1 AGATGCTCGACCATGCTTTTGTCCAGCAGCAAAAT 39  
XX  
RESULT 9  
ADU22741 ID ADU22741 standard; DNA; 50 BP.  
XX  
AC ADU22741;  
XX  
DT 27-JUN-2005 (first entry)  
XX

DE Human transposable element representative sequence, SEQ ID 745.  
 XX  
 XX Human; ss; transposable element; DNA methylation; chromatin; cancer;  
 KM LINE; long interspersed nuclear element; SINE;  
 KM short interspersed nuclear element; HERV; human endogenous retrovirus;  
 KM microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004096021-A2.  
 XX  
 PD 11-NOV-2004.  
 XX  
 PF 29-APR-2004; 2004WO-US013522.  
 XX  
 PR 29-APR-2003; 2003US-0466798P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX  
 PI McDonald JF;  
 XX  
 DR WPI; 2004-804580/79.  
 XX  
 PT Determining expression, methylation or chromatin status pattern of  
 PT families of transposable elements in a sample e.g. for diagnosing cancer,  
 PT comprises determining the expression, methylation or chromatin status of  
 PT the elements.  
 XX  
 PS Disclosure; SEQ ID NO 745; 68bp; English.  
 XX  
 CC The invention relates to determining expression, methylation or chromatin  
 CC status pattern of one or more families of transposable elements in a  
 CC sample comprising determining expression, methylation or chromatin status  
 CC of one or more families of transposable elements. Also included are a  
 CC method of assigning an expression pattern of transposable elements to a  
 CC type of cancerous cell in a sample, a method of diagnosing cancer, a  
 CC method of determining the effectiveness of an anti-cancer therapeutic in  
 CC a subject, a method of assigning a methylation pattern of one or more  
 CC families of transposable elements to a type of cancerous cell in a sample  
 CC and a method of assigning a chromatin status pattern of transposable  
 CC elements to a type of cancerous cell in a sample. The method is useful in  
 CC determining an expression, methylation or chromatin status pattern of one  
 CC or more families of transposable elements (e.g. LINE, long interspersed  
 CC nuclear element, SINE, short interspersed nuclear element, or HERV, human  
 CC endogenous retrovirus) in a sample for diagnosing cancer or determining  
 CC the effectiveness of an anti-cancer therapeutic. The present sequence is  
 CC a representative sequence for a human transposable element, used in a  
 CC microarray to study the expression, methylation or chromatin status  
 CC pattern of the transposable elements.  
 XX  
 SQ Sequence 50 BP, 10 A; 11 C; 12 G; 17 T; 0 U; 0 Other;  
 XX  
 Query Match 9.6%; Score 22.6; DB 13; Length 50;  
 Best Local Similarity 86.2%; Pred. No. 2.9e+03;  
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 149 CTTCTCTCTGCGCATGATTTTAAGATTC 177  
 DB 22 CTTCCCTTCGCGCATGATTTGAAGTTTC 50  
 XX  
 RESULT 10  
 ADU22730  
 ID ADU22730 standard; DNA; 50 BP.  
 XX  
 AC ADU22730;  
 XX  
 DT 27-JUN-2005 (first entry)  
 XX  
 DE Human transposable element representative sequence, SEQ ID 734.  
 XX  
 KM Human; ss; transposable element; DNA methylation; chromatin; cancer;  
 KM LINE; long interspersed nuclear element; SINE;

KM short interspersed nuclear element; HERV; human endogenous retrovirus;  
 KM microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004096021-A2.  
 XX  
 PD 11-NOV-2004.  
 XX  
 PF 29-APR-2004; 2004WO-US013522.  
 XX  
 PR 29-APR-2003; 2003US-0466798P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX  
 PI McDonald JF;  
 XX  
 DR WPI; 2004-804580/79.  
 XX  
 PT Determining expression, methylation or chromatin status pattern of  
 PT families of transposable elements in a sample e.g. for diagnosing cancer,  
 PT comprises determining the expression, methylation or chromatin status of  
 PT the elements.  
 XX  
 PS Disclosure; SEQ ID NO 734; 68bp; English.  
 XX  
 CC The invention relates to determining expression, methylation or chromatin  
 CC status pattern of one or more families of transposable elements in a  
 CC sample comprising determining expression, methylation or chromatin status  
 CC of one or more families of transposable elements. Also included are a  
 CC method of assigning an expression pattern of transposable elements to a  
 CC type of cancerous cell in a sample, a method of diagnosing cancer, a  
 CC method of determining the effectiveness of an anti-cancer therapeutic in  
 CC a subject, a method of assigning a methylation pattern of one or more  
 CC families of transposable elements to a type of cancerous cell in a sample  
 CC and a method of assigning a chromatin status pattern of transposable  
 CC elements to a type of cancerous cell in a sample. The method is useful in  
 CC determining an expression, methylation or chromatin status pattern of one  
 CC or more families of transposable elements (e.g. LINE, long interspersed  
 CC nuclear element, SINE, short interspersed nuclear element, or HERV, human  
 CC endogenous retrovirus) in a sample for diagnosing cancer or determining  
 CC the effectiveness of an anti-cancer therapeutic. The present sequence is  
 CC a representative sequence for a human transposable element, used in a  
 CC microarray to study the expression, methylation or chromatin status  
 CC pattern of the transposable elements.  
 XX  
 SQ Sequence 50 BP, 14 A; 13 C; 10 G; 12 T; 0 U; 1 Other;  
 XX  
 Query Match 9.6%; Score 22.6; DB 13; Length 50;  
 Best Local Similarity 71.8%; Pred. No. 2.9e+03;  
 Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
 XX  
 QY 197 AATGCTAACGCCATGCTTTGTTGCTGCAAACT 235  
 DB 1 AGATGCTGACACATGCTTTTGTCCAGCCAGCAAGAAVT 39  
 XX  
 RESULT 11  
 ABZ79597C  
 ID ABZ79597 standard; DNA; 41 BP.  
 XX  
 AC ABZ79597;  
 XX  
 DT 27-JUN-2003 (first entry)  
 XX  
 DE Quinoprotein dehydrogenase 12.10 related probe #SEQ ID 8.  
 XX  
 KM Quinoprotein dehydrogenase; 12.10; enzyme; malignant tumour; haemopathy;  
 KM Human immunodeficiency virus; HIV; immunological disease; inflammation;  
 KM probe; ss.  
 XX  
 OS Unidentified.  
 XX

PN CN1380401-A.  
XX  
PD 20-NOV-2002.  
XX  
PF 10-APR-2001; 2001CN-00105895.  
XX  
PR 10-APR-2001; 2001CN-00105895.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
PS WPI; 2003-230985/23.  
XX  
DR A polypeptide-quinoprotein dehydrogenase-12.10 and polynucleotide for  
PT coding this polypeptide.  
XX  
PS Example 7; Page 22 (disclosure); 30pp; Chinese.  
XX  
CC The present invention discloses a polypeptide for a quinoprotein  
CC dehydrogenase 12.10, the polynucleotide for coding the polypeptide, and a  
CC method for producing this polypeptide using DNA recombination technology.  
CC Also disclosed is a method for curing several diseases, such as malignant  
CC tumour, haemopathy, Human Immunodeficiency virus (HIV) infection,  
CC immunological disease and various inflammatory virus. The invention also  
CC discloses the antagonist for resisting this polypeptide, and its  
CC therapeutic action. The current sequence represents a quinoprotein  
CC dehydrogenase 12.10 related probe  
XX  
SQ Sequence 41 BP; 11 A; 7 C; 18 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 9.5%; Score 22.4; DB 8; Length 41;  
Best Local Similarity 81.2%; Pred. No. 3.1e+03;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
XX  
QY 132 TGAGACACCTGCTCCCTCTCTCTCTGCA 163  
DB 32 TGCTACACCGCTTCCCTTGTCTTGTGCA 1  
XX  
RESULT 12  
AB246086  
ID AB246086 standard; DNA; 41 BP.  
XX  
AC AB246086;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human organic anion transporter OATP2 gene polymorphic site, #2870.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT replace(21,A)  
FT /tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKE ) RIKEN KK.

XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
XX  
XX  
XX Claim 23; Page 112; 2785pp; English.  
XX  
CC Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 4 A; 16 C; 7 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 9.3%; Score 22; DB 6; Length 41;  
Best Local Similarity 73.7%; Pred. No. 4.3e+03;  
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
XX  
QY 141 TGCTCCCTTCATCTTCGCAATGATTTAAGATTCC 178  
DB 2 TGCTCTTCCTTATCTTCGCCAATGATTTGTGAGGCCCC 39  
XX  
RESULT 13  
AB248256  
ID AB248256 standard; DNA; 41 BP.  
XX  
AC AB248256;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human organic anion transporter OATP2 gene polymorphic site, #5039.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH replacement  
FT variation /tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX WO200252044-A2.  
XX 04-JUL-2002.  
XX 27-DEC-2001; 2001WO-JP011592.  
XX 27-DEC-2000; 2000JP-00399443.  
XX 02-MAY-2001; 2001JP-00135256.  
XX 27-AUG-2001; 2001JP-00256862.  
XX (RIKE ) RIKEN KK.  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
PI WPI; 2002-583571/62.  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
XX Claim 23; Page 161; 2785pp; English.  
XX  
XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolizing enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
XX Sequence 41 BP; 4 A; 16 C; 7 G; 14 T; 0 U; 0 Other;  
SQ  
Query Match 9.3%; Score 22; DB 6; Length 41;  
Best Local Similarity 73.7%; Pred. No. 4.3e+03;  
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 141 TGCCTCCCTTCCTTCGCGCATGATTTAGATTC 178  
DB 2 TGCCTTCCTTCATCTTCGCGCATGATGAGGCC 39

RESULT 14  
ADU25276  
ID ADU25276 standard; DNA; 50 BP.  
XX  
XX ADU25276;  
XX  
XX 27-JAN-2005 (first entry)  
XX  
XX Retroelement consensus sequence identifier oligonucleotide #746.  
XX  
XX Expression pattern; transposable element; developmental potential;  
XX stem cell; cellular differentiation induction factor;  
XX methylation pattern; chromatin status pattern; endogenous retrovirus;  
XX ERV; short interspersed nuclear element; SINE;  
XX long interspersed nuclear element; LINE; retroelement; SE.  
XX  
XX Synthetic.  
XX  
XX WO2004097005-A2.  
XX  
XX 11-NOV-2004.  
XX  
XX 29-APR-2004; 2004WO-US013667.  
XX  
XX 29-APR-2003; 2003US-046801P.  
XX  
XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
XX McDonald JF;  
XX  
XX WPI; 2004-804756/79.  
XX  
XX Assigning an expression pattern of transposable elements to the level of  
PT developmental potential of a cell comprises determining expression of one  
PT or more families of transposable elements, and assigning the expression  
PT pattern.  
XX  
XX Disclosure: SEQ ID NO 747; 50pp; English.  
XX  
XX The invention relates to a method of assigning an expression pattern of  
CC transposable elements to a level of developmental potential of a cell.  
CC The method comprises determining the expression of one or more families  
CC of transposable elements, and assigning the expression pattern obtained  
CC to the level of developmental potential of a cell. Also disclosed are a  
CC method of determining the developmental potential of a stem cell, a  
CC method of identifying a cellular differentiation induction factor, a  
CC method of identifying a factor that increases the developmental potential  
CC of a cell, a method of assigning a methylation pattern of transposable  
CC elements to the level of developmental potential of a cell, and a method  
CC of assigning a chromatin status pattern of transposable elements to the  
CC level of developmental potential of a cell. In assigning an expression  
CC pattern of transposable elements to the level of developmental potential  
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
CC cell, or a differentiated cell. The expression pattern is determined by  
CC microarray analysis. One or more of the families of transposable elements  
CC are retroelement families, or DNA element families. One or more of the  
CC families of retroelements is selected from the group consisting of  
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
CC elements (SINES) and a family of long interspersed nuclear elements  
CC (LINEs). The expression of the transposable elements is measured by  
CC assaying for the mRNA transcribed from the genes or proteins translated  
CC from an mRNA transcribed from the genes. The expression of two or more  
CC families of transposable elements is determined and used to form the  
CC pattern of expression. The methylation of the transposable element genes  
CC is monitored by enzymatic means, microarray analysis, or methylation-  
CC specific PCR. The methylation pattern is determined by microarray  
CC analysis. The method of the invention are useful for assigning an  
CC expression pattern of transposable elements to the level of developmental  
CC potential of a cell. This sequence represents an oligonucleotide  
CC identifier of a retroelement consensus sequence.  
XX  
XX Sequence 50 BP; 13 A; 15 C; 9 G; 13 T; 0 U; 0 Other;  
SQ



Query Match 9.3%; Score 22; DB 13; Length 50;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 207 GCCATGCTTCTTGTCTGTCTGCAAACTG 236  
 |||||  
 Db 1 GCCATGCTTCTTGTCTGTCTGCAAACTG 30

QY 207 GCCATGCTTCTTGTCTGTCTGCAAACTG 236  
 |||||  
 Db 1 GCCATGCTTCTTGTCTGTCTGCAAACTG 30

Search completed: October 1, 2006, 00:26:41  
 Job time : 325.377 secs

RESULT 15  
 ID ADU22743 standard; DNA: 50 BP.  
 XX  
 AC ADU22743;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Human transposable element representative sequence, SEQ ID 747.  
 XX  
 KM Human; ss; transposable element; DNA methylation; chromatin; cancer;  
 KM LINE; long interspersed nuclear element; SINE;  
 KM short interspersed nuclear element; HERV; human endogenous retrovirus;  
 XX microarray.  
 OS Homo sapiens.  
 XX  
 PN WO2004096021-A2.  
 XX  
 PD 11-NOV-2004.  
 XX  
 PF 29-APR-2004; 2004MO-US013522.  
 XX  
 PR 29-APR-2003; 2003US-0466798P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX  
 PI McDonald JF;  
 XX  
 DR WPI; 2004-804580/79.  
 XX  
 PT Determining expression, methylation or chromatin status pattern of  
 PT families of transposable elements in a sample e.g. for diagnosing cancer.  
 PT comprises determining the expression, methylation or chromatin status of  
 PT the elements.  
 XX  
 PS Disclosure; SEQ ID NO 747; 68bp; English.  
 XX  
 CC The invention relates to determining expression, methylation or chromatin  
 CC status pattern of one or more families of transposable elements in a  
 CC sample comprises determining expression, methylation or chromatin status  
 CC of one or more families of transposable elements. Also included are a  
 CC method of assigning an expression pattern of transposable elements to a  
 CC type of cancerous cell in a sample, a method of diagnosing cancer, a  
 CC method of determining the effectiveness of an anti-cancer therapeutic in  
 CC a subject, a method of assigning a methylation pattern of one or more  
 CC families of transposable elements to a type of cancerous cell in a sample  
 CC and a method of assigning a chromatin status pattern of transposable  
 CC elements to a type of cancerous cell in a sample. The method is useful in  
 CC determining an expression, methylation or chromatin status pattern of one  
 CC or more families of transposable elements (e.g. LINE, long interspersed  
 CC nuclear element, SINE, short interspersed nuclear element, or HERV, human  
 CC endogenous retrovirus) in a sample for diagnosing cancer or determining  
 CC the effectiveness of an anti-cancer therapeutic. The present sequence is  
 CC a representative sequence for a human transposable element, used in a  
 CC microarray to study the expression, methylation or chromatin status  
 CC pattern of the transposable elements.  
 CC  
 CC Sequence 50 BP; 13 A; 15 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 9.3%; Score 22; DB 13; Length 50;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 68606
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-68606
```

```
Query Match 11.4%; Score 26.8; DB 16; Length 50;
Best Local Similarity 77.5%; Pred. No. 73;
Matches 31; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 14 GGGGCGATCCCGCATGATGTTAGTCCCTCG 53
Db 11 GAGGGTGCTCTTGAYGATGTTAGAGCATCCCTCG 50
```

## RESULT 3

```
US-11-175-859-51557/c
/ Sequence 51557, Application US/11175859
/ Publication No. US20060024715A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Liu, Guoying et al.
/ TITLE OF INVENTION: Method of Analysis of Human Polymorphism
/ FILE REFERENCE: 3690.1
/ CURRENT APPLICATION NUMBER: US/11/175,859
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 51557
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-51557
```

```
Query Match 10.8%; Score 25.4; DB 16; Length 50;
Best Local Similarity 71.1%; Pred. No. 2.3e+02;
Matches 32; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
```

```
Qy 136 ACAACGTGCTCCCTCTCCCTCGCATGATTTAGATTCAG 180
Db 45 ACACCCACTGCTACTGCTCTACTACCATTAATTGATTCAG 1
```

## RESULT 4

```
US-10-891-260-437
/ Sequence 437, Application US/10891260
/ Publication No. US2005022724A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Mei, Rui
/ TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
/ FILE REFERENCE: 3522.3
/ CURRENT APPLICATION NUMBER: US/10/891,260
/ CURRENT FILING DATE: 2004-07-13
/ PRIOR APPLICATION NUMBER: 10/681,773
/ PRIOR FILING DATE: 2003-10-07
/ NUMBER OF SEQ ID NOS: 10244
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 437
/ LENGTH: 33
/ TYPE: DNA
/ ORGANISM: homo sapien
US-10-891-260-437
```

```
Query Match 9.8%; Score 23.2; DB 10; Length 33;
```

```
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 14 GGGGCGATCCCGCATGATGTTAGTCCG 43
Db 1 GGGGCGATCCCTTACCAATGCTGTGTGC 30
```

## RESULT 5

```
US-10-891-260-1034/c
/ Sequence 1034, Application US/10891260
/ Publication No. US2005022724A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Mei, Rui
/ TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
/ FILE REFERENCE: 3522.3
/ CURRENT APPLICATION NUMBER: US/10/891,260
/ CURRENT FILING DATE: 2004-07-13
/ PRIOR APPLICATION NUMBER: 10/681,773
/ PRIOR FILING DATE: 2003-10-07
/ NUMBER OF SEQ ID NOS: 10244
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 1034
/ LENGTH: 33
/ TYPE: DNA
/ ORGANISM: homo sapien
US-10-891-260-1034
```

```
Query Match 9.6%; Score 22.6; DB 10; Length 33;
Best Local Similarity 80.6%; Pred. No. 1.9e+03;
Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 70 CGTGAGCTGGTGTGTTGAAAGAGCTGCG 100
Db 32 CATGAGACTGATGTYTGAAAGAGCTGCG 2
```

## RESULT 6

```
US-11-175-859-57653/c
/ Sequence 57653, Application US/11175859
/ Publication No. US20060024715A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Liu, Guoying et al.
/ TITLE OF INVENTION: Method of Analysis of Human Polymorphism
/ FILE REFERENCE: 3690.1
/ CURRENT APPLICATION NUMBER: US/11/175,859
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 57653
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-57653
```

```
Query Match 9.5%; Score 22.4; DB 16; Length 50;
Best Local Similarity 72.5%; Pred. No. 2.6e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 105 TCTCATTTCTCTCTCCCACTTTGATGAGACACTGCT 144
Db 48 TCTCTATTTCTGTTCCAAATTCATATGACACAGCTGT 9
```

## RESULT 7

```
US-10-310-914A-1140145/c
/ Sequence 1140145, Application US/10310914A
/ Publication No. US20060003322A1
```

GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Biointentionally detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1140145  
LENGTH: 28  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1140145

Query Match 9.4%; Score 22.2; DB 11; Length 28;  
Best Local Similarity 98.9%; Pred. No. 2.5e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GGGGCGAGATCCCTCATGATGTTTA 39  
DB 27 GAGGCGAGATCCCTTATGATGTTCA 1

RESULT 8  
US-11-175-859-55008/c  
Sequence 55008, Application US/11175859  
Publication No. US20060024715A1  
GENERAL INFORMATION:  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
FILE REFERENCE: 3690.1  
CURRENT APPLICATION NUMBER: US/11/175.859  
CURRENT FILING DATE: 2005-07-05  
PRIOR APPLICATION NUMBER: US 60/585,352  
PRIOR FILING DATE: 2004-07-02  
NUMBER OF SEQ ID NOS: 116251  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 55008  
LENGTH: 50  
TYPE: DNA  
ORGANISM: homo sapien  
US-11-175-859-55008

Query Match 9.4%; Score 22.2; DB 16; Length 50;  
Best Local Similarity 66.7%; Pred. No. 3.1e+03;  
Matches 30; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 TGTCTGGTCAATGGGCGAGATCCCTCATGATGTTTAAAGCCCA 45  
DB 50 TGTCTGGTCAATGAGATTCACACSTCATGATGATTAATGACCA 6

RESULT 9  
US-11-060-756-81484/c  
Sequence 81484, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060.756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 81484  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe

US-11-060-756-81484

Query Match 9.2%; Score 21.8; DB 13; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.2e+03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 149 CTTCTCCTTCGCGATGATTTTAA 173  
DB 25 CTTACCTTCGCGATGATTTTAA 1

RESULT 10  
US-11-060-756-81500/c  
Sequence 81500, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060.756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 81500  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-81500

Query Match 9.2%; Score 21.8; DB 13; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.2e+03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 148 CTTCTCCTTCGCGATGATTTTAA 172  
DB 25 CTTACCTTCGCGATGATTTTAA 1

RESULT 11  
US-11-060-756-81511/c  
Sequence 81511, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060.756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 81511  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-81511

Query Match 9.2%; Score 21.8; DB 13; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.2e+03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 154 CTTCTCCTTCGCGATGATTTTAA 178  
DB 25 CTTCTCCTTCGCGATGATTTTAA 1

RESULT 12  
US-11-175-859-75179  
Sequence 75179, Application US/11175859  
Publication No. US20060024715A1

```
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75179
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-175-859-75179

Query Match
Best Local Similarity 9.2%; Score 21.8; DB 16; Length 50;
Best Local Similarity 74.3%; Pred. No. 4.3e+03;
Matches 26; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 103 CCTCTCATTTCTCCGCTCCCACTTTGACAGAGC 137
DB 10 CCTCTCATTTCTCTCYAATATTTCACAGTAGAGC 44

RESULT 13
US-10-035-833A-2870
; Sequence 2870, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2870
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-2870

Query Match
Best Local Similarity 9.2%; Score 21.6; DB 8; Length 41;
Best Local Similarity 71.1%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 141 TGTCTCCCTTCCTCTGCGATGATTTAAGATTCC 178
DB 2 TGTCTCTTCCTTCATCTTCRCATGATGTGAGGCCCC 39

RESULT 14
US-10-035-833A-5039
; Sequence 5039, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5039
; LENGTH: 41
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-5039

Query Match
Best Local Similarity 9.2%; Score 21.6; DB 8; Length 41;
Best Local Similarity 71.1%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 141 TGTCTCCCTTCCTCTGCGATGATTTAAGATTCC 178
DB 2 TGTCTCTTCCTTCATCTTCRCATGATGTGAGGCCCC 39

RESULT 15
US-10-310-914A-1072814/C
; Sequence 1072814, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1072814
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1072814

Query Match
Best Local Similarity 9.1%; Score 21.4; DB 11; Length 23;
Best Local Similarity 95.7%; Pred. No. 4.3e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 CATCCCTTGTGATGAGTAGT 66
DB 23 CATCTCTTGTGATGAGTAGT 1
```

Search completed: October 1, 2006, 01:09:51  
Job time : 773.184 secs



```
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 518
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: 37
; OTHER INFORMATION: n=G, A, T, or C
US-10-554-759-518
```

```
Query Match 13.8%; Score 32.6; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.27;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 61 GTGAGTCACGAGAGCTGTTGTAAGAGCCCTGCCCCCTC 108
Db 2 GTTAGTTCACCGAGATCTGCTTTTAAAGAGTTGGACCTCCCC 49
```

```
RESULT 3
US-10-554-711-770
; Sequence 770, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-770
```

```
Query Match 13.6%; Score 32; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.43;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 139 CTTGCTCCCCCTTCTCTTGCATGATTTTAAGATTCAGGACTT 186
Db 3 CTTGCTCCCCCTTCTCTTGCATGATTTTAAGATTCAGGACTT 50
```

```
RESULT 4
US-10-554-759-770
; Sequence 770, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
```

```
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-770
```

```
Query Match 13.6%; Score 32; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.43;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 139 CTTGCTCCCCCTTCTCTTGCATGATTTTAAGATTCAGGACTT 186
Db 3 CTTGCTCCCCCTTCTCTTGCATGATTTTAAGATTCAGGACTT 50
```

```
RESULT 5
US-10-554-711-48
; Sequence 48, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-48
```

```
Query Match 12.3%; Score 29; DB 6; Length 50;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 37 TTAGTGCATCCCTTCTCTTGCATGATTTTAAGATTCAGGACTT 81
Db 6 TTAGTGTCTCTCTGATGATGATGATTTCTCGAGATCTGG 50
```

```
RESULT 6
US-10-554-759-48
; Sequence 48, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
```



```
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-759-48
```

```
Query Match          12.3%; Score 29; DB 6; Length 50;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy      37  TTAGTCCATCCCTTGATGATGAGTTCACGTGAGAGCTGG 81
Db      6  TTGATCTGCTCTCTGATGATGAGTTCCTGATGATCTGG 50
```

```
RESULT 7
; Sequence 734, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-734
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 71.8%; Pred. No. 6.2e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy      197  AATGCTAACGCCATGCTTCTGTTCTGTCGAAACT 235
Db      1  AGATGCTGCGACCATGCTTTTGTCCAGCCAGCAAAAT 39
```

```
RESULT 8
; Sequence 745, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 745
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-745
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 86.2%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      149  CTCTCCTTCGCGCATGATTTTAAGATTC 177
Db      22  CTTCCTTCGCGCATGATTTTAAGATTC 50
```

```
RESULT 9
; Sequence 734, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-759-734
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 71.8%; Pred. No. 6.2e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy      197  AATGCTAACGCCATGCTTCTGTTCTGTCGAAACT 235
Db      1  AGATGCTGCGACCATGCTTTTGTCCAGCCAGCAAAAT 39
```

```
RESULT 10
; Sequence 745, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 745
; LENGTH: 50
; TYPE: DNA
```

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
OTHER INFORMATION: Synthetic Construct  
US-10-554-759-745

Query Match 9.6%; Score 22.6; DB 6; Length 50;  
Best Local Similarity 86.2%; Pred. No. 6.2e+02;  
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCTGCCATGATTTTAAGATTC 177  
Db 22 CTTCCCTCCGCGCATGATTTGTAAGTTTC 50

RESULT 11  
US-10-554-711-747  
Sequence 747, Application US/10554711  
Publication No. US20060115806A1  
GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
TITLE OF INVENTION: as Molecular Markers of Cancer  
FILE REFERENCE: 21099.0075P1  
CURRENT APPLICATION NUMBER: US/10/554,711  
CURRENT FILING DATE: 2005-10-28  
PRIOR APPLICATION NUMBER: 60/466,798  
PRIOR FILING DATE: 2003-04-29  
NUMBER OF SEQ ID NOS: 778  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 747  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
OTHER INFORMATION: Synthetic Construct  
US-10-554-711-747

Query Match 9.3%; Score 22; DB 6; Length 50;  
Best Local Similarity 83.3%; Pred. No. 9.9e+02;  
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 207 GCCATGCTTCTGTGTGTCGCAAACTG 236  
Db 1 GCCATGCTTCTGTACAGCTCGCAACCG 30

RESULT 12  
US-10-554-759-747  
Sequence 747, Application US/10554759  
Publication No. US2006017825A1  
GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
APPLICANT: McDonald, John F.  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem  
TITLE OF INVENTION: Cells  
FILE REFERENCE: 21099.0077P1  
CURRENT APPLICATION NUMBER: US/10/554,759  
CURRENT FILING DATE: 2005-10-28  
PRIOR APPLICATION NUMBER: 60/466,801  
PRIOR FILING DATE: 2003-04-29  
NUMBER OF SEQ ID NOS: 770  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 747  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
OTHER INFORMATION: Synthetic Construct

US-10-554-759-747

Query Match 9.3%; Score 22; DB 6; Length 50;  
Best Local Similarity 83.3%; Pred. No. 9.9e+02;  
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 207 GCCATGCTTCTGTGTGTCGCAAACTG 236  
Db 1 GCCATGCTTCTGTACAGCTCGCAACCG 30

RESULT 13  
US-10-554-711-746  
Sequence 746, Application US/10554711  
Publication No. US20060115806A1  
GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
TITLE OF INVENTION: as Molecular Markers of Cancer  
FILE REFERENCE: 21099.0075P1  
CURRENT APPLICATION NUMBER: US/10/554,711  
CURRENT FILING DATE: 2005-10-28  
PRIOR APPLICATION NUMBER: 60/466,798  
PRIOR FILING DATE: 2003-04-29  
NUMBER OF SEQ ID NOS: 778  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 746  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
OTHER INFORMATION: Synthetic Construct  
NAME/KEY: misc\_feature  
LOCATION: 8  
OTHER INFORMATION: n=g, A, T, or C  
US-10-554-711-746

Query Match 9.2%; Score 21.8; DB 6; Length 50;  
Best Local Similarity 76.5%; Pred. No. 1.2e+03;  
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 163 ATGATTTAAGATTCAGAGGACTTCACAGAAGC 196  
Db 1 ATGATTTAAGATTCCTGAGGCTCTCACAGAGC 34

RESULT 14  
US-10-554-759-746  
Sequence 746, Application US/10554759  
Publication No. US2006017825A1  
GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
APPLICANT: McDonald, John F.  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem  
TITLE OF INVENTION: Cells  
FILE REFERENCE: 21099.0077P1  
CURRENT APPLICATION NUMBER: US/10/554,759  
CURRENT FILING DATE: 2005-10-28  
PRIOR APPLICATION NUMBER: 60/466,801  
PRIOR FILING DATE: 2003-04-29  
NUMBER OF SEQ ID NOS: 770  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 746  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
OTHER INFORMATION: Synthetic Construct

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: n-G, A, T, or C
US-10-554-759-746

```

```

Query Match          9.2%; Score 21.8; DB 6; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      163 ATGATTTAAGATTCGAGGACTTCACAGAAGC 196
      ||||| ||||| ||||| ||||| |||||
Db      1 ATGATGNAAGCTTCTGTGAGGCTTCACCAAGC 34

```

```

RESULT 15
US-10-554-711-640
; Sequence 640; Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; PRIOR APPLICATION NUMBER: 2005-10-28
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 640
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-640

```

```

Query Match          9.0%; Score 21.2; DB 6; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      163 ATGATTTAAGATTCGAGGACTTCACAGAAGC 196
      ||||| ||||| ||||| ||||| |||||
Db      1 ATGATGTAAGTTCTGTGAGGCTTCACCAAGC 34

```

Search completed: October 1, 2006, 01:14:07  
 Job time : 123.925 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:29:43 ; Search time 3520.25 Seconds  
(without alignments)  
3748.870 Million cell updates/sec

Title: US-10-642-946-6\_COPY\_3002\_3237

Perfect score: 236  
Sequence: 1 tgcctcggcgcacgaggggagcag.....tgcctcgcgcgaacacg 236

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gse1:\*  
12: gb\_gse2:\*  
13: gb\_gse3:\*  
14: gb\_gse4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	9.0	45	13	CL529018 HIV55C09
2	19.8	8.4	44	11	AZ862104 HIV69D04
3	19.6	8.3	44	11	BH804777 1008098B1
4	19.4	8.2	31	1	A1022023
5	19.2	8.1	49	10	DT933089 BH006A10
6	19.2	8.1	50	10	DV774160 MCG11nc
7	19.2	8.1	37	11	AZ836826 2M0131A20
8	19.2	8.1	41	14	BX128197 Dania rex
9	18.8	8.0	44	11	AZ868544 2M0240C20
10	18.8	8.0	46	14	BX650405 Arabidops
11	18.8	8.0	50	11	AZ765968 1M0563N12
12	18.8	8.0	50	13	CZ194703 PST6723-N
13	18.6	7.9	43	11	AZ862121 2M0169H01
14	18.6	7.9	47	11	AZ831496 1M0059P21
15	18.6	7.9	50	8	CX001254 1V40A04.D
16	18.4	7.8	48	1	A1941313 6B87E01.Y
17	18.4	7.8	46	1	A1749566 ac30F01.X
18	18.2	7.7	40	1	AA257023 z84e02.s
19	18.2	7.7	49	4	CA966474 CCLX05a17

20	18.2	7.7	50	7	BE882523
21	18	7.6	45	11	AZ504116
22	18	7.6	49	1	A1521631
23	18	7.6	49	11	AZ407440
24	18	7.6	50	7	BE299660 600944319
25	17.8	7.5	33	9	D45809
26	17.8	7.5	40	11	AZ789792 2M0037J19
27	17.8	7.5	45	5	CF334268 JMT--03-H
28	17.8	7.5	48	7	BF507210 3659P-23
29	17.8	7.5	49	1	A1334100 qp97C03.X
30	17.8	7.5	49	11	AZ324079
31	17.8	7.5	50	1	AU104247
32	17.6	7.5	43	5	CF306079
33	17.6	7.5	44	2	BU001599
34	17.6	7.5	45	5	CF30467
35	17.6	7.5	47	8	CV721217 YBR--03-F
36	17.6	7.5	48	5	CF304105 ABF1--04-F
37	17.6	7.5	49	1	AV674036 AV674036
38	17.6	7.5	49	5	CF322787 HNN--02-B
39	17.6	7.5	49	7	AV965544
40	17.6	7.5	50	1	AJ920737
41	17.4	7.4	32	11	AZ387638
42	17.4	7.4	34	1	A1561118
43	17.4	7.4	38	11	AZ479185
44	17.4	7.4	40	11	AZ328467
45	17.4	7.4	40	11	AZ793917

## ALIGNMENTS

RESULT 1  
CL529018  
LOCUS  
DEFINITION  
HIV55C09.fwd HIV-vector integration sites in human IMR90 primary lung fibroblasts Homo sapiens genomic clone HIV55C09.fwd, genomic survey sequence.

ACCESSION  
CL529018  
VERSION  
CL529018.1 GI:474222229  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Frederic Bushman  
Salk Institute Infectious Disease Laboratory  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1630  
Fax: 858 554 0341  
Email: bushman@salk.edu  
Class: PCR with specific primers.  
Location/Qualifiers  
1. 45

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone.lib="HIV55C09.fwd"  
/clone.lib="HIV-vector integration sites in human IMR90 primary lung fibroblasts"  
/note="Human primary lung fibroblasts (IMR90) were infected with an HIV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the HIV cDNA. Junctions between integrated HIV proviruses

ORIGIN and cellular DNA were cloned and sequenced."

Query Match 9.0%; Score 21.2; DB 13; Length 45;  
Best Local Similarity 88.5%; Pred. No. 2.5e+05;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGGTCATGGGGCAGATCCCTCATGA 31  
|||||  
Db 14 GGGTCATGAGGCGAGACCTCATGA 39

RESULT 2  
AZ862104/c 44 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0169D04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
DEFINITION Clone UGCG2M0169D04 R, genomic survey sequence.

ACCESSION AZ862104  
VERSION AZ862104.1 GI:13059089  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 44)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weles, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0169 row: D column: 04  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 44.

FEATURES  
source  
1. 44  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0169D04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PWD42nv. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
ligated DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (GI4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into

ORIGIN chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 8.4%; Score 19.8; DB 11; Length 44;  
Best Local Similarity 69.2%; Pred. No. 6.5e+05;  
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 137 CACCGCTCCCCCTTCCTTCGCCAGATTAAAGT 175  
|||||  
Db 39 CCCCTCCCTCCCTTCCTTCGCCAGATTAAATAT 1

RESULT 3  
BH804777/c 44 bp DNA linear GSS 25-APR-2002  
LOCUS 1008096B10.2EL\_x1 1008 - Rescuedu Grid I Zea mays genomic, genomic  
DEFINITION survey sequence.

ACCESSION BH804777  
VERSION BH804777.1 GI:20321384  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 44)

Walbot, V.  
Maize genomic sequences found using engineered Rescuedu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1008098 row: 14  
Class: transposon-tagged.  
Location/Qualifiers  
1. 44  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/AL88/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1008 - Rescuedu Grid I"  
/note="Organ: leaf; Vector: Rescuedu (engineered from  
pBluescript backbone); Site: 1: BamHI, Site 2: BglII;  
Rescuedu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescuedu, go to the web  
site www.zmdb.jaxrate.edu and follow the links for  
'Rescuedu.' Grid I was grown at Berkeley in 2001. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

## ORIGIN

Query Match 8.3%; Score 19.6; DB 11; Length 44;  
Best Local Similarity 66.7%; Pred. No. 7.5e+05;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 20 GATCCCTATGATAGTTAGTCCATCCCTTGATGATGAG 61  
|||||  
Db 44 GATCCGAATATATGCGTGTGCTTCCTTATGATGATGAG 3

RESULT 4  
LOCUS AI022023  
DEFINITION ov72a02.x1 Soares\_fetal\_liver\_spleen\_INFLS\_S1 Homo sapiens cDNA clone IMAGE1652330 3' similar to TR:069340 069340 ORF1, ORF2, AND ORF3; contains TARI. c3 TARI repetitive element; mRNA sequence.  
ACCESSION AI022023  
VERSION AI022023.1 GI:3239376  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 31)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: e9apbs-f@mail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert length: 864 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..31  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1652330"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; This is a subcloned version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGACAGATTAATTAAGACTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Benito Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 8.2%; Score 19.4; DB 1; Length 31;  
Best Local Similarity 79.3%; Pred. No. 7e+05;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 94 GCCTGGCCCTCTCATCTCTCCCTGCC 122  
|||||  
3 GCCTGGCCCTCTCTCCCTCTCTGCC 31

RESULT 5  
LOCUS DT933089  
DEFINITION BH006A10 Leptospaeria starvation library Leptospaeria maculans cDNA, mRNA sequence.  
ACCESSION DT933089  
VERSION DT933089.1 GI:75966345  
KEYWORDS EST.  
SOURCE Leptospaeria maculans (blackleg of rapeseed fungus)  
ORGANISM Leptospaeria maculans  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Leptospaeriaceae; Leptospaeria; Leptospaeria maculans complex.

REFERENCE 1 (bases 1 to 49)  
AUTHORS Gardiner, D.M., Cozijnsen, A.J. and Howlett, B.J.  
TITLE Leptospaeria maculans EST's  
JOURNAL Unpublished (2005)  
COMMENT Contact: Cozijnsen A.J.  
Blackleg Group  
The School of Botany, The University of Melbourne  
The University of Melbourne, Victoria 3010, Australia  
Tel: + 61 3 8344 5056  
Fax: + 61 3 9347 5406  
Email: a.cozijnsen@unimelb.edu.au.  
Location/Qualifiers  
1..49  
/organism="Leptospaeria maculans"  
/mol\_type="mRNA"  
/strain="IBCN18 (M1)"  
/db\_xref="taxon:5022"  
/sex="MART-2"  
/tissue\_type="Mycelium"  
/clone\_lib="Leptospaeria starvation library"

ORIGIN

Query Match 8.1%; Score 19.2; DB 10; Length 49;  
Best Local Similarity 70.6%; Pred. No. 1e+06;  
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 167 TTTTAAGATTCGAGACTTCACAGAGCAANT 200  
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3 TTTTAAGATTCGAGACTTCACAGATTAANT 36

RESULT 6  
LOCUS DV774160/c  
DEFINITION DV774160 50 bp mRNA linear EST 23-NOV-2005  
ACCESSION DV774160  
VERSION DV774160.1 GI:82627020  
KEYWORDS EST.  
SOURCE Homarus americanus (American lobster)  
ORGANISM Homarus americanus  
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.  
REFERENCE 1 (bases 1 to 50)  
Stepanyan, R., Day, K., Urban, J., Hardin, D.L., Shetty, R.S., Derby, C.D., Ache, B.W. and McClintock, T.S.  
Gene expression and specificity in the mature zone of the lobster olfactory organ  
Unpublished (2005)  
JOURNAL Contact: McClintock TS  
COMMENT Department of Physiology  
University of Kentucky  
800 Rose St., Lexington, KY 40536-0298, USA  
Tel: 859 323 1083  
Fax: 859 323 1070  
Email: mcclint@uky.edu.  
Location/Qualifiers  
1..50  
/organism="Homarus americanus"  
/mol\_type="mRNA"  
/db\_xref="taxon:6706"  
/clone="McClintock24\_C06.ab1"  
/sex="male and female"  
/tissue\_type="mature zone"  
/dev\_stage="adult"  
/lab\_host="Dh5alpha"  
/note="Organ: Olfactory organ; lateral ramus of first antennae; Vector: pBluescript; Site\_1: NciI; Site\_2: SalI; 5'-end sequences from a subcloned cDNA library. The frequency of common sequences in this library was reduced by screening filter lifts of colonies with complex probes"









/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGCM0169H01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGCM0059P21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 7.9%; Score 18.6; DB 11; Length 43;  
Best Local Similarity 65.9%; Pred. No. 1.5e+06;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

## ORIGIN

Query Match 7.9%; Score 18.6; DB 11; Length 47;  
Best Local Similarity 72.7%; Pred. No. 1.5e+06;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 112 CTCCTGCTCCACTCTTGATGAGACACGCTCCCTTC 152  
DB 42 CACATGCTCACACATGCTCCACACATGACGCGATTC 2

QY 71 GTGAGAGCTGCTGTTTGAAGAAGCTGCGCCC 103  
DB 33 GTGGATGTGTGCTTGAATGAATGATGCCCC 1

RESULT 14  
LOCUS AZ331496 47 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0059P21F Mouse 10kb plasmid UGGC1M library Mus musculus genomic  
ACCESSION AZ331496  
VERSION AZ331496.1 GI:10394261  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0059 row: P column: 21  
Seq primer: CGTTGTAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 47.  
Location/Qualifiers  
1..47  
/organism="Mus musculus"

RESULT 15  
LOCUS CX001254 50 bp mRNA linear EST 03-DEC-2004  
DEFINITION 1v40a04.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
ACCESSION CX001254  
VERSION CX001254.1 GI:56272670  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Balija, V.S., Nascimben, L.V. and McCombie, W.R.  
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
JOURNAL Unpublished (2004)  
COMMENT Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.  
Location/Qualifiers  
1..50  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_1ib="Left Cardiac Ventricle (DOGEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site 1: BSCR1; Site 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

ORIGIN

Query Match 7.9%; Score 18.6; DB 8; Length 50;  
 Best Local Similarity 72.7%; Pred. No. 1.5e+06;  
 Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 95 CCTGGCCCCCTCATCTCTCTGCTCCCACTCT 127  
 |||||  
 DB 5 CCGGGCCCTCTCTCTCTCTCTCTCTCTCT 37

Search completed: October 1, 2006, 06:42:23  
 Job time : 3524.25 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:58:57 ; Search time 127.075 Seconds  
(without alignments)  
3514.157 Million cell updates/sec

Title: US-10-642-946-6\_COPY\_1967\_2208

Perfect score: 242

Sequence: 1 ttctccagcacagcagcgcga.....ccaactaaactgagtcac 242

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: 3153450

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New:\*  
1: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
8: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
9: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
10: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	9.1	50	US-10-554-711-527	Sequence 527, App
2	22	9.1	50	US-10-554-759-527	Sequence 527, App
3	20.8	8.6	50	US-11-155-444-16	Sequence 16, Appl
4	19.2	7.9	50	US-10-554-711-723	Sequence 723, App
5	19.2	7.9	50	US-10-554-759-723	Sequence 723, App
6	19.2	7.9	50	US-10-554-759-723	Sequence 723, App
7	19.2	7.9	50	US-10-554-759-723	Sequence 723, App
8	17.8	7.4	47	US-11-370-584-2387	Sequence 2387, App
9	17.8	7.4	47	US-11-217-529-49117	Sequence 49117, A
10	17.2	7.1	25	US-11-370-584-1835	Sequence 1835, App
11	17.2	7.1	25	US-11-217-529-22009	Sequence 22009, A
12	17.2	7.1	25	US-11-217-529-99537	Sequence 99537, A
13	17	7.0	50	US-10-511-937-263	Sequence 263, App
14	16.8	6.9	25	US-11-348-413-461909	Sequence 461909, A
15	16.8	6.9	25	US-11-348-413-461910	Sequence 461910, A
16	16.8	6.9	25	US-11-348-413-461911	Sequence 461911, A
17	16.8	6.9	25	US-11-348-413-461912	Sequence 461912, A
18	16.8	6.9	25	US-11-348-413-1104344	Sequence 1104344, A
19	16.8	6.9	25	US-11-348-413-1104345	Sequence 1104345, A
20	16.8	6.9	41	US-11-166-003-139	Sequence 139, App
21	16.8	6.9	41	US-11-264-784-205	Sequence 205, App
22	16.8	6.9	41	US-11-264-737-310	Sequence 310, App
23	16.8	6.9	41	US-11-265-761-220	Sequence 220, App

C	24	16.6	6.9	25	8	US-11-217-529-15423	Sequence 15423, A
	25	16.6	6.9	25	9	US-11-348-413-36613	Sequence 36613, A
	26	16.6	6.9	25	9	US-11-348-413-36614	Sequence 36614, A
	27	16.6	6.9	25	9	US-11-348-413-36615	Sequence 36615, A
	28	16.6	6.9	25	9	US-11-348-413-50182	Sequence 50182, A
	29	16.6	6.9	25	9	US-11-348-413-100416	Sequence 100416, A
	30	16.6	6.9	25	9	US-11-348-413-624681	Sequence 624681, A
	31	16.6	6.9	25	9	US-11-348-413-624682	Sequence 624682, A
	32	16.6	6.9	25	9	US-11-348-413-824683	Sequence 824683, A
	33	16.6	6.9	25	9	US-11-348-413-624722	Sequence 624722, A
	34	16.6	6.9	25	9	US-11-348-413-683036	Sequence 683036, A
	35	16.6	6.9	25	9	US-11-348-413-923505	Sequence 923505, A
	36	16.6	6.9	25	9	US-11-348-413-923506	Sequence 923506, A
	37	16.6	6.9	25	9	US-11-348-413-923507	Sequence 923507, A
	38	16.6	6.9	25	9	US-11-348-413-952627	Sequence 952627, A
	39	16.6	6.9	25	9	US-11-348-413-952628	Sequence 952628, A
	40	16.6	6.9	25	9	US-11-348-413-952629	Sequence 952629, A
	41	16.6	6.9	25	9	US-11-370-584-275	Sequence 275, App
	42	16.4	6.8	25	9	US-11-348-413-852337	Sequence 852337, A
	43	16.4	6.8	43	7	US-11-043-842-584	Sequence 584, App
	44	16.4	6.8	48	7	US-11-368-338-30	Sequence 30, Appl
	45	16.2	6.7	25	8	US-11-217-529-153307	Sequence 153307, A

#### ALIGNMENTS

RESULT 1  
US-10-554-711-527  
; Sequence 527, Application US/10554711  
; Publication No. US20060115806A1  
; GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
APPLICANT: McDonald, John F.  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
FILE REFERENCE: 21099.0075P1  
CURRENT APPLICATION NUMBER: US/10/554, 711  
CURRENT FILING DATE: 2005-10-28  
PRIOR APPLICATION NUMBER: 60/466, 798  
PRIOR FILING DATE: 2003-04-29  
NUMBER OF SEQ ID NOS: 778  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 527  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
US-10-554-711-527  
Query Match 9.1%; Score 22; DB 6; Length 50;  
Best Local Similarity 64.6%; Pred. No. 9.1e+02;  
Matches 31; Conservative 1; Mismatches 16; Indels 0; Gaps 0;  
OY 133 TCTTTGGAGCAGCTCTCAGCTGAGCTGAACGAACGACCTTTAA 180  
Db 1 TTTGTTGGGACACCAAGAGCTGGAAGCTGACACGACCAKCTGTGTA 48  
RESULT 2  
US-10-554-759-527  
; Sequence 527, Application US/10554759  
; Publication No. US20060117825A1  
; GENERAL INFORMATION:  
APPLICANT: University of Georgia Research Foundation  
APPLICANT: McDonald, John F.  
TITLE OF INVENTION: Global Analysis of Transposable Elements  
FILE REFERENCE: 21099.0077P1  
CURRENT APPLICATION NUMBER: US/10/554, 759

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; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 527
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-527
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Query Match          9.1%; Score 22; DB 6; Length 50;
Best Local Similarity 64.6%; Pred. No. 9.1e+02;
Matches 31; Conservative 1; Mismatches 16; Indels 0; Gaps 0;
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QY      133 TCTCTTTGAGACACCTCTCAAGTGGAGCTGAAAGAAAGACTGTAA 180
Db      1 TTTGTTTGGAGCACCAAGAGCCTGGAACTGCACGACCAKCTGTAA 48
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RESULT 3
US-11-155-444-16/c
; Sequence 16, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
; APPLICANT: GARDER, ELLEN
; APPLICANT: BAILLY, VEROIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: BGN168CN
; CURRENT APPLICATION NUMBER: US/11/155,444
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-11-155-444-16
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Query Match          8.6%; Score 20.8; DB 8; Length 50;
Best Local Similarity 70.0%; Pred. No. 2.3e+03;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY      37 GGGAGCTCCACCTCCCGAGCTGCTGCTCCTCCTTTC 76
Db      50 GGATCTTCACCTCTGAGCGCGCGCTCATTTATCTCC 11
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RESULT 4
US-10-554-711-343
; Sequence 343, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
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; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-343
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Query Match          7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY      39 GAGCTCCACCTCCCGAGCTGCTGCTCCTCCTG 70
Db      12 GACCTTCACCTCCCGAGCTCCTCCCAATG 43
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RESULT 5
US-10-554-711-723
; Sequence 723, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 723
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-723
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```

Query Match          7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY      39 GAGCTCCACCTCCCGAGCTGCTGCTCCTCCTG 70
Db      12 GACCTTCACCTCCCGAGCTCCTCCCAATG 43
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```

RESULT 6
US-10-554-759-343
; Sequence 343, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
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SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 343  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/note =  
US-10-554-759-343

Query Match 7.9%; Score 19.2; DB 6; Length 50;  
Best Local Similarity 75.0%; Pred. No. 8e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCCTCAGCTG 70  
Db 12 GACCTTCACTTCCCGAGCTCCTCCCACTTGG 43

RESULT 7  
US-10-554-759-723  
; Sequence 723; Application US/10554759  
; Publication No. US20060177825A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Georgia Research Foundation  
; APPLICANT: McDonald, John F.  
; TITLE OF INVENTION: Global Analysis of Transposable Elements  
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem  
; TITLE OF INVENTION: Cells  
; FILE REFERENCE: 21099.0077P1  
; CURRENT APPLICATION NUMBER: US/10/554,759  
; CURRENT FILING DATE: 2005-10-28  
; PRIOR APPLICATION NUMBER: 60/466,801  
; PRIOR FILING DATE: 2003-04-29  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 723  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-554-759-723

Query Match 7.9%; Score 19.2; DB 6; Length 50;  
Best Local Similarity 75.0%; Pred. No. 8e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCCTCAGCTG 70  
Db 12 GACCTTCACTTCCCGAGCTCCTCCCACTTGG 43

RESULT 8  
US-11-370-584-2387/c  
; Sequence 2387; Application US/11370584  
; Publication No. US20060177863A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Ballelic markers for use in constructing a high  
; TITLE OF INVENTION: density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/11/370,584  
; CURRENT FILING DATE: 2006-03-08  
; PRIOR APPLICATION NUMBER: US/10/349,143  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 2387  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-10720-63 : polymorphic base A or G  
US-11-370-584-2387

Query Match 7.4%; Score 17.8; DB 7; Length 47;  
Best Local Similarity 67.6%; Pred. No. 2.3e+04;  
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 161 TGAACAGACGACCTGTTAAGCCGCTGCTGTTA 197  
Db 39 TTATCGAAGACCAAGTGAAGCCCTGTTCTTTAA 3

RESULT 9  
US-11-217-529-49117  
; Sequence 49117; Application US/11217529  
; Publication No. US2006009612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 49117  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-49117

Query Match 7.3%; Score 17.6; DB 8; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2e+04;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 97 GTAACATATTGTTGCCCACTAC 120  
Db 1 GAAGTACATTGTTGCCCACTAC 24

RESULT 10  
US-11-370-584-1835  
; Sequence 1835; Application US/11370584  
; Publication No. US20060177863A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Ballelic markers for use in constructing a high  
; TITLE OF INVENTION: density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/11/370,584  
; CURRENT FILING DATE: 2006-03-08  
; PRIOR APPLICATION NUMBER: US/10/349,143  
; PRIOR FILING DATE: 2003-01-21

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; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1835
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6730-356 : polymorphic base A or G
US-11-370-584-1835
```

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Query Match          7.2%; Score 17.4; DB 7; Length 47;
Best Local Similarity 60.0%; Pred. No. 3.1e+04;
Matches 27; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
```

```
QY      5 CCAGCAGACGCTGATTTTGTCTGCTGCTGAGCTCCACT 49
Db      3 CTAGACCAGAACTTAATTTCTCTCTCTTCTTCTTCTTCA 47
```

```
RESULT 11
US-11-217-529-22009/c
; Sequence 22009, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-22009
```

```
Query Match          7.1%; Score 17.2; DB 8; Length 25;
Best Local Similarity 86.4%; Pred. No. 2.8e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      180 AGCCACCGCTCTGTTAGGCT 201
Db      25 AGCCACCGCTCTGTTAAAGT 4
```

```
RESULT 12
US-11-217-529-99537
; Sequence 99537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
```

```
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99537
```

```
Query Match          7.1%; Score 17.2; DB 8; Length 25;
Best Local Similarity 86.4%; Pred. No. 2.8e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      203 GTCTAGGCTGTATCATACCC 224
Db      1 GTCCAGGCTGTATCAGACAACC 22
```

```
RESULT 13
US-10-511-937-263
; Sequence 263, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Roseberry, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 263
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-263
```

```
Query Match          7.0%; Score 17; DB 6; Length 50;
Best Local Similarity 69.7%; Pred. No. 4.4e+04;
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY      149 CTCACGTGAGCTGACAGACGACCTGTTAG 181
Db      9 CCCAAGTGAGACAGAACAGAGGATTTGGGAGG 41
```

```
RESULT 14
US-11-348-413-461909
; Sequence 461909, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
```



Search completed: October 1, 2006, 01:14:07  
Job time : 128.075 secs

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; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 461909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13836; WANO1UPTD; Start 105; Stop 129;
; OTHER INFORMATION: 000000000011110
US-11-348-413-461909

```

```

Query Match          6.9%; Score 16.8; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 3.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      94 ACGGTAACATTTTGTGC 113
Db      5 ACTATACTACATTTTGTGC 24

```

```

RESULT 15
US-11-348-413-461910
; Sequence 461910, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 461910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13836; WANO1UPTD; Start 106; Stop 130;
; OTHER INFORMATION: 000000000011110
US-11-348-413-461910

```

```

Query Match          6.9%; Score 16.8; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 3.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      94 ACGGTAACATTTTGTGC 113
Db      4 ACTATACTACATTTTGTGC 23

```

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:15:33 : Search time 332.623 seconds  
(without alignments)  
5072.656 Million cell updates/sec

Title: US-10-642-946-6\_COPY\_1967\_2208

Perfect score: 242  
Sequence: 1 tctctccagcagcagcactgga.....ccaactaaactgattcac 242

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq.8:\*

1:	geneseqn1980a:*
2:	geneseqn1990a:*
3:	geneseqn2000a:*
4:	geneseqn2001a:*
5:	geneseqn2001b:*
6:	geneseqn2002a:*
7:	geneseqn2002b:*
8:	geneseqn2003a:*
9:	geneseqn2003b:*
10:	geneseqn2003c:*
11:	geneseqn2003d:*
12:	geneseqn2004a:*
13:	geneseqn2004b:*
14:	geneseqn2005a:*
15:	geneseqn2006a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	9.1	50	13	ADU25056	ADU25056 Retroelem
2	22	9.1	50	13	ADU22523	ADU22523 Human tra
3	20.8	8.6	50	6	ABZ07908	ABZ07908 Human leu
4	20.8	8.6	50	13	ADQ12194	ADQ12194 Primer of
5	20.4	8.4	41	6	ABZ47186	ABZ47186 Human ATP
6	20.4	8.4	41	6	ABZ44689	ABZ44689 Human ATP
7	20.2	8.3	48	6	ABK97936	ABK97936 DNA encod
8	19.6	8.1	31	3	AAAS1766	AAAS1766 31-mer CT
9	19.6	8.1	42	2	AAQ74160	AAQ74160 Mouse hea
10	19.6	8.1	50	6	ABZ01168	ABZ01168 Human leu
11	19.2	7.9	39	2	AAAT97180	AAAT97180 T cell re
12	19.2	7.9	42	2	AAV16931	AAV16931 Sense PCR
13	19.2	7.9	42	2	AAV16941	AAV16941 Antisense
14	19.2	7.9	42	2	AAV16801	AAV16801 Pea Rubis
15	19.2	7.9	42	2	AAV16811	AAV16811 Pea Rubis
16	19.2	7.9	50	13	ADU25252	ADU25252 Retroelem
17	19.2	7.9	50	13	ADU24873	ADU24873 Retroelem
18	19.2	7.9	50	13	ADU22340	ADU22340 Human tra

19	19.2	7.9	50	13	ADU22719	ADU22719 Human tra
20	19	7.9	39	8	ABK979718	ABK979718 EST polym
21	19	7.9	41	6	ABK99795	ABK99795 Human zin
22	19	7.9	41	12	ADH05426	ADH05426 Gene poly
23	19	7.9	41	12	ADH91213	ADH91213 I-beta-me
24	19	7.9	50	4	AAI28699	AAI28699 Human SNP
25	19	7.9	50	6	ABZ06403	ABZ06403 Human leu
26	19	7.9	50	6	ABZ06793	ABZ06793 Human leu
27	19	7.9	50	9	AAAS6821	AAAS6821 MT413 VL
28	18.8	7.8	46	4	ABJ51688	ABJ51688 Human GFR
29	18.6	7.7	25	14	ABE90482	ABE90482 127B prob
30	18.6	7.7	43	5	AAAS09540	AAAS09540 Antibody
31	18.6	7.7	47	2	AAV02490	AAV02490 Bridge o1
32	18.6	7.7	47	2	AAV02469	AAV02469 Primer MP
33	18.6	7.7	47	4	AAAC81686	AAAC81686 Chimeric
34	18.6	7.7	50	2	AAAC69754	AAAC69754 Herpes s1
35	18.6	7.7	50	2	AAAT64216	AAAT64216 HSV-1 b'8
36	18.6	7.7	50	2	AAAT17504	AAAT17504 Test sequ
37	18.6	7.7	50	6	ABK82995	ABK82995 DNA blind
38	18.6	7.7	50	12	ADBE80534	ADBE80534 Duplex o1
39	18.4	7.6	24	6	ABL40677	ABL40677 Parkinson
40	18.4	7.6	28	13	ADZ48190	ADZ48190 Cutaneous
41	18.4	7.6	40	3	AAZ96036	AAZ96036 Polynucle
42	18.4	7.6	41	6	ABV72866	ABV72866 Mouse bra
43	18.4	7.6	41	6	ABV72867	ABV72867 Mouse bra
44	18.4	7.6	45	5	AAAS10797	AAAS10797 Bovine MH
45	18.4	7.6	45	5	AAAT1381	AAAT1381 Bovine MH

## ALIGNMENTS

RESULT 1	
ID	ADU25056
AC	ADU25056 standard; DNA; 50 BP.
XX	
XX	ADU25056;
XX	
DT	27-JAN-2005 (first entry)
XX	
DE	Retroelement consensus sequence identifier oligonucleotide #526.
XX	
XX	Expression pattern; transposable element; developmental potential;
KW	stem cell; cellular differentiation induction factor;
KW	methylation pattern; chromatin status pattern; endogenous retrovirus;
KW	ERV; short interspersed nuclear element; SINE;
KW	long interspersed nuclear element; LINE; retroelement; ss.
OS	Synthetic.
XX	
XX	WO2004097005-A2.
PN	
PD	11-NOV-2004.
XX	
PF	29-APR-2004; 2004WO-US013667.
XX	
PR	29-APR-2003; 2003US-0466801P.
XX	
PA	(UYGB-) UNIV GEORGIA RES FOUND INC.
XX	
P1	Mcdonald JF;
XX	
XX	
DR	WPI; 2004-804756/79.
XX	
PT	Assigning an expression pattern of transposable elements to the level of
PT	developmental potential of a cell comprises determining expression of one
PT	or more families of transposable elements, and assigning the expression
PT	pattern.
XX	
XX	Disclosure; SEQ ID NO 527; 50pp; English.
XX	
CC	The invention relates to a method of assigning an expression pattern of
CC	transposable elements to the level of developmental potential of a cell.

The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of determining the developmental potential of a stem cell, a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential of a cell, a method of assigning a methylation pattern of transposable elements to the level of developmental potential of a cell, and a method of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell. In assigning an expression pattern of transposable elements to the level of developmental potential of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements are retroelement families, or DNA element families. One or more of the families of retroelements is selected from the group consisting of endogenous retroviruses (ERVs), a family of short interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (LINEs). The expression of the transposable elements is measured by assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the pattern of expression. The methylation of the transposable element genes is monitored by enzymatic means, microarray analysis, or methylation-specific PCR. The methylation pattern is determined by microarray analysis. The methods of the invention are useful for assigning an expression pattern of transposable elements to the level of developmental potential of a cell. This sequence represents an oligonucleotide identifier of a retroelement consensus sequence.

Sequence 50 BP; 13 A; 13 C; 12 G; 10 T; 0 U; 2 Other;

Query Match	9.1%	Score 22;	DB 13;	Length 50;
Best Local Similarity	64.6%	Pred. No. 4e+03;		
Matches 31; Conservative	1;	Mismatches 16;	Indels 0;	Gaps 0;

QY	133 TCTTTGGAGCACCCTCTCACTGAGCTGAACAGAACGACTGTAA 180                     :
Db	1 TTGTGTTGGACAACCAAGAGCCTGGAACCTGCACRGACCAKCTGTAA 48 

RESULT 2  
ADU22523  
ID ADU22523 standard; DNA; 50 BP.

XX  
AC ADU22523;

XX  
DT 27-JAN-2005 (first entry)

XX Human transposable element representative sequence, SEQ ID 527.

Human; ss; transposable element; DNA methylation; chromatin; cancer;  
 KW LINE; long interspersed nuclear element; SINE;  
 KW short interspersed nuclear element; HBRV; human endogenous retrovirus;  
 KW microarray.

xx OS Homo sapiens.

AA  
PN WO2004096021-A2.

AA PD 11-NOV-2004

AA  
PF 29-APR-2004; 2004WO-US013522.

PR 29-APR-2003; 2003US-0466798P.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

PI McDonald JF

AA WPI; 2004-804580/79.  
DR

XX Determining expression, methylation or chromatin status pattern of PT

PT families of transposable elements in a sample e.g. for diagnosing cancer.  
PT comprises determining the expression, methylation or chromatin status of  
PT the elements.

PS Disclosure; SEQ ID NO 527; 68bp; English

The invention relates to determining expression, methylation or chromatin status pattern of one or more families of transposable elements in a sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a method of assigning an expression pattern of transposable elements to a type of cancerous cell in a sample, a method of diagnosing cancer, a method of determining the effectiveness of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more families of transposable elements to a type of cancerous cell in a sample and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed nuclear element, SINE, short interspersed nuclear element, or HENV, human endogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status pattern of the transposable elements.

Sequence 50 BP; 13 A; 13 C; 12 G; 10 T; 0 U; 2 Other;

Query Match	9.1%	Score 22;	DB 13;	length 50;
Best Local Similarity	64.6%	Pred. No. 4e+03;		
Matches 31; Conservative	1;	Mismatches	0;	Gaps 0

```

Ox      133 TCTCTTTGAGACCTCTTCACGTGAGCTGAAACAGAAAGACCTGTTAA 180
          |||||      |||||      |||||      |||||
Db      1   TTTGTTTGGACACCAAGAGCCTGGAAGCTGCACRGACCAKCTGTAA 48

```

RESULT 3  
ABZ07908  
ID ABZ07908 standard; DNA; 50 BP.

AA ABZ07908;  
AC

MM	09-JAN-2003	(First entry)
DT		

XX	Human leukocyte gene expression profiling probe SEQ ID NO 7899.
DE	

AA  
KW  
T7; leukocyte; gene expression profiling; allograft rejection;

KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

Model	SS
KM	11.1
KW	8.5

OS Homo sapiens.

AA WO200257414-A2.  
PN

AA PD 25-JUL-2002.

AA 22-OCT-2001; 2001WO-US047856.  
PF

PR 20-OCT-2000; 2000US-0241994P.

[illegible]

3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

PI Ly N, Woodward R, Quettermous T, Johnson F;

WPI; 2002-636525/68.

PT New system for leukocyte expression profiling, diagnosing a disease, or

PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 582; Opp; English.

XX The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the two corresponds to any of 8143 oligonucleotides  
CC (AB20010-AB208152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,  
CC predicting disease complications in an individual or monitoring response  
CC to treatment in an individual. The diseases include cardiac allograft  
CC rejection, kidney allograft rejection, liver allograft rejection,  
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 12 A; 11 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 8.6%; Score 20.8; DB 6; Length 50;  
Best Local Similarity 70.0%; Pred. No. 1e+04;  
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 54 AGCTGCTGCTCCTCAGCTGCTTTTCCAAACCCACCTGTAA 93  
Db 1 AGCTGCTGCTTCTCTTTCAGTTCGAATGCAACCTGTAA 40

RESULT 4  
ADQ12194/c  
ID ADQ12194 standard; DNA; 50 BP.

AC ADQ12194;

DT 07-OCT-2004 (first entry)  
XX Primer of the invention #6.

DE Lymphotoxin-beta receptor; LT- $\beta$ gr-R; Cytostatic; cancer; tumour;  
KM hucB211; hucB1A10; primer; ss.

XX Unidentified.

OS WO2004058191-A2.

PN 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US041393.

XX 20-DEC-2002; 2002US-0435154P.

XX (BIOG-) BIOGEN IDEC MA INC.

XX Garder E, Bailly V, Browning JL;

XX MPI; 2004-525790/50.

XX New multivalent antibody constructs specific for the human lymphotoxin-  
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting  
PT tumour volume.

XX Example 5; SEQ ID NO 16; 85bp; English.

XX The present invention relates to a multivalent antibody comprising at  
CC least one antigen recognition site specific for a lymphotoxin-beta  
CC receptor (LT- $\beta$ gr-R) epitope. The antibody is useful for preparing a  
CC medicament for the treatment of cancer. The composition and method are  
CC used for diagnosing or treating cancer and for inhibiting tumour volume.  
CC The present sequence represents a primer of the invention.

XX Sequence 50 BP; 13 A; 12 C; 19 G; 6 T; 0 U; 0 Other;

Query Match 8.6%; Score 20.8; DB 13; Length 50;  
Best Local Similarity 70.0%; Pred. No. 1e+04;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 37 GGAGCTCCACCTCCCGACCTGCTGCTCCTTTC 76  
Db 50 GGATCTCCACCTCTGAGCGGCGCTCATTTGATCTCC 11

RESULT 5

ID AB247186/c  
AB247186 standard; DNA; 41 BP.

XX AB247186;

DT 26-JUN-2003 (first entry)

XX Human ATP-binding cassette ABCB9 gene polymorphic site, #3970.

XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 12;

XX polymorphic site; drug evaluation; drug screening; genotyping;

XX genetic profiling; therapeutic customisation; adverse reaction;

XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX variation replace(21,T)

XX /\*tag=a

XX /standard\_name="Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

XX 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;

XX MPI; 2002-583571/62.

XX Claim 23; Page 136; 2785bp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur

CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolizing enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.

CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also

CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy

SQ Sequence 41 BP; 9 A; 10 C; 20 G; 2 T; 0 U; 0 Other;

Query Match 8.4%; Score 20.4; DB 6; Length 41;  
Best Local Similarity 71.1%; Pred. No. 1.3e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 21 TTTTGTGACCTGCTGGAGCTCCACCTCCCACTG 58  
||||| ||||| ||||| ||||| ||||| |||||  
Db 41 TTTTGCACCGCTGTGGCGGTACCCCTCCCGCTG 4

RESULT 6  
ABZ44689/c  
ID ABZ44689 standard; DNA; 41 BP.  
XX ABZ44689;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX Human ATP-binding cassette ABCB9 gene polymorphic site, #1473.  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;  
XX polymorphic site; drug evaluation; drug screening; genotyping;  
XX genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX FT variation /tag= a  
XX FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
XX PN WO200252044-A2.  
XX  
XX PD 04-JUL-2002.  
XX  
XX PF 27-DEC-2001; 2001WO-JP011592.  
XX  
XX PR 27-DEC-2000; 2000JP-00399443.  
XX PR 02-MAY-2001; 2001JP-00135256.  
XX PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX PA (RIKE ) RIKEN KK.  
XX  
XX PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
XX WPI; 2002-583571/62.  
XX  
XX PT Identifying individuals having a polymorphism, useful for determining the  
XX PT effectiveness or side effect of a drug or treatment protocol, comprises  
XX PT detecting at least one polymorphism in the drug metabolizing enzyme  
XX PT nucleic acid.  
XX  
XX PS Claim 23; Page 88; 2785pp; English.  
XX  
XX CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
XX CC encoding enzymes associated with drug metabolism. The invention relates  
XX CC to methods and compositions for identifying individuals who have at least  
XX CC one polymorphism in such drug metabolising enzyme-encoding genes. The

CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy

SQ Sequence 41 BP; 9 A; 10 C; 20 G; 2 T; 0 U; 0 Other;

Query Match 8.4%; Score 20.4; DB 6; Length 41;  
Best Local Similarity 71.1%; Pred. No. 1.3e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 21 TTTTGTGACCTGCTGGAGCTCCACCTCCCACTG 58  
||||| ||||| ||||| ||||| ||||| |||||  
Db 41 TTTTGCACCGCTGTGGCGGTACCCCTCCCGCTG 4

RESULT 7  
ABK97936/c  
ID ABK97936 standard; DNA; 48 BP.  
XX ABK97936;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX DE DNA encoding IFN-Con IRRP1 peptide #1.  
XX  
XX  
XX Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;  
XX immunosuppressive; antiairnetic; cytokine receptor; interferon; IFN;  
XX cancer; haematological malignancy; viral infection; hepatitis; human;  
XX multiple sclerosis; autoimmune disease; arthritis; ds; gene.  
XX  
XX OS Synthetic.  
XX  
XX PN WO200244197-A2.  
XX  
XX PD 06-JUN-2002.  
XX  
XX PF 30-NOV-2001; 2001WO-CA001701.  
XX  
XX PR 01-DEC-2000; 2000US-00727388.  
XX  
XX PA (FISH/) FISH E N.  
XX  
XX PI Fish EN;  
XX  
XX WPI; 2002-547689/58.  
XX PR P-PSDB; ABG68863.  
XX  
XX

PT Cytokine receptor binding peptide construct, in particular interferon  
PT receptor binding peptide construct for use as an interferon mimetic,  
PT comprising a cytokine receptor binding domain incorporated in a molecular  
PT scaffold.  
XX  
XX Example 8; Page 52; 105pp; English.  
XX  
CC This invention relates to a novel cytokine receptor binding peptide  
CC construct comprising a cytokine receptor binding domain incorporated in a  
CC suitable molecular scaffold so that the scaffold maintains the binding  
CC domain in a configuration suitable for binding to the cytokine receptor.  
CC The peptides of the invention may have cytoskeletal, virocidic,  
CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and  
CC antitumor activities. A new interferon receptor binding peptide  
CC construct is useful in the manufacture of a medicament with an interferon  
CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in  
CC medical therapies for cancer, haematological malignancies, viral  
CC infections (hepatitis B or C), multiple sclerosis and autoimmune diseases  
CC such as arthritis, to detect modulators of IFN action, in screening  
CC assays to compare the activity and/or interaction with another molecule  
CC or potential IFN modulator and also in the diagnosis of IFN activity  
CC related disorders. A nucleic acid encoding the peptide of the invention  
CC or is useful for the treatment and therapy of the mentioned medical  
CC conditions. The peptide of the invention has less side effect than those  
CC of native cytokines. The present sequence represents an interferon  
CC receptor binding peptide associated DNA of the invention  
CC  
SQ Sequence 48 BP; 5 A; 10 C; 25 G; 8 T; 0 U; 0 Other;  
  
Query Match 8.3%; Score 20.2; DB 6; Length 48;  
Best Local Similarity 68.3%; Pred. No. 1.6e+04;  
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
  
QY 31 CTGGCTGGAGCTCCACCTCCCGAGCTGCTGCTCCTCACCCTGC 71  
DB 45 CAGACAGAACCTCCACCGCCGCGCGCGCTCCCGC 5  
  
RESULT 8  
AA51766  
ID AAA51766 standard; DNA; 31 BP.  
XX  
AC AAA51766;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE 31-mer CYP3A5 wild-type -147A oligonucleotide.  
XX  
KM CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;  
KM Activator protein-3 motif; AP-3; basic transcription element;  
KM drug metabolism; phenotype; variant; ds.  
XX  
OS Homo sapiens.  
XX  
OS WO200039332-A1.  
XX  
PN 06-JUL-2000.  
XX  
PD 22-DEC-1999; 99WO-GB004380.  
XX  
PF 23-DEC-1998; 98GB-00028619.  
XX  
PR (JANC ) JANSSEN PHARM NV.  
XX  
PA Paulussen ADC, Armstrong M;  
XX  
PI WPI; 2000-452418/39.  
XX  
DR Identifying subjects with a high drug metabolizing phenotype associated  
PT with cytochrome CYP3A5 expression for establishing whether a drug will be  
PT metabolized by the subject.  
XX  
PS Disclosure; Page 31; 68pp; English.

XX  
CC 31-mer double stranded oligonucleotides corresponding to the cytochrome  
CC P450 subfamily CYP3A5 5' untranslated region containing a polymorphism at  
CC -147 (G) or wild-type (A) sequence were used in an electrophoretic  
CC mobility shift assay (EMSA). The assay showed that -147 polymorphism  
CC might create a binding site for the transcription factor Sp1. CYP3A5  
CC transcription regulatory regions can be screened for the presence/absence  
CC of a polymorphic variant, preferably at positions -475 or -147 of the DNA  
CC of the 5' flanking region adjacent to the CYP3A5 coding sequence. The  
CC variants are present in an activator protein-3 (AP-3) motif and/or a  
CC basic transcription element (BRE). The polymorphisms cause increased  
CC CYP3A5 gene expression and this has been linked to drug metabolic  
CC activity. Screening for the presence of variants can be used to identify  
CC subjects with a high or low drug metabolizing phenotype associated with  
CC cytochrome CYP3A5 expression. Primers are used which in addition to  
CC hybridizing to the site of interest, are capable of introducing a  
CC restriction site which is absent in either the wild type sequence or  
CC polymorphic variants. Restriction enzyme cleavage analysis can then be  
CC used to indicate the presence or absence of the variant. The methods are  
CC used to establish, before treatment with a drug, whether the drug will be  
CC effectively metabolized by the patient, to identify compounds and  
CC transcription factors that can bind to a DNA sequence encoding CYP3A5,  
CC diagnosing susceptibility to a disease which is caused by toxins or  
CC procarcinogens metabolized by CYP3A5 and for identifying mutagenic  
CC effects of a compound  
XX  
SQ Sequence 31 BP; 5 A; 15 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 8.1%; Score 19.6; DB 3; Length 31;  
Best Local Similarity 84.6%; Pred. No. 2.1e+04;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 53 CAGCTGCTGGCTCACCCTGCTTTCCA 78  
DB 3 CAGCTGACAGCCCACTCTCTCCA 28  
  
RESULT 9  
AAQ74160/c  
ID AAQ74160 standard; DNA; 42 BP.  
XX  
AC AAQ74160;  
XX  
DT 07-FEB-1996 (first entry)  
XX  
DE Mouse heavy chain 3' amplification primer ICG2a,b RIL.  
XX  
XX  
KM Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;  
KM antibody; immunotolerance; animal; variegated display library;  
KM variable region; antigen; immunorecessive; cell surface marker; foetal;  
KM cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;  
KM familial hypercholesterolaemia; binding affinity; ss.  
XX  
XX  
OS Synthetic.  
XX  
OS WO9515982-A2.  
XX  
PN 15-JUN-1995.  
XX  
PD 08-DEC-1994; 94WO-US014106.  
XX  
PF 08-DEC-1993; 93US-00164022.  
XX  
PR 06-DEC-1994; 94US-00350400.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;  
XX  
DR WPI; 1995-224291/29.  
XX  
PT Generating new antibodies specific for immunorecessive epitopes - by  
PT selection from variegated V gene library cloned from immuno:tolerance  
PT derived antibody repertoire, useful in diagnosis, purificn. and therapy.

PR e.g. of cancer.  
 XX  
 PS Example; Fig 1A, 109pp; English.  
 XX  
 CC primers AA074153-74 are a set of degenerate primers used to amplify 90%  
 CC of the mouse kappa chain and heavy chain Fab coding sequences from  
 CC antibodies in an immunotolerant animal. This primer binds to the 3' of  
 CC the heavy chain coding region. The amplified products are cloned to  
 CC produce a variegated display library (VDL) of antibody variable regions.  
 CC The antibodies are generated by an immunotolerant individual against an  
 CC antigen. The VDL can be used to generate an antibody against a  
 CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or  
 CC stem cell, which can differentiate between variant or related forms of  
 CC the antigen. The antibodies generated can be used in the diagnosis, e.g.  
 CC detection of the immunorecessive antigen, or in therapy e.g. of cancer.  
 CC Alzheimer's disease or familial hypercholesterolaemia. The method of  
 CC production of the antibody allows rapid and sensitive isolation of  
 CC antibodies that would be difficult to isolate by standard methods. The  
 CC antibodies produced have greater binding affinity than those produced by  
 CC combinatorial/hybridoma methods  
 CC  
 SQ Sequence 42 BP; 7 A; 13 C; 13 G; 9 T; 0 U; 0 Other;  
 XX  
 Query Match 8.1%; Score 19.6; DB 2; Length 42;  
 Best Local Similarity 66.7%; Pred. No. 2.3e+04;  
 Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 177 TTAGCCACCGCTGCTGTAGGCTTGTAGGCTGTATCAG 218  
 DB 42 TTGAGCCACGCGCGCCCACTAGTATCTGTGCGCGAACACAG 1  
 RESULT 10  
 AB201168/c  
 ID AB201168 standard; DNA; 50 BP.  
 XX  
 AC AB201168;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE Human leukocyte gene expression profiling probe SEQ ID NO 1159.  
 XX  
 KW T7; leukocyte; gene expression profiling; allograft rejection;  
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257414-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-OCT-2001; 2001WO-US047856.  
 XX  
 PR 20-OCT-2000; 2000US-0241994P.  
 PR 08-JUN-2001; 2001US-0296764P.  
 XX  
 PA (BIOC-) BIOCARDIA INC.  
 XX  
 PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
 PI Ly N, Woodward R, Queternous T, Johnson F;  
 XX  
 DR WPI; 2002-636525/68.  
 XX  
 PT New system for leukocyte expression profiling, diagnosing a disease, or  
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX  
 PS Claim 1; Page 361; Opp; English.  
 CC The invention relates to a system for detecting gene expression, which  
 CC comprises one or two isolated DNA molecules that detect expression of a

CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 CC  
 SQ Sequence 50 BP; 15 A; 9 C; 20 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 8.1%; Score 19.6; DB 6; Length 50;  
 Best Local Similarity 66.7%; Pred. No. 2.5e+04;  
 Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 35 CTGGAGCTCCACCTCCACGCTGCTGCTGCTGCTTTTC 76  
 DB 50 CTGGCGCTTCCCTTCCAGTTACAGCCACGCTTCTTC 9  
 RESULT 11  
 AAT97180/c  
 ID AAT97180 standard; DNA; 39 BP.  
 XX  
 AC AAT97180;  
 XX  
 DT 11-MAY-1998 (first entry)  
 XX  
 DE T cell receptor alpha chain 3' PCR primer.  
 XX  
 KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;  
 KW gene amplification; immunotherapy; therapy; T cell receptor; human; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9741244-A1.  
 XX  
 PD 06-NOV-1997.  
 XX  
 PF 25-APR-1997; 97WO-US007039.  
 XX  
 PR 01-MAY-1996; 96US-00644664.  
 PR 06-DEC-1996; 96US-00761277.  
 XX  
 PA (GENI-) GENITOPE CORP.  
 XX  
 PI Denney DW;  
 XX  
 DR WPI; 1997-549743/50.  
 XX  
 PT Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at  
 PT least 2 different recombinant variable regions of immunoglobulin  
 PT molecules derived from B cell lymphoma cells.  
 XX  
 PS Example 9; Page 86; 177pp; English.  
 XX  
 CC This 3' primer is used with a consensus 5' primer (see AAT97179) for the  
 CC PCR amplification of the human T cell receptor (TCR) alpha chain  
 CC extracellular domain DNA. The 3' connection for the TCR alpha chain is  
 CC made after Aen-110 of the constant region of the alpha chain. The methods  
 CC of the invention allow large quantities of soluble TCR to be produced in  
 CC a rapid manner. Customised tumour cell vaccines comprising soluble TCR  
 CC are obtained for the treatment of lymphoma and leukaemia  
 CC  
 SQ Sequence 39 BP; 9 A; 7 C; 9 G; 14 T; 0 U; 0 Other;  
 XX  
 Query Match 7.9%; Score 19.2; DB 2; Length 39;  
 Best Local Similarity 75.0%; Pred. No. 3.1e+04;  
 Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;





```
OS Synthetic.
OS Pisum sativum.
XX US5866394-A.
XX
XX 02-FEB-1999.
XX
XX 31-OCT-1996; 96US-00741931.
XX
XX 21-FEB-1995; 95US-00391000.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Houtz RU;
XX
XX WPI; 1999-141928/12.
XX
XX Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the
XX lysine epsilon-amino group of Rubisco.
XX
XX Example 4; Col 13-14; 28pp; English.
XX
XX This sequence represents a primer from a degenerate pool of primers
XX synthesised based on the peptide P18 (AAW75489) from the pea Rubisco
XX (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N
XX -methyltransferase (LSMT). The primer is based on the sense strand
XX encoding the peptide P18 and is used in the isolation of the pea Rubisco
XX LSMT from a cDNA library. The Rubisco LSMT gene encodes a protein of 489
XX amino acids with a predicted molecular weight of 55 kD. Recombinant
XX Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of
XX the epsilon-amino group of Lys-14 in the large subunit of Rubisco
XX
XX SQ Sequence 42 BP; 9 A; 14 C; 8 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 19.2; DB 2; Length 42;
XX Best Local Similarity 75.0%; Pred. No. 3.2e+04;
XX Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 39 GAGCTCCACTCCCGAGCTGCTGCTCACTG 70
XX ||||| ||||| ||||| |||||
XX DB 8 GAAGCTGCTCCTGCTGCTGCTGCTTACCTG 39
XX
XX RESULT 15
XX AAX16811/c
XX ID AAX16811 standard; DNA; 42 BP.
XX
XX AAX16811;
XX
XX 27-APR-1999 (first entry)
XX
XX Dea Rubisco LSMT P18-derived degenerate primer #13.
XX
XX Pea; rubisco; ribulose-1,5-bisphosphate carboxylase/oxygenase; primer;
XX epsilon-N-methyltransferase; PCR; amplification; methyltransferase;
XX methylation; ss.
XX
XX OS Synthetic.
XX OS Pisum sativum.
XX
XX US5866394-A.
XX
XX 02-FEB-1999.
XX
XX 31-OCT-1996; 96US-00741931.
XX
XX 21-FEB-1995; 95US-00391000.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Houtz RU;
XX
XX WPI; 1999-141928/12.
XX
```

```
XX
XX Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the
XX lysine epsilon-amino group of Rubisco.
XX
XX Example 4; Col 13-14; 28pp; English.
XX
XX This sequence represents a primer from a degenerate pool of primers
XX synthesised based on the peptide P18 (AAW75489) from the pea Rubisco
XX (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N
XX -methyltransferase (LSMT). The primer is based on the antisense strand
XX encoding the peptide P18 and is used in the isolation of the pea Rubisco
XX LSMT from a cDNA library. The Rubisco LSMT gene encodes a protein of 489
XX amino acids with a predicted molecular weight of 55 kD. Recombinant
XX Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of
XX the epsilon-amino group of Lys-14 in the large subunit of Rubisco
XX
XX SQ Sequence 42 BP; 11 A; 8 C; 14 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 19.2; DB 2; Length 42;
XX Best Local Similarity 75.0%; Pred. No. 3.2e+04;
XX Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 39 GAGCTCCACTCCCGAGCTGCTGCTCACTG 70
XX ||||| ||||| ||||| |||||
XX DB 35 GAAGCTGCTCCTGCTGCTGCTGCTTACCTG 4
XX
XX Search completed: October 1, 2006, 00:26:40
XX Job time : 334.623 secs
XX
```

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:40:27 ; Search time 791.816 Seconds  
(without alignments)  
3755.428 Million cell updates/sec

Title: US-10-642-946-6\_COPY\_1967\_2208

Perfect score: 242  
Sequence: 1 ttctccagcacacgacgtga.....ccaactaaactgacac 242

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11E\_PUBCOMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	9.9	50	US-11-175-859-40976	Sequence 40976, A
2	20.8	8.6	50	US-10-131-827-7899	Sequence 7899, Ap
3	20.8	8.6	50	US-11-175-859-61965	Sequence 61965, A
4	20.2	8.3	50	US-11-175-859-73641	Sequence 73641, A
5	20.2	8.3	50	US-11-175-859-75378	Sequence 75378, A
6	20.2	8.3	50	US-11-175-859-94006	Sequence 94006, A
7	20	8.3	41	US-10-035-833A-1473	Sequence 1473, Ap
8	20	8.3	41	US-10-035-833A-3970	Sequence 3970, Ap
9	20	8.3	41	US-11-175-859-61890	Sequence 61890, A
10	19.8	8.2	50	US-11-036-317-987319	Sequence 987319, A
11	19.8	8.2	50	US-11-175-859-40305	Sequence 40305, A
12	19.8	8.2	50	US-11-175-859-61232	Sequence 61232, A
13	19.6	8.1	50	US-10-131-827-1159	Sequence 1159, Ap
14	19.6	8.1	50	US-11-175-859-89374	Sequence 89374, A
15	19.6	8.1	50	US-11-175-859-96830	Sequence 96830, A
16	19.4	8.0	48	US-10-035-833A-4173	Sequence 4173, Ap
17	19.4	8.0	50	US-11-175-859-2047	Sequence 2047, Ap

18	19.4	8.0	50	US-11-175-859-9678	Sequence 9678, Ap
19	19.4	8.0	50	US-11-175-859-64743	Sequence 64743, A
20	19.4	8.0	50	US-11-175-859-100374	Sequence 100374, A
21	19.2	7.9	39	US-09-925-664-35	Sequence 35, Appl
22	19.2	7.9	39	US-09-925-192-35	Sequence 192, Appl
23	19.2	7.9	39	US-11-175-859-102443	Sequence 102443, A
24	19	7.9	50	US-10-131-827-6394	Sequence 6394, Ap
25	19	7.9	50	US-10-131-827-6784	Sequence 6784, Ap
26	19	7.9	50	US-10-499-151A-46	Sequence 46, Appl
27	19	7.9	50	US-11-175-859-13869	Sequence 13869, A
28	19	7.9	50	US-11-175-859-64934	Sequence 64934, A
29	19	7.9	50	US-11-175-859-74739	Sequence 74739, A
30	18.8	7.8	50	US-11-175-859-4623	Sequence 4623, Ap
31	18.8	7.8	50	US-11-175-859-58714	Sequence 58714, A
32	18.8	7.8	50	US-11-175-859-111918	Sequence 111918, A
33	18.6	7.7	43	US-10-184-508A-2	Sequence 2, Appl
34	18.6	7.7	43	US-10-186-186-2	Sequence 12, Appl
35	18.6	7.7	50	US-09-993-346-504	Sequence 504, Appl
36	18.6	7.7	50	US-11-175-859-66081	Sequence 66081, A
37	18.4	7.6	29	US-10-084-839A-18234	Sequence 3861, Ap
38	18.4	7.6	32	US-10-939-294A-18234	Sequence 18234, A
39	18.4	7.6	45	US-09-748-111B-12	Sequence 12, Appl
40	18.4	7.6	45	US-09-794-366-12	Sequence 12, Appl
41	18.4	7.6	50	US-11-175-859-3989	Sequence 3989, Ap
42	18.4	7.6	50	US-11-175-859-37922	Sequence 37922, A
43	18.4	7.6	50	US-11-175-859-80567	Sequence 80567, A
44	18.4	7.6	50	US-11-175-859-89058	Sequence 89058, A
45	18.2	7.5	24	US-10-310-914A-116991	Sequence 116991, A

ALIGNMENTS

RESULT 1  
US-11-175-859-40976  
; Sequence 40976, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affimetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; PRIOR FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 40976  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-40976

Query Match 9.9%; Score 24; DB 16; Length 50;  
Best Local Similarity 66.0%; Pred. No. 6.3e+02;  
Matches 33; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 56 CTGCTGCTTCACTGCTTTTCAACCCACCTGTAAACGCTACTACATA 105  
Db 1 CTGCTGCTTCTGCTGCTGCTTTTAAYGCTTCAAGAGACAGACACCCCA 50

RESULT 2  
US-10-131-827-7899  
; Sequence 7899, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Day  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

```

; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7899
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7899

Query Match
Best Local Similarity 70.0%; Score 20.8; DB 7; Length 50;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 54 AGCTGCTGCTCCTACCTGCTTTCCAAACCCACCCCTGAA 93
Db 1 AGCTGCTGCTTCTCTTTTCAGTTGCAATGCAAACTGTTA 40

RESULT 3
US-11-175-859-61985
; Sequence 61985, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61985
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-61985

Query Match
Best Local Similarity 66.7%; Score 20.8; DB 16; Length 50;
Matches 28; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Oy 50 CCCGAGCTGCTGCTCCTACCTGCTTTCCAAACCCACCCCTGT 91
Db 8 CCACAGCATCTGCCCTACATCTGCTCCAAATCAATACCCCT 49

RESULT 4
US-11-175-859-73641/c
; Sequence 73641, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73641
; LENGTH: 50
; TYPE: DNA

; ORGANISM: homo sapien
US-11-175-859-73641

Query Match
Best Local Similarity 65.1%; Score 20.2; DB 16; Length 50;
Matches 28; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Oy 68 CTCGTTTCCAAACCCACCCCTGTAAACGTAACACTATTG 110
Db 47 CTCGTTTCCAAACCTCAACCTTTGATGATGTAATTCCTTTG 5

RESULT 5
US-11-175-859-75378/c
; Sequence 75378, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75378
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-75378

Query Match
Best Local Similarity 71.4%; Score 20.2; DB 16; Length 50;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy 197 AGGGTTGCTAGGCTGATCAGATACCAACTAA 231
Db 36 AAGGCTGACTRATCTGATCAAAAACCAAAATAA 2

RESULT 6
US-11-175-859-94006/c
; Sequence 94006, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94006
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-94006

Query Match
Best Local Similarity 68.3%; Score 20.2; DB 16; Length 50;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 69 TGCTTTCCAAACCCACCCCTGTAACGGTAACATTTT 109
Db 50 TGATTTCCAGATCTTACCCTGTTAATATATCCAGATTTT 10

RESULT 7
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US-10-035-833A-1473/c
; Sequence 1473, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035, 833A
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1473
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-1473

```

```

Query Match      8.3% Score 20; DB 8; Length 41;
Best Local Similarity 68.4%; Pred. No. 1.6e+04;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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Qy 21 TTTTGTCACCTGGCTGGAGCTCCACCTCCCGCAGCTG 58
Db 41 TTTTGCCACCGGTCTGGCGCRGTACCTCCCGCGCTG 4

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RESULT 8
US-10-035-833A-3970/c
; Sequence 3970, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035, 833A
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3970
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-3970

```

```

Query Match      8.3% Score 20; DB 8; Length 41;
Best Local Similarity 68.4%; Pred. No. 1.6e+04;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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Qy 21 TTTTGTCACCTGGCTGGAGCTCCACCTCCCGCAGCTG 58
Db 41 TTTTGCCACCGGTCTGGCGCRGTACCTCCCGCGCTG 4

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RESULT 9
US-11-175-859-61890/c
; Sequence 61890, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Aftymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175, 859
; NUMBER OF SEQ ID NOS: 2005-07-05
; PRIOR FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/585,352
; NUMBER OF SEQ ID NOS: 116251

```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61890
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-61890

```

```

Query Match      8.3% Score 20; DB 16; Length 50;
Best Local Similarity 63.0%; Pred. No. 1.7e+04;
Matches 29; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

```

```

Qy 180 AGCCACCGTGTCTGTAGGTTGTTAGGCTGATACGATACCA 225
Db 49 ATCCACGCTGTCTGTAGGTTGTTAGGCTGATACGATACCA 4

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```

RESULT 10
US-11-036-317-987319
; Sequence 987319, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; NUMBER OF SEQ ID NOS: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 987319
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987319

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```

Query Match      8.2% Score 19.8; DB 13; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.6e+04;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 TTCTCCAGCAGCAGCTGATTT 23
Db 1 TTCTCCAGCAGCAGCTGATTT 23

```

```

RESULT 11
US-11-175-859-20305/c
; Sequence 20305, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Aftymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175, 859
; NUMBER OF SEQ ID NOS: 2005-07-05
; PRIOR FILING DATE: 2004-07-02
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20305
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-20305

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```

Query Match      8.2% Score 19.8; DB 16; Length 50;
Best Local Similarity 61.2%; Pred. No. 2e+04;
Matches 30; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

```

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Qy 39 GAGTCCACCTCCCGCTGCTGCTCAGCTTTTCCAAACCCACC 87

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Db 50 GAGCTCCCATCTTCAAGTCTAGCTGACAGCTGATCCCAAGCAACC 2

RESULT 12

US-11-175-859-61232

; Sequence 61232, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; PRIOR FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 61232

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-61232

Query Match 8.2%; Score 19.8; DB 16; Length 50;

Best Local Similarity 61.2%; Pred. No. 2e+04;

Matches 30; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

OY 21 TTTTGTCACCTGCTGGAAGCTCCACCTCCCAAGCTGCTGCTCACT 69

Db 2 TTGTCGACCTGACTGAGCTGACACCTGACACCCCAAGCTGCTGCT 50

RESULT 13

US-10-131-827-1159/c

; Sequence 1159, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131, 827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1159

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-1159

Query Match 8.1%; Score 19.6; DB 7; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.3e+04;

Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 35 CTGGAGCTCCAGCTCCCAAGCTGCTGCTCACTGCTTTTC 76

Db 50 CTGTGCGCTTCCCTTTCCAGTTACAGCCCAAGCTCTTCTC 9

RESULT 14

US-11-175-859-89374

; Sequence 89374, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; APPLICANT: Liu, Guoying et al.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; PRIOR FILING DATE: 2004-07-02

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 89374

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-89374

Query Match 8.1%; Score 19.6; DB 16; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.3e+04;

Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 201 TTTGCTAGCTGTATCAGATACCACTAAACTGATTCAC 242

Db 9 TGGGTAGGGGCTGACATATACAAATATAGCTGGGGTAC 50

RESULT 15

US-11-175-859-96830

; Sequence 96830, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; PRIOR FILING DATE: 2004-07-02

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 96830

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-96830

Query Match 8.1%; Score 19.6; DB 16; Length 50;

Best Local Similarity 69.4%; Pred. No. 2.3e+04;

Matches 25; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

OY 199 GGTGTCTAGCTGTATCAGATACCACTAAACT 234

Db 2 GGGTGTAAATGTTTCAGATAGTCAGGAAAGT 37

Search completed: October 1, 2006, 01:09:50

Job time : 792.816 secs

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%, *length 10-241 nt.*

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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Query Match 7.5%; Score 17.6; DB 1; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 5.6;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 174 ATTCAGGAGACTGCACAGAAGCA 197  
 DB 25 ATACCAGCAGCTGCACAAAAGCA 2

RESULT 3  
 US-11-348-413-779975  
 ; Sequence 779975, Application US/11348413  
 ; Publication No. US20060160121A1  
 ; GENERAL INFORMATION:

APPLICANT: Wyeth  
 APPLICANT: Mounts, William M  
 APPLICANT: Murphy, Ellen  
 APPLICANT: Olmsted, Stephen  
 TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 FILE REFERENCE: 031896-084100 (Am 101724)  
 CURRENT FILING DATE: 2006-02-07  
 PRIOR FILING DATE: 2005-10-05  
 PRIOR APPLICATION NUMBER: PCT/US05/035471  
 PRIOR FILING DATE: 2005-10-05  
 PRIOR APPLICATION NUMBER: US 11/243,445  
 PRIOR FILING DATE: 2005-10-05  
 PRIOR APPLICATION NUMBER: US 60/615,573  
 PRIOR FILING DATE: 2004-10-05  
 NUMBER OF SEQ ID NOS: 1276209  
 SEQ ID NO 779975  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Artificial

FEATURE:  
 OTHER INFORMATION: probe  
 NAME/KEY: misc feature  
 LOCATION: (1)\_(125)  
 OTHER INFORMATION: SEQ ID NO: 5002; MAN01PA72\_at; Start 23; Stop 47;  
 ; US-11-348-413-779975

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 5.6;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 188 ACAAGAACAATGCTAACGCCAT 211  
 DB 2 ACGAGAAGCAAACTCTATGCCAT 25

RESULT 4  
 US-11-078-073-81/c  
 ; Sequence 81, Application US/11078073  
 ; Publication No. US20060094032A1  
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin  
 APPLICANT: Frank-Kamenetsky, Maria  
 APPLICANT: Manoharan, Muthiah  
 APPLICANT: Rajeev, Kallanthottathil G.  
 APPLICANT: Hadwiger, Philipp  
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF  
 FILE REFERENCE: 14174-085001  
 CURRENT FILING DATE: 2005-03-11  
 PRIOR FILING DATE: 2004-03-12  
 PRIOR APPLICATION NUMBER: US 60/552,620  
 PRIOR FILING DATE: 2004-03-12  
 PRIOR APPLICATION NUMBER: US 60/559,824  
 PRIOR FILING DATE: 2004-04-05  
 PRIOR APPLICATION NUMBER: US 60/647,191  
 PRIOR FILING DATE: 2005-01-25  
 NUMBER OF SEQ ID NOS: 1061

SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 81  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-078-073-81

Query Match 7.4%; Score 17.4; DB 1; Length 23;  
 Best Local Similarity 94.7%; Pred. No. 5.4;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTTGCCATG 165  
 DB 23 CCCTCCTCCTTGCCATG 5

RESULT 5  
 US-11-078-073-82/c  
 ; Sequence 82, Application US/11078073  
 ; Publication No. US20060094032A1  
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin  
 APPLICANT: Frank-Kamenetsky, Maria  
 APPLICANT: Manoharan, Muthiah  
 APPLICANT: Rajeev, Kallanthottathil G.  
 APPLICANT: Hadwiger, Philipp  
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF  
 FILE REFERENCE: 14174-085001  
 CURRENT FILING DATE: 2005-03-11  
 PRIOR FILING DATE: 2005-03-11  
 PRIOR APPLICATION NUMBER: US 60/552,620  
 PRIOR FILING DATE: 2004-03-12  
 PRIOR APPLICATION NUMBER: US 60/559,824  
 PRIOR FILING DATE: 2004-04-05  
 PRIOR APPLICATION NUMBER: US 60/647,191  
 PRIOR FILING DATE: 2005-01-25  
 NUMBER OF SEQ ID NOS: 1061  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 82  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-078-073-82

Query Match 7.4%; Score 17.4; DB 1; Length 23;  
 Best Local Similarity 94.7%; Pred. No. 5.4;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTTGCCATG 165  
 DB 22 CCCTCCTCCTTGCCATG 4

RESULT 6  
 US-11-078-073-83/c  
 ; Sequence 83, Application US/11078073  
 ; Publication No. US20060094032A1  
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin  
 APPLICANT: Frank-Kamenetsky, Maria  
 APPLICANT: Manoharan, Muthiah  
 APPLICANT: Rajeev, Kallanthottathil G.  
 APPLICANT: Hadwiger, Philipp  
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF  
 FILE REFERENCE: 14174-085001  
 CURRENT FILING DATE: 2005-03-11  
 PRIOR FILING DATE: 2005-03-11  
 PRIOR APPLICATION NUMBER: US 60/552,620  
 PRIOR FILING DATE: 2004-03-12  
 PRIOR APPLICATION NUMBER: US 60/559,824  
 PRIOR FILING DATE: 2004-04-05  
 PRIOR APPLICATION NUMBER: US 60/647,191  
 PRIOR FILING DATE: 2005-01-25

```
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-83
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      21 CCCTCTCTCTCTGCCATG 3
```

```
RESULT 7
US-11-078-073-84/c
; Sequence 84, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-84
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      20 CCCTTCCTCTCTGCCATG 2
```

```
RESULT 8
US-11-078-073-85/c
; Sequence 85, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
```

```
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-85
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      19 CCCTCTCTCTCTGCCATG 1
```

```
RESULT 9
US-11-078-073-80/c
; Sequence 80, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-80
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      148 CCTTCCTCTCTGCCATG 165
Db      23 CCTTCCTCTCTGCCATG 6
```

```
RESULT 10
US-11-078-073-86/c
; Sequence 86, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
```

```
; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-86
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      147 CCCTTCCTCTCTGCAT 164
          |||||
Db       18 CCCTCTCTCTCTGCAT 1
```

```
RESULT 11
US-11-323-061-4
; Sequence 4, Application US/11323061
; Publication No. US20060177851A1
; GENERAL INFORMATION:
; APPLICANT: Brennan, Mark David
; APPLICANT: Condra, Jodi Ann
; APPLICANT: Maesey, Amy Tabb
; APPLICANT: Wei, Wei
; APPLICANT: Neibergs, Holly
; TITLE OF INVENTION: GENETIC MARKERS OF SCHIZOPHRENIA
; FILE REFERENCE: 17929-002001
; CURRENT APPLICATION NUMBER: US/11/323,061
; CURRENT FILING DATE: 2005-12-30
; PRIOR APPLICATION NUMBER: US 60/640,707
; PRIOR FILING DATE: 2004-12-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-323-061-4
```

```
Query Match          6.6%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 9;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      144 TCCCTTCCTCTCTGCATG 165
          |||||
Db       1 TTCTCTTCACTTCTCTGCATG 22
```

```
RESULT 12
US-10-511-937-2014/c
; Sequence 2014, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
```

```
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2014
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2014
```

```
Query Match          6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.1;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      134 AGACCTGCTCCCTCTCT 153
          |||||
Db       20 AGACCTCTCTCTCTCTCT 1
```

```
RESULT 13
US-11-346-145-6/c
; Sequence 6, Application US/11346145
; Publication No. US20060178333A1
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Saidman, Shlomo
; APPLICANT: Eyron, Tama
; TITLE OF INVENTION: Antisense Oligonucleotide Against Human Acetylcholinesterase
; FILE REFERENCE: 13122/US/01
; CURRENT APPLICATION NUMBER: US/11/346,145
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: ID 143379
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/IL02/00411
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat inverse EN102
US-11-346-145-6
```

```
Query Match          6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.1;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      102 CCCTTCATCTCTCTGCTC 121
          |||||
Db       20 CCCTCTCTCTCTCTCTCTC 1
```

```
RESULT 14
US-11-233-507-43/c
; Sequence 43, Application US/11233507
; Publication No. US20060099616A1
; GENERAL INFORMATION:
; APPLICANT: Ommen van, Garrit-Jan B.
; APPLICANT: Deutekom van, Judith C.T.
; APPLICANT: Dunnen den, Johannes T.
; APPLICANT: Aartsma-Rus, Annemeke
; TITLE OF INVENTION: Modulation of exon recognition in pre-mRNA by
; TITLE OF INVENTION: interfering with the secondary RNA structure
; FILE REFERENCE: P63917US00
; CURRENT APPLICATION NUMBER: US/11/233,507
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: PCT/NL2004/00196
```

PRIOR FILING DATE: 2004-03-22 PCT/NL03/00214  
PRIOR APPLICATION NUMBER: PCT  
PRIOR FILING DATE: 2003-03-21  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: h59A0N2  
US-11-233-507-43

Query Match 6.3%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 9.7;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 171 AAGATTCAGGAGCTTCA 188  
DB 19 AAGACTCCAGGACTTCA 2

RESULT 15  
US-11-223-738-35  
Sequence 35, Application US/11223738  
Publication No. US2006009682A1  
GENERAL INFORMATION:  
APPLICANT: DELANY, Samantha  
APPLICANT: SANSEAU, Philippe  
APPLICANT: TATE, Simon Nicholas  
TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES  
FILE REFERENCE: PG3606D1  
CURRENT APPLICATION NUMBER: US/11/223,738  
CURRENT FILING DATE: 2005-09-09  
PRIOR APPLICATION NUMBER: 09/857,123  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: PCT/EP99/09284  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: GB98265593  
PRIOR FILING DATE: 1998-12-01  
NUMBER OF SEQ ID NOS: 40  
SEQ ID NO 35  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-11-223-738-35

Query Match 6.1%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 CTGCTCCCACTCTTGC 130  
DB 2 CTGCTCCCACTCTTGC 17

RESULT 16  
US-10-511-937-857  
Sequence 857, Application US/10511937  
Publication No. US2006008836A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, Macdonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946  
PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 857  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-511-937-857

Query Match 6.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 135 GACACCTGCTCCCTTCT 153  
DB 1 GACCCCTCTTCCCTTCT 19

RESULT 17  
US-11-370-584-10001/c  
Sequence 10001, Application US/11370584  
Publication No. US20060177863A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high  
density...  
FILE REFERENCE: GENSET.020CP1  
CURRENT APPLICATION NUMBER: US/11/370,584  
CURRENT FILING DATE: 2006-03-08  
PRIOR APPLICATION NUMBER: US/10/349,143  
PRIOR FILING DATE: 2003-01-21  
PRIOR APPLICATION NUMBER: US/09/422,978  
PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: US 09/298,850  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US 60/109,732  
PRIOR FILING DATE: 1998-11-23  
PRIOR APPLICATION NUMBER: US 60/082,614  
PRIOR FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 10001  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136,  
US-11-370-584-10001

Query Match 6.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 209 CATGCTCTGTCTGTCT 227  
DB 19 CTTACTTCTTGTGTCT 1

RESULT 18  
US-11-233-507-15  
Sequence 15, Application US/11233507



```
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4193
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ 259,
US-11-370-584-4193

Query Match          5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCGCACTC 126
Db      17 TTCTCTATATCCCACTC 1

RESULT 23
US-11-293-697-5018/c
; Sequence 5018, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5018
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized F
US-11-293-697-5018

Query Match          5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      100 CCCCTCTCATCTCTCT 116
Db      18 CCCCTTCTCACTCTCT 2

RESULT 24
US-11-321-991-8
; Sequence 8, Application US/11321991
```

```
; Publication No. US20060115877A1
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PARACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/11/321,991
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: US/11/024,426
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-11-321-991-8

Query Match          5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      32 ATGGTTAGTGCATTC 48
Db      2 ATGGCTTAGTGCATTC 18

RESULT 25
US-11-255-139A-6881/c
; Sequence 6881, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0.
; SEQ ID NO 6881
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6881

Query Match          5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      148 CCTTCTCTCTTCTGCC 162
Db      16 CTGTCTCTCTCTGCC 2

RESULT 26
US-11-255-139A-6882/c
; Sequence 6882, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
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; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6882
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6882
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Query March 5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 148 CCTTCTCCTCTGCC 162
Db 15 CCTGCTCCTCTGCC 1
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RESULT 27
US-11-370-584-11764
; Sequence 11764, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
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```
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marra
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
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; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in
; OTHER INFORMATION: complement
US-11-370-584-11764
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Query March 5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 113 TCCTGCTCCACTCT 127
Db 2 TCCTTCTCCACTCT 16
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RESULT 28
US-11-102-097-1540
; Sequence 1540, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
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; SEQ ID NO 1540
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
US-11-102-097-1540
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Query March 5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 190 AAGAGCAATGCTA 204
Db 4 AAGAGCAATGCTA 18
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RESULT 29
US-11-102-097-1541
; Sequence 1541, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1541
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
; OTHER INFORMATION: Influenza virus.
US-11-102-097-1541
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Query March 5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 190 AAGAGCAATGCTA 204
Db 3 AAGAGCAATGCTA 17
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```
RESULT 30
US-11-102-097-1542
; Sequence 1542, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1542
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
; OTHER INFORMATION: Influenza virus.
US-11-102-097-1542
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Query March 5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 190 AAGAGCAATGCTA 204  
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Db 1 AAGAGTAAATCTA 15

RESULT 31  
US-11-370-584-7274/c  
; Sequence 7274, Application US/11370584  
; Publication No. US2006017763A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high  
; TITLE OF INVENTION: density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/11/370,584  
; CURRENT FILING DATE: 2006-03-08  
; PRIOR APPLICATION NUMBER: US/10/349,143  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 7274  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..18  
; OTHER INFORMATION: upstream amplification primer 99-3391 for SEQ 3340,  
US-11-370-584-7274

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 15;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 CTCATGATGCTTGTG 42  
| | | | |  
Db 18 CTCATCAATGCTGTG 1

RESULT 32  
US-11-268-341-1/c  
; Sequence 1, Application US/11268341  
; Publication No. US2006009574A1  
; GENERAL INFORMATION:  
; APPLICANT: Omar, Abdul Rahman  
; APPLICANT: Hair-Bejo, Mord  
; APPLICANT: Aini, Ideris  
; APPLICANT: Hamzah, Hairul Aini  
; TITLE OF INVENTION: DETECTION AND DISTINGUISHING INFECTIONS BURSAL DISEASE VIRUS  
; TITLE OF INVENTION: (IBDV) STRAINS BY MOLECULAR BIOLOGY METHOD  
; FILE REFERENCE: S1436.70010US00  
; CURRENT APPLICATION NUMBER: US/11/268,341  
; CURRENT FILING DATE: 2005-11-07  
; PRIOR APPLICATION NUMBER: MY PI 20044610  
; PRIOR FILING DATE: 2004-11-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-11-268-341-1

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 15;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 90 AAGAGCTGGCCCTCT 107  
| | | | |  
Db 18 AATAGCTGGCACTCT 1

RESULT 33  
US-11-255-139A-3650/c  
; Sequence 3650, Application US/11255139A  
; Publication No. US20060154271A1  
; GENERAL INFORMATION:  
; APPLICANT: Sigma Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/11/255,139A  
; CURRENT FILING DATE: 2005-10-20  
; NUMBER OF SEQ ID NOS: 8014  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3650  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-255-139A-3650

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 16;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 142 GCTCCCTCTCTCTT 157  
| | | | |  
Db 16 GCTCCCTCTCTCTT 1

RESULT 34  
US-11-293-697-5010  
; Sequence 5010, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5010  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p  
US-11-293-697-5010

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 17;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 134 AGACACCTGCTCCCC 149  
| | | | |  
Db 3 ACACCTGCTCCAC 18

RESULT 35  
US-11-177-646-509  
; Sequence 509, Application US/1177646

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; Publication No. US20060210967A1
; GENERAL INFORMATION:
; APPLICANT: AGAN, BRIAN
; APPLICANT: ROWLEY, ROBB
; APPLICANT: SETO, DONALD
; APPLICANT: STENGER, DAVID
; APPLICANT: THORNTON, JENNIFER
; APPLICANT: TIBBETTS, CLARK
; APPLICANT: THACH, DZUNG
; APPLICANT: VORA, GARY
; APPLICANT: WALTER, ELIZABETH
; APPLICANT: WANG, ZHENG
; TITLE OF INVENTION: RE-SEQUENCING PATHOGEN MICROARRAY
; FILE REFERENCE: APD 735
; CURRENT APPLICATION NUMBER: US/11/177,646
; PRIOR FILING DATE: 2005-07-02
; PRIOR APPLICATION NUMBER: 60/590931
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 509
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-177-646-509

Query Match      5.3%; Score 12.6; DB 1; Length 18;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      113 TCGTCTCCCACT 125
Db      2  TCTGCTCCCACT 14

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Search completed: October 2, 2006, 15:40:32  
 Job time : 0.001 secs



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RESULT 4
LOCUS CS155866/c 19 bp RNA linear PAT 07-SEP-2005
DEFINITION Sequence 57 from Patent WO2005078097.
ACCESSION CS155866
VERSION CS155866.1 GI:74271014
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Jadhav,V.
AUTHORS Patent: WO 2005078097-A 57 25-AUG-2005;
JOURNAL Sitma Therapeutics, Inc. (US)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTGCGCAT 164
Db 18 CCTCTCTCTCTGCGCAT 1

RESULT 5
LOCUS CS155924 19 bp RNA linear PAT 07-SEP-2005
DEFINITION Sequence 115 from Patent WO2005078097.
ACCESSION CS155924
VERSION CS155924.1 GI:74271072
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Jadhav,V.
AUTHORS Patent: WO 2005078097-A 115 25-AUG-2005;
JOURNAL Sitma Therapeutics, Inc. (US)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTGCGCAT 164
Db 2 CCTCTCTCTCTGCGCAT 19

RESULT 6
LOCUS ARI18904 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 30 from patent US 6150092.
ACCESSION ARI18904
VERSION ARI18904.1 GI:14100814
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 Unclasiified.
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.

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TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 30 21-NOV-2000;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 6.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.2;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTGCGCAT 164
Db 3 CCTCTCTCTCTGCGCAT 20

RESULT 7
LOCUS BD089856 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD089856
VERSION BD089856.1 GI:22635466
KEYWORDS JP 2001321190-A/2100.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Soeda,E.
JOURNAL A method of arraying genome clone
TITLE Patent: JP 2001321190-A 2100 20-NOV-2001;
JOURNAL THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT
OS Artificial Sequence
PN JP 2001321190-A/2100
PD 20-NOV-2001 JP 2001068285
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/00,C12M1/68,G01N33/53,G01N33/566,PC
C12N15/00
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
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FT source
FT Location/Qualifiers
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/organism="Artificial Sequence".
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1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 6.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.2;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 CTCATCTCTCTGCTCC 121
Db 1 CTCATCTCTCTGCTCC 18

RESULT 8
LOCUS AB068203 20 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-D1S1400
at 1936.
ACCESSION AB068203
VERSION AB068203.1 GI:15129007
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,

```

Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoehi, M., Horii, A. and Soda, E.  
 A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36  
 JOURNAL Genomics 74 (1), 55-70 (2001)  
 PUBMED 11374902  
 REFERENCE 2 (bases 1 to 20)  
 AUTHORS Horii, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
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 /note="reverse primer for human STS sts-D1S1400 at 1p36 sts-D1S1400 obtained from clones B279N/6, B3328, B156C13, B370J6, B310A20, B359U17, B45N15, B63P6, Human BAC library RPCT-11"  
 Query Match 6.9%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 3.2;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 104 CTCATCTCTCTCTCTCC 121  
 Db 1 CTCATCTCTCTCTCTCC 18  
 RESULT 9  
 AR207191 20 bp DNA linear PAT 20-JUN-2002  
 LOCUS AR207191 Sequence 85 from patent US 6372492.  
 DEFINITION AR207191  
 ACCESSION AR207191  
 VERSION AR207191.1 GI:21506024  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Bennett, C. Frank, and Cowsett, L. M.  
 TITLE Antisense modulation of talin expression  
 JOURNAL Patent: US 6372492-A 85 16-APR-2002;  
 FEATURES  
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 /mol\_type="unassigned DNA"  
 Query Match 6.8%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 105 TCTCATTTCTCTGCTC 120  
 Db 3 TCTCATTTCTCTGCTC 18  
 RESULT 10  
 AX590845/c 20 bp DNA linear PAT 27-JAN-2003  
 LOCUS AX590845 Sequence 285 from Patent WO02086113.  
 DEFINITION AX590845  
 ACCESSION AX590845  
 VERSION AX590845.1 GI:27949394  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Cookson, W. O., Moffat, M. F., Allen, M. and Lench, N.

TITLE Enzyme and snp marker for disease  
 JOURNAL Patent: WO 02086113-A 285 31-OCT-2002;  
 REFERENCE Isis Innovation Limited (GB)  
 FEATURES  
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 Location/Qualifiers  
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 /db\_xref="taxon:32630"  
 /note="Primer"  
 Query Match 6.8%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 191 AGAGCAAAATGCTAAC 206  
 Db 18 AGAGCAAAATGCTAAC 3  
 RESULT 11  
 AB166649/c 21 bp DNA linear SYN 07-OCT-2004  
 LOCUS AB166649 Synthetic construct DNA, reverse primer for microsatellite DIK4617.  
 DEFINITION AB166649  
 ACCESSION AB166649  
 VERSION AB166649.1 GI:51850039  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Ihara, N., Takasuga, A., Mizoshita, K., Takeda, H., Sugimoto, M., Mizoguchi, Y., Hirano, T., Itoh, T., Matanabe, T., Reed, K. M., Sneling, W. M., Kappes, S. M., Beattie, C. W., Bennett, G. L. and Sugimoto, Y.  
 TITLE A comprehensive genetic map of the cattle genome based on 3802 microsatellites  
 JOURNAL Genome Res. 14 (10), 1987-1998 (2004)  
 PUBMED 15466297  
 REFERENCE 2 (bases 1 to 21)  
 AUTHORS Sugimoto, Y., Ihara, N. and Takasuga, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shiraoka Institute of Animal Genetics, Odakura, Nishigo, Niishi-Shirakawa, Fukushima 961-8061, Japan (E-mail: kazusug@isag.or.jp, Tel:81-248-25-5641, Fax:81-248-25-5725)  
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 /mol\_type="other DNA"  
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 /chromosome="4"  
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 /note="reverse primer for microsatellite DIK4617"  
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 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 Db 19 CTCCTCTCTCTCTCTCC 1  
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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GenEmbl: \*  
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2: gb\_pat: \*  
3: gb\_ph: \*  
4: gb\_pl: \*  
5: gb\_pr: \*  
6: gb\_ro: \*  
7: gb\_sts: \*  
8: gb\_sy: \*  
9: gb\_un: \*  
10: gb\_vl: \*  
11: gb\_ov: \*  
12: gb\_hcg: \*  
13: gb\_in: \*  
14: gb\_cm: \*  
15: gb\_da: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	21.6	9.2	41	2	AX516672 Sequence
3	21.6	9.2	41	2	AX518841 Sequence
4	21.2	9.0	49	2	BD190591 Bioreact1
5	21.2	9.0	49	2	AR405844 Sequence
6	20.8	8.8	43	2	I41116 Sequence 19
7	20.8	8.8	43	2	I41117 Sequence 20
8	19.8	8.4	50	2	CQ004290 Sequence
9	19.6	8.3	50	2	AR681155 Sequence
10	19.4	8.2	45	2	AR147108 Sequence
11	19.4	8.2	45	2	AR158296 Sequence
12	19.4	8.2	45	2	AR267871 Sequence
13	19.4	8.2	45	2	AR365906 Sequence
14	19.4	8.2	50	2	AR684817 Sequence
15	19.4	8.2	50	2	AR684983 Sequence
16	19.2	8.1	50	2	AR682008 Sequence
17	19.2	8.1	50	2	AX162664 Sequence
18	19	8.1	36	2	E13977 PCR primer

19	19	8.1	36	2	E14911	E14911 PCR primer
20	19	8.1	36	2	E64709	E64709 Anti-pathog
21	19	8.1	36	2	AR559761	AR559761 Sequence
22	19	8.1	42	2	AX512498	AX512498 Sequence
23	19	8.1	42	2	AX573414	AX573414 Sequence
24	19	8.1	42	2	AX746300	AX746300 Sequence
25	19	8.1	43	2	AR238006	AR238006 Sequence
26	19	8.1	50	2	E25630	E25630 RNA-DNA chl
27	19	8.1	50	2	AR682371	AR682371 Sequence
28	18.8	8.0	37	2	CQ004681	CQ004681 Sequence
29	18.6	7.9	49	2	E29443	E29443 Oligonucleo
30	18.6	7.9	49	2	I05520	I05520 Sequence 8
31	18.6	7.9	50	2	CQ002636	CQ002636 Sequence
32	18.6	7.9	50	2	AR682820	AR682820 Sequence
33	18.4	7.8	41	2	AX516639	AX516639 Sequence
34	18.4	7.8	41	2	AX518809	AX518809 Sequence
35	18.4	7.8	47	2	AR289030	AR289030 Sequence
36	18.4	7.8	50	2	BD223995	BD223995 Near infr
37	18.4	7.8	50	2	AR200395	AR200395 Sequence
38	18.4	7.8	50	2	AR682631	AR682631 Sequence
39	18.2	7.7	39	2	CQ970252	CQ970252 Sequence
40	18.2	7.7	41	2	AX516265	AX516265 Sequence
41	18.2	7.7	41	2	AX518600	AX518600 Sequence
42	18.2	7.7	44	2	AR210406	AR210406 Sequence
43	18.2	7.7	44	2	I90213	I90213 Sequence 39
44	18.2	7.7	47	2	BD204757	BD204757 Method of
45	18.2	7.7	47	2	AR290979	AR290979 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS BX545753  
DEFINITION Arabidopsis thaliana transposon insertion STS SM\_3.36298, sequence tagged site.  
ACCESSION BX545753  
VERSION BX545753.1 GI:32168986  
KEYWORDS STS, sequence tagged site.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Walsh,S., Langham,S., Legry,C., Jones,J.D.G. and Bevan,M.





Db 35 CCGCTGTCTCATCTCCAGCTCTACCTTGCTG 2

RESULT 6  
LOCUS 141116 43 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 19 from patent US 5624803.  
ACCESSION 141116  
VERSION 141116.1 GI:2081706  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 43)  
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.  
TITLE In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom  
JOURNAL Patent: US 5624803-A 19 29-APR-1997;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Query Match 8.8%; Score 20.8; DB 2; Length 43;  
Best Local Similarity 78.1%; Pred. No. 6.9e+05;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168  
Db 10 CTCCTCTCCACTCTCTCTCTCTGATTT 41

RESULT 7  
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DEFINITION Sequence 20 from patent US 5624803.  
ACCESSION 141117  
VERSION 141117.1 GI:2081707  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 43)  
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.  
TITLE In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom  
JOURNAL Patent: US 5624803-A 20 29-APR-1997;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 8.8%; Score 20.8; DB 2; Length 43;  
Best Local Similarity 78.1%; Pred. No. 6.9e+05;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168  
Db 34 CTCCTCTCCACTCTCTCTCTCTGATTT 3

RESULT 8  
LOCUS CQ004290 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 2330 from Patent WO0147944.  
ACCESSION CQ004290  
VERSION CQ004290.1 GI:41010922  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shimkete,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 2930 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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/note="Nucleotide deleted between bases 25 and 26  
Accession number cg43976335"

ORIGIN  
Query Match 8.4%; Score 19.8; DB 2; Length 50;  
Best Local Similarity 69.2%; Pred. No. 1.3e+06;  
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 88 GAAAGAGCTGGCCCTCTCATTTCTGCTCCGACATC 126  
Db 12 GAAAGGCTATGCCCTCCACTCCCTCTCTACCATC 50

RESULT 9  
LOCUS AR681155 50 bp DNA linear PAT 12-SEP-2005  
DEFINITION Sequence 584 from patent US 6905827.  
ACCESSION AR681155  
VERSION AR681155.1 GI:74462925  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wohlgemuth,J., Fry,K., Woodward,R. and Ly,N.  
TITLE Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases  
JOURNAL Patent: US 6905827-A 584 14-JUN-2005;  
Expression Diagnostics, Inc.; So. San Francisco, CA  
FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

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Query Match 8.3%; Score 19.6; DB 2; Length 50;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGTGTTTGAAGAAGCTGGCCCTCTCATTT 112  
Db 6 GTGAGCCGTGTGTTTAAATATCTCTTCCCATGTCATTC 47

RESULT 10  
LOCUS AR147108 45 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 210 from patent US 6221361.  
ACCESSION AR147108  
VERSION AR147108.1 GI:15110911  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Cochran,M.D. and Junker,D.E.  
TITLE Recombinant swinepox virus

JOURNAL Patent: US 6221361-A 210 24-APR-2001;  
FEATURES Location/Qualifiers

source

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Best Local Similarity 70.3%; Pred. No. 1.8e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTGTTCTGTCGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 11  
LOCUS AR158296 45 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 210 from patent US 6251403.  
ACCESSION AR158296  
VERSION AR158296.1 GI:16220314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)  
AUTHORS Cochran,M.D. and Junker,D.E.  
TITLE Recombinant swinepox virus  
JOURNAL Patent: US 6251403-A 210 26-JUN-2001;  
FEATURES Location/Qualifiers

source

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ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;  
Best Local Similarity 70.3%; Pred. No. 1.8e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTGTTCTGTCGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 12  
LOCUS AR267871 45 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 210 from patent US 6497882.  
ACCESSION AR267871  
VERSION AR267871.1 GI:29697996  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)  
AUTHORS Cochran,M.D. and Junker,D.E.  
TITLE Recombinant swinepox virus  
JOURNAL Patent: US 6497882-A 210 24-DEC-2002;  
FEATURES Location/Qualifiers

source

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/organism="unknown"  
/mol\_type="genomic DNA"

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Query Match 8.2%; Score 19.4; DB 2; Length 45;  
Best Local Similarity 70.3%; Pred. No. 1.8e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTGTTCTGTCGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 13  
LOCUS AR365906 45 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 210 from patent US 6328975.  
ACCESSION AR365906  
VERSION AR365906.1 GI:34598093  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)  
AUTHORS Cochran,M.D. and Junker,D.E.  
TITLE Recombinant swinepox virus  
JOURNAL Patent: US 6328975-A 210 11-DEC-2001;  
FEATURES Location/Qualifiers

source

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/organism="unknown"  
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ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;  
Best Local Similarity 70.3%; Pred. No. 1.8e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTGTTCTGTCGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 14  
LOCUS AR684817 50 bp DNA linear PAT 12-SEP-2005  
DEFINITION Sequence 4246 from patent US 6905827.  
ACCESSION AR684817  
VERSION AR684817.1 GI:74466587  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Wolgemuth,J., Fry,K., Woodward,R. and Ly,N.  
TITLE Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases  
JOURNAL Patent: US 6905827-A 4246 14-JUN-2005;  
FEATURES Expression Diagnostics, Inc.; So. San Francisco, CA  
Location/Qualifiers

source

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ORIGIN

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Best Local Similarity 79.3%; Pred. No. 1.8e+06;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 104 CTCTCATTCCTCTGCTCCCATCTTGCAAT 132

DB 22 CCTCATCTCTCTGCTCACTCTCTTCAT 50

RESULT 15  
LOCUS AR684983 50 bp DNA linear PAT 12-SEP-2005  
DEFINITION Sequence 4412 from patent US 6905827.  
ACCESSION AR684983  
VERSION AR684983.1 GI:74466753  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

Query Match 8.2%; Score 19.4; DB 2; Length 50;  
Best Local Similarity 79.3%; Pred. No. 1.8e+06;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 104 CTCTCATTCCTCTGCTCCCATCTTGCAAT 132

DB 22 CCTCATCTCTCTGCTCACTCTCTTCAT 50

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REFERENCE 1 (bases 1 to 50)
AUTHORS  Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
TITLE     Methods and compositions for diagnosing or monitoring auto immune
          and chronic inflammatory diseases
JOURNAL   Patent: US 6905827-A 4412 14-JUN-2005;
          Expression Diagnostics, Inc.; So. San Francisco, CA
FEATURES  Location/Qualifiers
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ORIGIN

Query Match      8.2%; Score 19.4; DB 2; Length 50;
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Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCCACTTTCATGAGACA 138
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DB      13 TTATCTGCTCCACTATGACATGATCA 41
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## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.2	7.5	25	1	US-09-396-196G-18892
2	15.8	6.5	21	1	US-09-657-472-768
3	15.6	6.4	22	1	US-10-085-612A-23
4	15.2	6.3	20	1	US-09-216-393B-262
5	15.2	6.3	21	1	US-09-526-193A-240
6	15	6.2	18	1	US-08-846-020A-32
7	15	6.2	18	1	US-09-617-871-32
8	15	6.2	21	1	US-09-657-472-1850
9	14.2	5.9	20	1	US-09-021-701-404
10	14.2	5.9	20	1	US-09-021-701-405
11	14.2	5.9	20	1	US-09-487-368A-97
12	14.2	5.9	20	1	US-09-629-644A-97
13	14.2	5.9	20	1	US-09-629-644A-97
14	14.2	5.9	20	1	US-09-198-452A-3809
15	14.2	5.9	20	1	US-09-198-452A-6637
16	14.2	5.9	20	1	US-09-495-714C-138
17	14.2	5.9	20	1	US-09-601-844B-23
18	14.2	5.9	20	1	US-09-726-345-2
19	14.2	5.9	20	1	US-10-209-405-27
20	14.2	5.9	20	1	US-10-209-405-96
21	13.8	5.7	19	1	US-09-422-978-6418
22	13.4	5.5	17	1	US-10-156-306B-6888
23	13.4	5.5	17	1	US-10-156-306B-6889
24	13.4	5.5	18	1	US-08-632-673B-9
25	13.4	5.5	18	1	US-09-357-072-17
26	13.4	5.5	18	1	US-08-652-265-17
27	13.4	5.5	18	1	US-08-834-497A-17
28	13.4	5.5	18	1	US-09-503-444A-17
29	13.4	5.5	18	1	US-09-341-700A-294
30	13.4	5.5	19	1	US-08-546-130A-24
31	13.4	5.5	19	1	US-08-680-395-32
32	13.4	5.5	19	1	US-09-066-641-31
33	13.4	5.5	19	1	US-08-893-695-45

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34	13.2	5.5	18	1	US-08-572-126-3	Sequence 3, Appl
35	13.2	5.5	18	1	US-09-003-199-17	Sequence 17, Appl
36	13.2	5.5	18	1	US-09-003-199-19	Sequence 19, Appl
37	13.2	5.5	18	1	US-08-757-023A-3	Sequence 3, Appl
38	13.2	5.5	18	1	US-08-651-155B-1	Sequence 1, Appl
39	13.2	5.5	18	1	US-09-321-797-3	Sequence 3, Appl
40	13.2	5.5	18	1	US-10-006-937-7	Sequence 7, Appl
41	13.2	5.5	18	1	US-09-194-036B-1	Sequence 1, Appl
42	13	5.4	17	1	US-09-866-108A-9217	Sequence 9217, Ap
43	13	5.4	17	1	US-09-866-108A-9218	Sequence 9218, Ap
44	13	5.4	17	1	US-09-866-108A-9219	Sequence 9219, Ap
45	13	5.4	17	1	US-09-866-108A-9220	Sequence 9220, Ap
46	13	5.4	17	1	US-09-866-108A-9221	Sequence 9221, Ap
47	12.8	5.3	17	1	US-08-584-040-5554	Sequence 5754, Ap
48	12.8	5.3	17	1	US-09-474-432B-580	Sequence 580, Ap
49	12.8	5.3	17	1	US-09-371-772B-2633	Sequence 2633, Ap
50	12.8	5.3	17	1	US-09-476-387-579	Sequence 579, Ap
51	12.8	5.3	17	1	US-09-866-108A-119	Sequence 119, Ap
52	12.8	5.3	17	1	US-09-866-108A-120	Sequence 120, Ap
53	12.8	5.3	17	1	US-09-866-108A-1319	Sequence 1319, Ap
54	12.8	5.3	17	1	US-09-866-108A-1320	Sequence 1320, Ap
55	12.8	5.3	17	1	US-09-866-108A-5889	Sequence 5889, Ap
56	12.8	5.3	17	1	US-09-866-108A-5890	Sequence 5890, Ap
57	12.8	5.3	17	1	US-09-866-108A-7503	Sequence 7503, Ap
58	12.8	5.3	17	1	US-09-866-108A-7504	Sequence 7504, Ap
59	12.8	5.3	17	1	US-09-685-664B-2633	Sequence 2633, Ap
60	12.8	5.3	17	1	US-10-156-306B-4949	Sequence 4949, Ap
61	12.8	5.3	17	1	US-10-138-674B-2633	Sequence 2633, Ap
62	12.8	5.3	18	1	US-09-280-409-127	Sequence 127, Ap
63	12.8	5.3	18	1	US-09-344-520-29	Sequence 29, Appl
64	12.8	5.3	18	1	US-09-474-922A-42	Sequence 42, Appl
65	12.8	5.3	18	1	US-09-475-947A-333	Sequence 333, Appl
66	12.8	5.3	18	1	US-09-544-338B-406	Sequence 406, Appl
67	12.8	5.3	18	1	US-09-543-771B-406	Sequence 406, Appl
68	12.4	5.1	17	1	US-08-758-306-691	Sequence 691, Appl
69	12.4	5.1	17	1	US-08-292-620A-1715	Sequence 1715, Ap
70	12.4	5.1	17	1	US-08-292-620A-1918	Sequence 1918, Ap
71	12.4	5.1	17	1	US-08-292-620A-1952	Sequence 1952, Ap
72	12.4	5.1	17	1	US-09-071-845-1715	Sequence 1715, Ap
73	12.4	5.1	17	1	US-09-071-845-1918	Sequence 1918, Ap
74	12.4	5.1	17	1	US-09-071-845-1952	Sequence 1952, Ap
75	12.4	5.1	17	1	US-08-834-497A-49	Sequence 49, Appl
76	12.4	5.1	17	1	US-08-834-497A-50	Sequence 50, Appl
77	12.4	5.1	17	1	US-08-866-108A-5891	Sequence 5891, Ap
78	12.4	5.1	17	1	US-08-866-108A-5892	Sequence 5892, Ap
79	12.4	5.1	17	1	US-10-156-306B-5820	Sequence 5820, Ap

ALIGNMENTS

RESULT 1  
US-09-396-196G-18892  
Sequence 18892, Application US/09396196G  
Parent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mitmann  
APPLICANT: David Mack  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09396,196G  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18892  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-18892

Query Match 7.5%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGCAGCTGATTT 23  
Db 3 TTCTCCAGCAGCAGCTGATTT 25

## RESULT 2

US-09-657-472-768/c  
Sequence 768, Application US/09657472  
Patent No. 6727063  
GENERAL INFORMATION:  
APPLICANT: Lander, Eric S.  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Bolik, Stacey  
APPLICANT: Daley, George O.  
APPLICANT: McCarthy, Jeanette J.  
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
FILE REFERENCE: 2825.1027-001  
CURRENT FILING DATE: 2000-09-07  
CURRENT APPLICATION NUMBER: US/09/657,472  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 60/153,357  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: US 60/220,947  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 60/225,724  
NUMBER OF SEQ ID NOS: 2551  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 768  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-657-472-768

Query Match 6.5%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 10;  
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCGACGACGACTGATTT 23  
Db 21 CTCGACGACGACTGATTT 1

## RESULT 3

US-10-085-612A-23  
Sequence 23, Application US/10085612A  
Patent No. 6929912  
GENERAL INFORMATION:  
APPLICANT: Guida, Marco  
APPLICANT: Hall, Jeff  
APPLICANT: Petros, William  
APPLICANT: Colvin, Oliver  
APPLICANT: Vredenburgh, James  
APPLICANT: Marks, Jeffrey  
TITLE OF INVENTION: METHODS FOR EVALUATING THE ABILITY TO METABOLIZE PHARMACEUTICALS  
FILE REFERENCE: DNA-5-C1  
CURRENT FILING DATE: 2002-02-26  
CURRENT APPLICATION NUMBER: US/10/085,612A  
PRIOR FILING DATE: 1998-08-31/144,367  
PRIOR APPLICATION NUMBER: 60/271,630  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 23  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-085-612A-23

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 11;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 56 CTGCTGCTCAGCTGCTTTCC 77  
Db 1 CTGAGCCCACTCTTCTCC 22

## RESULT 4

US-09-216-393B-262  
Sequence 262, Application US/09216393B  
Patent No. 6514694  
GENERAL INFORMATION:  
APPLICANT: Milhausen, Michael James  
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: TX-1-C2  
CURRENT FILING DATE: 1998-12-18  
CURRENT APPLICATION NUMBER: US/09/216,393B  
PRIOR FILING DATE: 1997-12-19  
PRIOR APPLICATION NUMBER: 08/994,825  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 262  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Primer  
US-09-216-393B-262

Query Match 6.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 189 TGTCTGTAGGTTGTCTAG 208  
Db 1 TGGCTGTTGGCTTGTCTGG 20

## RESULT 5

US-09-526-193A-240  
Sequence 240, Application US/09526193A  
Patent No. 6617122  
GENERAL INFORMATION:  
APPLICANT: Hayden, Michael R.  
APPLICANT: Brooks-Wilson, Angela R.  
APPLICANT: Pimstone, Simon N.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
FILE REFERENCE: 50110/002005  
CURRENT FILING DATE: 2000-03-15  
CURRENT APPLICATION NUMBER: US/09/526,193A  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 240  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-526-193A-240

Query Match 6.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 13;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 58 GGTGCTCACCCTTTCC 77  
|||  
Db 1 GCAGCTCACCCTTTCC 20

RESULT 6  
US-08-846-020A-32  
; Sequence 32, Application US/08846020A  
; Patent No. 6090547  
; GENERAL INFORMATION:  
; APPLICANT: Drazen M.D., Jeffrey M.  
; APPLICANT: In M.D., Kwang-Ho  
; APPLICANT: Asano M.D., Koichiro  
; APPLICANT: Beier, David  
; APPLICANT: Grobholz, James  
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence  
; TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHOATE, HALL & STEWART  
; STREET: 53 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2891  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,020A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jarrell Ph.D., Brenda H.  
; REGISTRATION NUMBER: 39,223  
; REFERENCE/DOCKET NUMBER: 0092662-0012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-5000  
; TELEFAX: (617) 248 4000  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
; IMMEDIATE SOURCE:  
; CLONE: Exon 9 sense primer  
; US-08-846-020A-32

Query Match 6.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CCTCCCGAGCTGCTG 61  
|||  
Db 2 CCTCCCGAGCTGCTG 16

RESULT 7  
US-09-617-871-32  
; Sequence 32, Application US/09617871  
; Patent No. 6355434  
; GENERAL INFORMATION:  
; APPLICANT: Drazen M.D., Jeffrey M.  
; APPLICANT: In M.D., Kwang-Ho  
; APPLICANT: Asano M.D., Koichiro  
; APPLICANT: Beier, David

APPLICANT: Grobholz, James  
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence  
; TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHOATE, HALL & STEWART  
; STREET: 53 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2891  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/617,871  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,020  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jarrell Ph.D., Brenda H.  
; REGISTRATION NUMBER: 39,223  
; REFERENCE/DOCKET NUMBER: 0092662-0012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-5000  
; TELEFAX: (617) 248 4000  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
; IMMEDIATE SOURCE:  
; CLONE: Exon 9 sense primer  
; US-09-617-871-32

Query Match 6.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CCTCCCGAGCTGCTG 61  
|||  
Db 2 CCTCCCGAGCTGCTG 16

RESULT 8  
US-09-657-472-1850/C  
; Sequence 1850, Application US/09657472  
; Patent No. 6727063  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolik, Stacey  
; APPLICANT: Daley, George O.  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
; FILE REFERENCE: 2825.1027-001  
; CURRENT APPLICATION NUMBER: US/09/657,472  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/153,357  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 60/220,947  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: US 60/225,724  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2551





US-09-487-368A-97

## Query Match

Best Local Similarity 5.9%; Score 14.2; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGTCG 62  
1 CAACCTCCCGAGCGGC 19RESULT 12  
US-09-629-644A-97

Sequence 97, Application US/09629644A

Patent No. 6492345

GENERAL INFORMATION:

APPLICANT: Lex M. Cowbert

APPLICANT: Jacqueline Wyatt

APPLICANT: Susan M. Freiler

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: ISPH-0478

CURRENT APPLICATION NUMBER: US/09/629,644A

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/487,368

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 97

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-629-644A-97

Query Match 5.9%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGTCG 62  
1 CAACCTCCCGAGCGGC 19RESULT 13  
US-09-629-644A-97

Sequence 97, Application US/09629644A

Patent No. 6602857

GENERAL INFORMATION:

APPLICANT: Lex M. Cowbert

APPLICANT: Jacqueline Wyatt

APPLICANT: Susan M. Freiler

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: ISPH-0478

CURRENT APPLICATION NUMBER: US/09/629,644A

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/487,368

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 97

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-629-644A-97

Query Match 5.9%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGTCG 62  
1 CAACCTCCCGAGCGGC 19RESULT 14  
US-09-198-452A-3809/C

Sequence 3809, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Grifflais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

PRIOR FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 3809

LENGTH: 20

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3809

Query Match 5.9%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

122 CCTGTTCCATCTTTG 140  
19 CCTGTTCCATCTTTG 1RESULT 15  
US-09-198-452A-6637/C

Sequence 6637, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Grifflais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

PRIOR FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 6637

LENGTH: 20

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-6637

Query Match 5.9%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

58 GCTGCTCACCTGCTTTC 76  
20 GCTGCTCACCTGCTTTC 2RESULT 16  
US-09-495-714C-138/C

Sequence 138, Application US/09495714C

Patent No. 6670465

GENERAL INFORMATION:

APPLICANT: University Technologies International Inc.

TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE

FILE REFERENCE: 45499.4 (formerly 45074.6)

CURRENT APPLICATION NUMBER: US/09/495,714C

US-09-495-714C-138/C

Query Match 5.9%; Score 14.2; DB 1; Length 20;

; CURRENT FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 138  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-495-714C-138

Query Match 5.9%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 AGCAGACGACTGGATTG 25  
Db 19 ACCGACTCTCGATTG 1

RESULT 17  
US-09-601-844B-23/C  
; Sequence 23 Application US/09601844B  
; Patent No. 6716621  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, No. 6716621yoshi  
; APPLICANT: Mizuno, Yoshihumi  
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease  
; FILE REFERENCE: 0652 210000  
; CURRENT APPLICATION NUMBER: US/09/601,844B  
; CURRENT FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: PCT/JP99/00545  
; PRIOR FILING DATE: 1999-02-09  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(10)  
; OTHER INFORMATION: Exon 8  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (11)..(20)  
; OTHER INFORMATION: Intron  
US-09-601-844B-23

Query Match 5.9%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 58 GCTGCTCCTGCTGCTTTC 76  
Db 20 GCTCCTCCTGCTGCTTTC 2

RESULT 18  
US-09-726-345-2  
; Sequence 2 Application US/09726345  
; Patent No. 6855521  
; GENERAL INFORMATION:  
; APPLICANT: Naval Medical Research Center  
; TITLE OF INVENTION: Serotype and Dengue Group Specific Fluorogenic Probe-Based PCR  
; TITLE OF INVENTION: (TagMan) Assays Against the Respective C and NS5 Genomic and 3'  
; TITLE OF INVENTION: No. 6855521-Coding Regions of Dengue Virus  
; FILE REFERENCE: NC 82197  
; CURRENT APPLICATION NUMBER: US/09/726,345  
; CURRENT FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: DNA

; ORGANISM: Dengue virus  
US-09-726-345-2

Query Match 5.9%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 CACCTGAGCTGAGCTCCA 46  
Db 1 CACCTGAGCTGAGCTCCA 19

RESULT 19  
US-10-209-405-27/C  
; Sequence 27 Application US/10209405  
; Patent No. 6906186  
; GENERAL INFORMATION:  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freiler  
; TITLE OF INVENTION: ANTISENSE MODULATION OF POLO-LIKE KINASE EXPRESSION  
; FILE REFERENCE: RTS-0131  
; CURRENT APPLICATION NUMBER: US/10/209,405  
; CURRENT FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 129  
; SEQ ID NO 27  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-209-405-27

Query Match 5.9%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 TCTCAGCTGAGCTGACCA 166  
Db 20 TCTCCTGAGCTGACCA 2

RESULT 20  
US-10-209-405-96  
; Sequence 96 Application US/10209405  
; Patent No. 6906186  
; GENERAL INFORMATION:  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freiler  
; TITLE OF INVENTION: ANTISENSE MODULATION OF POLO-LIKE KINASE EXPRESSION  
; FILE REFERENCE: RTS-0131  
; CURRENT APPLICATION NUMBER: US/10/209,405  
; CURRENT FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 129  
; SEQ ID NO 96  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-209-405-96

Query Match 5.9%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 TCTCAGCTGAGCTGACCA 166  
Db 1 TCTCCTGAGCTGACCA 19

RESULT 21  
US-09-422-978-6418/C  
; Sequence 6418 Application US/09422978  
; Patent No. 6537751

```

; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Bacterial markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6418
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11313 for SEQ 2484,
US-09-422-978-6418

Query Match          5.7%  Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%  Pred. No. 20;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      165 CAGACGACCTGTTAG 181
DB      17 CATACGACCTGATTAG 1

RESULT 22
US-10-156-306B-6888/C
; Sequence 6888, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSW19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6888

Query Match          5.5%  Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%  Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      38 GGAGCTCCACCTCCC 52
DB      16 GGTCCTCCACCTCCC 2

RESULT 23
US-10-156-306B-6889/C
; Sequence 6889, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSW19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
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; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6889
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6889

Query Match          5.5%  Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%  Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      38 GGAGCTCCACCTCCC 52
DB      15 GGTCCTCCACCTCCC 1

RESULT 24
US-08-632-673B-9/C
; Sequence 9, Application US/08632673B
; Patent No. 5712098
; GENERAL INFORMATION:
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Gnikre, Andreas
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Ruddy, David
; APPLICANT: Wolff, Roger K.
; APPLICANT: Feder, John N.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
; TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREM LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,673B
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 017957-000410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-632-673B-9

Query Match          5.5%  Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%  Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      35 CTGGAGCTCCACCT 49
```

```
Db      17  CTGGGTCTCCACCT 3
      ||||| ||||| |||||
RESULT 25
US-09-357-072-17/c
; Sequence 17, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-17

Query Match      5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      162  GACGACGACGACCTG 176
      ||||| ||||| |||||
Db      18  GACGACGACGACCTG 4
      ||||| ||||| |||||

RESULT 26
US-08-652-265-17/c
; Sequence 17, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Galtke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated
; OTHER INFORMATION: guanine (G-dig)"
US-08-652-265-17

Query Match      5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      35  CTGGGAGCTCCACCT 49
      ||||| ||||| |||||
Db      17  CTGGGTCTCCACCT 3
      ||||| ||||| |||||

RESULT 27
US-08-834-497A-17/c
; Sequence 17, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Galtke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Penile & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
```

REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0056-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0088-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 18  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated  
OTHER INFORMATION: guanine (G-dig)"  
US-08-834-497A-17

Query Match 5.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 22;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 CTGGAGCTCCACCT 49  
DB 17 CTGGGTGCTCCACCT 3

RESULT 28  
US-09-503-444A-17/C  
Sequence 17, Application US/09503444A  
Patent No. 6228594  
GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
APPLICANT: Drayna, Dennis T.  
APPLICANT: Feder, John N.  
APPLICANT: Gnirke, Andreas  
APPLICANT: Ruddy, David  
APPLICANT: Tsuchihashi, Zenta  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect Version 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/503,444A  
FILING DATE: 14-Feb-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/652,265  
FILING DATE: 23-May-1996  
APPLICATION NUMBER: 08/632,673  
FILING DATE: 16-Apr-1996  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/630,912  
FILING DATE: 04-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0088-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 18  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated  
OTHER INFORMATION: guanine (G-dig)"  
US-09-503-444A-17

Query Match 5.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 22;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 CTGGAGCTCCACCT 49  
DB 17 CTGGGTGCTCCACCT 3

RESULT 29  
US-09-341-700A-294/C  
Sequence 294, Application US/09341700A  
Patent No. 6372171  
GENERAL INFORMATION:  
APPLICANT: Schlingensiepen, Karl-Hermann  
APPLICANT: Brysch, Wolfgang  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
FILE REFERENCE: 10496/P63763USO  
CURRENT APPLICATION NUMBER: US/09/341,700A  
CURRENT FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: PCT/EP98/00497  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: EP 97 101 531.8  
PRIOR FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 1764  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 294  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: antisense oligonucleotide  
US-09-341-700A-294

Query Match 5.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 22;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 CCAAGTGTGCTGCTCA 66  
DB 15 CCAAGTGTGCTGCTCA 1

```
RESULT 30
US-08-546-130A-24/C
; Sequence 24, Application US/08546130A
; Patent No. 5801021
; GENERAL INFORMATION:
; APPLICANT: Gray, Joe W.
; APPLICANT: Collins, Colin
; APPLICANT: Pinkel, Daniel
; APPLICANT: Kallioniemi, Olli-Pekka
; APPLICANT: Tanner, Minna M.
; TITLE OF INVENTION: Amplifications of Chromosomal Region
; TITLE OF INVENTION: 20q13 as a Prognostic Indicator in Breast Cancer
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/546,130A
; FILING DATE: 20-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-051630US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-546-130A-24

Query Match 5.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
Db 16 TTCTCCAGCAGACA 2

RESULT 31
US-08-680-395-32/C
; Sequence 32, Application US/08680395
; Patent No. 5892010
; GENERAL INFORMATION:
; APPLICANT: Gray, Joe W.
; APPLICANT: Collins, Colin
; APPLICANT: Hwang, Soo-in
; APPLICANT: Godfrey, Tony
; APPLICANT: Kowdel, David
; APPLICANT: Rommens, Johanna
; TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
; TITLE OF INVENTION: 20q13 as a Prognostic Indicator in Breast Cancer
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
```

```
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,395
; FILING DATE: 15-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 02307O-068900US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-680-395-32

Query Match 5.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
Db 16 TTCTCCAGCAGACA 2

RESULT 32
US-09-066-641-31/C
; Sequence 31, Application US/09066641
; Patent No. 6268184
; GENERAL INFORMATION:
; APPLICANT: GRAY, JOE W
; APPLICANT: COLLINS, COLIN
; APPLICANT: PINKEL, DANIEL
; APPLICANT: KALLIONIEMI, OLLI-PEKKA
; APPLICANT: TANNER, MINNA M
; TITLE OF INVENTION: AMPLIFICATIONS OF CHROMOSOMAL REGION 20Q13 AS A
; TITLE OF INVENTION: PROGNOSTIC INDICATOR IN BREAST CANCER
; FILE REFERENCE: 2500.136US2 20Q13
; CURRENT APPLICATION NUMBER: US/09/066,641
; CURRENT FILING DATE: 1998-04-24
; EARLIER APPLICATION NUMBER: 08/546,130
; EARLIER FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: reverse
; OTHER INFORMATION: primer
US-09-066-641-31

Query Match 5.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
Db 16 TTCTCCAGCAGACA 2
```

```
RESULT 33
US-08-892-695-45/c
Sequence 45, Application US/08892695A
Patent No. 6808878
GENERAL INFORMATION:
APPLICANT: Gray, Joe W
APPLICANT: Collins, Collin
APPLICANT: Hwang, Soo In
APPLICANT: Godfrey, Tony
APPLICANT: Kowel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: GENES FROM THE 20Q13 AMPLICON AND THEIR USES
FILE REFERENCE: 2500.124US3
CURRENT APPLICATION NUMBER: US/08/892,695A
CURRENT FILING DATE: 1997-07-15
EARLIER APPLICATION NUMBER: 08/785,532
EARLIER FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: 08/731,499
EARLIER FILING DATE: 1996-10-16
EARLIER APPLICATION NUMBER: 08/680,395
EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Backward
US-08-892-695-45

Query Match      5.5% Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTCCACGACGCA 15
Db      16 TTCTCCACGACGCA 2

RESULT 34
US-08-572-126-3
Sequence 3, Application US/08572126
Patent No. 5851806
GENERAL INFORMATION:
APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas E.
APPLICANT: Mcvey, Duncan L.
APPLICANT: Bruder, Joseph T.
APPLICANT: Lizonova, Alea
TITLE OF INVENTION: COMPLEMENTARY ADENO VIRAL VECTOR SYSTEMS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 08/258416
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kilya Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 74273
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-572-126-3

Query Match      5.5% Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      58 GCTGCTCACCCTGCTTT 75
Db      1 GCCGCTCATCCGCTTT 18
```

```
RESULT 35
US-09-003-199-17
Sequence 17, Application US/09003199
Patent No. 5985616
GENERAL INFORMATION:
APPLICANT: Parker, Eric M
APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPV Y5 RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: NJ
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,199
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thampoe, Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN0775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-5061
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-003-199-17

Query Match      5.5% Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 156 GGAGCTGAACAGACGAC 173  
|||||  
Db 1 GGAGCAAAACGACGAC 18

## RESULT 36

US-09-003-199-19  
Sequence 19, Application US/09003199  
Patent No. 5985616  
GENERAL INFORMATION:  
APPLICANT: Parker, Eric M  
APPLICANT: Strader, Catherine D  
APPLICANT: Rudinski, Mark S  
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: NJ  
COUNTRY: USA  
ZIP: 07033-0530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.5.3  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,199  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Thampoe, Immac J.  
REGISTRATION NUMBER: 36,322  
REFERENCE/DOCKET NUMBER: CU0775  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)298-5061  
TELEFAX: (908)298-5388  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-003-199-19

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 156 GGAGCTGAACAGACGAC 173  
|||||  
Db 1 GGAGCAAAACGACGAC 18

## RESULT 37

US-08-757-023A-3  
Sequence 3, Application US/08757023A  
Patent No. 5994106  
GENERAL INFORMATION:  
APPLICANT: Kovesdi, Imre  
APPLICANT: Brough, Douglas E.  
APPLICANT: McVey, Duncan L.  
APPLICANT: Bruder, Joseph T.  
APPLICANT: Lizanova, Alena  
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydis, Voic & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,023A  
FILING DATE: 26-NOV-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: 514  
APPLICATION NUMBER: US 08/258416  
FILING DATE: 10-JUN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilyk Jr., John  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 74273  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-757-023A-3

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 58 GCTGCTCACTGCTTTT 75  
|||||  
Db 1 GCGGCTCATCGCTTTT 18

## RESULT 38

US-08-651-155B-1  
Sequence 1, Application US/08651155B  
Patent No. 6365401  
GENERAL INFORMATION:  
APPLICANT: Mahan Dr., Michael J.  
APPLICANT: Conner Mr., Christopher P.  
APPLICANT: Hiethoff Mr., Douglas M.  
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION  
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST  
NUMBER OF SEQUENCES: 255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chrisman, Bynum & Johnson, P.C.  
STREET: 1900 Fifteenth Street  
CITY: Boulder  
STATE: CO  
COUNTRY: USA  
ZIP: 80302  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,155B  
FILING DATE: 17-MAY-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Peteren Mr., Steven C.  
REGISTRATION NUMBER: 36,238  
REFERENCE/DOCKET NUMBER: 17060.1



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/546-1300  
TELEFAX: 303/449-5426  
TELEX: ABA1475  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-651-155B-1

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 104 CATTGTGCGCCACTAG 121  
Db 1 CATTGCGTCCACTAG 18

RESULT 39  
US-09-321-797-3  
Sequence 3, Application US/09321797  
Patent No. 6482616  
GENERAL INFORMATION:  
APPLICANT: Koveadi, Imre  
Brough, Douglas E.  
Mcvey, Duncan L.  
Bruder, Joseph T.  
Lizanova, Alena  
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS  
AND CELL LINES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/321,797  
FILING DATE: 27-May-1999  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,023A  
FILING DATE: 26-Nov-1996  
APPLICATION NUMBER: US 08/258416  
FILING DATE: 10-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilyk Jr., John  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 74273  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5700  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-321-797-3

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 58 GCTGCTTACCTGCTTT 75  
Db 1 GCGCTTATCTCGCTTT 18

RESULT 40  
US-10-006-937-7  
Sequence 7, Application US/10006937  
Patent No. 6518047  
GENERAL INFORMATION:  
APPLICANT: Joniaux, Jean-Luc  
APPLICANT: Rauw, Karl  
APPLICANT: Thonart, Philippe  
APPLICANT: Davarin, Thierry  
TITLE OF INVENTION: ENZYME OR CELL PREPARATION WITH  
TITLE OF INVENTION: INULINASE ACTIVITY  
FILE REFERENCE: VANM237.001AUS  
CURRENT APPLICATION NUMBER: US/10/006,937  
CURRENT FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: EP 00870264.9  
PRIOR FILING DATE: 2000-11-09  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer for sequencing  
US-10-006-937-7

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TCTCAGCAGCAGCTG 19  
Db 1 TCTCCTGTAAGCACTG 18

RESULT 41  
US-09-194-036B-1  
Sequence 1, Application US/09194036B  
Patent No. 6548246  
GENERAL INFORMATION:  
APPLICANT: Mahan, Michael J.  
Conner, Christopher P.  
Hiehoff, Douglas M.  
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION  
OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST  
INFECTION  
NUMBER OF SEQUENCES: 255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Mountain View  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/194,036B  
FILING DATE: 17-No. 6548246-1998

```

; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US97/08208
;   FILING DATE: 1997-05-16
;   APPLICATION NUMBER: US 08/651,155
;   FILING DATE: 1996-05-17
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Shantanu Basu
;     REGISTRATION NUMBER: 43,318
;     REFERENCE/DOCKET NUMBER: 220002060601
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (650) 813-5995
;       TELEFAX: (650) 494-0792
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 18 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;       ORGANISM: DNA (other)
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-194-0368-1

Query Match          5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      104 CATTGTGCCCACTAGC 121
Db      1 CATTGGTGCCTAGC 18

RESULT 42
US-09-866-108A-9217/c
; Sequence 9217, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;   APPLICANT: GU, Yizhong
;   APPLICANT: JI, Yonggang
;   APPLICANT: PENN, Sharon G.
;   APPLICANT: HANZEL, David K.
;   APPLICANT: RANK, David R.
;   APPLICANT: CHEN, Wensheng
;   APPLICANT: SHANNON, Mark
;   TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;   FILE REFERENCE: AEOMICA-7
;   CURRENT APPLICATION NUMBER: US/09/866,108A
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: US 60/207,456
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: GB 24263.6
;   PRIOR FILING DATE: 2000-10-04
;   PRIOR APPLICATION NUMBER: US 60/236,359
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: PCT/US01/00666
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00667
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00664
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00669
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00665
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00668
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00663
;   PRIOR FILING DATE: 2001-01-30
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 15755
;   SOFTWARE: Aeomica Sequence Listing Engine
;   Patent No. 6686188
;   SEQ ID NO 9218
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9218
```

```

; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9217

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      31 CTGGCTGGAGCT 43
Db      17 CTGGCTGGAGCT 5

RESULT 43
US-09-866-108A-9218/c
; Sequence 9218, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;   APPLICANT: GU, Yizhong
;   APPLICANT: JI, Yonggang
;   APPLICANT: PENN, Sharon G.
;   APPLICANT: HANZEL, David K.
;   APPLICANT: RANK, David R.
;   APPLICANT: CHEN, Wensheng
;   APPLICANT: SHANNON, Mark
;   TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;   FILE REFERENCE: AEOMICA-7
;   CURRENT APPLICATION NUMBER: US/09/866,108A
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: US 60/207,456
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: GB 24263.6
;   PRIOR FILING DATE: 2000-10-04
;   PRIOR APPLICATION NUMBER: US 60/236,359
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: PCT/US01/00666
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00667
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00664
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00669
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00665
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00668
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00663
;   PRIOR FILING DATE: 2001-01-30
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 15755
;   SOFTWARE: Aeomica Sequence Listing Engine
;   Patent No. 6686188
;   SEQ ID NO 9218
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9218
```

```
US-09-866-108A-9219/c
; Sequence 9219, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9219
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9219

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CTGGCTGGAGCT 43
Db      15 CTGGCTGGAGCT 3

RESULT 45
US-09-866-108A-9220/c
; Sequence 9220, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

```
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.

US-09-866-108A-9220

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CTGGCTGGAGCT 43
Db      14 CTGGCTGGAGCT 2

RESULT 46
US-09-866-108A-9221/c
; Sequence 9221, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9221
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9221

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      31 CTGGCTGGAGCT 43
Db      13 CTGGCTGGAGCT 1

RESULT 47
US-08-584-040-5754
; Sequence 5754, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584, 040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5754:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5754

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

OY      153 CGTGAGCTGAACAGA 168
Db      2 CGUGAUCUGAAGA 17

RESULT 48
US-09-474-432B-580
; Sequence 580, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 580
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-580

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 26;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      34 GCTGGAGCTCCACCT 49
Db      2 GCUGGGGCTCCCTCU 17

RESULT 49
US-09-371-772B-2633
; Sequence 2633, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
```

US-09-371-772B-2633

Query Match 5.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 26;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 153 CGTGAGCTGACAGCA 168  
||:|||||:|||||  
Db 2 CGUGAGUCGAAACGA 17

RESULT 50  
US-09-476-387-579

Sequence 579, Application US/09476387

Patent No. 6617438

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpelisky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

FILE REFERENCE: MBH800-831-C (249/073)

CURRENT APPLICATION NUMBER: US/09/476,387

CURRENT FILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1524

SOFTWARE: PatentIn version 3.0

SEQ ID NO 579

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-09-476-387-579

Query Match 5.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 26;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GCTGGAGCTCCACT 49  
||:|||||:|||||  
Db 2 GCUGGGGCGCCUCCU 17

RESULT 51  
US-09-866-108A-119

Sequence 119, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A60MICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1575  
SOFTWARE: A60MICA Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 119  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-119

Query Match 5.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 31 CTGGCTGGAGCTCCA 46  
|||:|||||:|||||  
Db 2 CTGGCAGGAGCTCCA 17

RESULT 52  
US-09-866-108A-120

Sequence 120, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A60MICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

Remaining Prior Application data removed - See File Wrapper or PALM.

```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 120
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-120
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      31 CTGCGCTGGAGCTTCCA 46
Db      1 CTGCGAGAGACTTCCA 16
```

```
RESULT 53
US-09-866-108A-1319/c
; Sequence 1319, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1319
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1319
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      63 CTGACCTGCTTTCCA 78
Db      17 CTGACCTGCTTTCCA 2
```

```
RESULT 54
US-09-866-108A-1320/c
; Sequence 1320, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1320
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1320
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      63 CTGACCTGCTTTCCA 78
Db      16 CTGACCTGCTTTCCA 1
```

```
RESULT 55
US-09-866-108A-5889
; Sequence 5889, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
```

```
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 5889
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-5889
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      181 GCCCACCCTGTCTGTT 196
Db      2 GACCACCGTGTCTGTT 17
```

```
RESULT 56
US-09-866-108A-5890
;; Sequence 5890, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wenheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEOMICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
```

```
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 5890
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-5890
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      181 GCCCACCCTGTCTGTT 196
Db      1 GACCACCGTGTCTGTT 16
```

```
RESULT 57
US-09-866-108A-7503/C
;; Sequence 7503, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wenheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEOMICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 7503
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-7503
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      30 CTTGGCTGGAGCTCC 45
Db      17 CTTGGCTGTGAGCTCC 2
```

```
RESULT 58
US-09-866-108A-7504/C
; Sequence 7504, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7504
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7504

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      30 CCTGGCTGGAGCTCC 45
      |||||
Db      16 CCTGGCTGTCTAGCTCC 1

RESULT 59
US-09-685-664B-2633
; Sequence 2633, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

```
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2633

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      153 CGTGAGCTGACAGA 168
      |||||
Db      2 CGUGAUCUGAAAAGA 17

RESULT 60
US-10-156-306B-4949
; Sequence 4949, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-4949

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      64 TCACGCTTTTCCAA 79
      :|||
Db      1 UCACGAGCUCUCCAA 16

RESULT 61
US-10-138-674B-2633
; Sequence 2633, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674B-2633
```



```
Query Match          5.3% Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      153 CGTGAAGCTGAACAGA 168
      ||| ||| ||| ||| |||
Db      2   CGUGAUCUGAAAAGA 17

RESULT 62
US-09-344-520-29/c
; Sequence 29, Application US/09344520
; Patent No. 6037176
; GENERAL INFORMATION:
; APPLICANT: Frank Bennett
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF Integrin beta 3 EXPRESSION
; FILE REFERENCE: RTS-0070
; CURRENT APPLICATION NUMBER: US/09/344,520
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-520-29

Query Match          5.3% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      44  CCACCTCCCGACGATGC 59
      ||| ||| ||| ||| |||
Db      18  CCACCTGCCGAGATGC 3

RESULT 63
US-09-280-409-127/c
; Sequence 127, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 127
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-127

Query Match          5.3% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      36  TGGAGCTCCACCTCC 51
      ||| ||| ||| ||| |||
Db      18  TGGAGCTCCACCTCC 3

RESULT 64
US-09-474-922A-42/c
; Sequence 42, Application US/09474922A
; Patent No. 6187586

GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-474-922A-42

Query Match          5.3% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      204 TCTAGGCTGTATCAGA 219
      ||| ||| ||| ||| |||
Db      17  TCCAGGCTGTATCAGA 2

RESULT 65
US-09-475-947A-333
; Sequence 333, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-333

Query Match          5.3% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      50  CCCGAGCTGCTGCTC 65
      ||| ||| ||| ||| |||
Db      3   CCCGAGCTGCTGCTC 18

RESULT 66
US-09-544-398B-406/c
; Sequence 406, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Camilli, John P.
; APPLICANT: Little, Randali D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
```

;; PRIOR FILING DATE: 1998-10-23  
;; NUMBER OF SEQ ID NOS: 641  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 406  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-544-398B-406

Query Match 5.3%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 28;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCAGACAGCAGC 16  
Db 16 TTCCCACACAGCAGC 1

RESULT 67  
US-09-543-771B-406/C  
;; Sequence 406, Application US/09543771B  
;; Patent No. 6780609  
;; GENERAL INFORMATION:  
;; APPLICANT: Carulli, John P.  
;; APPLICANT: Little, Randall D.  
;; APPLICANT: Recker, Robert R.  
;; APPLICANT: Johnson, Mark L.  
;; TITLE OF INVENTION: High bone mass gene of 11q13.3  
;; FILE REFERENCE: 032796-014  
;; CURRENT APPLICATION NUMBER: US/09/543, 771B  
;; CURRENT FILING DATE: 2000-04-05  
;; PRIOR APPLICATION NUMBER: US 09/229,319  
;; PRIOR FILING DATE: 1999-01-13  
;; PRIOR APPLICATION NUMBER: US 60/071,449  
;; PRIOR FILING DATE: 1998-01-13  
;; PRIOR APPLICATION NUMBER: US 60/105,511  
;; PRIOR FILING DATE: 1998-10-23  
;; NUMBER OF SEQ ID NOS: 641  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 406  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-543-771B-406

Query Match 5.3%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 28;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCAGACAGCAGC 16  
Db 16 TTCCCACACAGCAGC 1

RESULT 68  
US-08-758-306-691/C  
;; Sequence 691, Application US/08758306  
;; Patent No. 5807743  
;; GENERAL INFORMATION:  
;; APPLICANT: Stinchcomb, Dan T.  
;; APPLICANT: McSwigen, James A.  
;; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
;; TITLE OF INVENTION: TREATMENT OF DISEASES  
;; TITLE OF INVENTION: ASSOCIATED WITH  
;; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
;; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
;; NUMBER OF SEQUENCES: 1379  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California

;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/758,306  
;; FILING DATE: December 3, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wartburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 212/132  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 691:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-758-306-691

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 133 TCTCTTGGAGCAGC 146  
Db 17 TCTCTTGGAGCAGC 4

RESULT 69  
US-08-292-620A-1715  
;; Sequence 1715, Application US/08292620A  
;; Patent No. 5837542  
;; GENERAL INFORMATION:  
;; APPLICANT: Susan Grimm  
;; APPLICANT: Dan T. Stinchcomb  
;; APPLICANT: James McSwigen  
;; APPLICANT: Sean Sullivan  
;; APPLICANT: Kenneth G. Draper  
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
;; TITLE OF INVENTION: DISEASES OR CONDITIONS  
;; TITLE OF INVENTION: RELATED TO LEVELS OF  
;; TITLE OF INVENTION: INTRACELLULAR ADHESION  
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
;; NUMBER OF SEQUENCES: 2390  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/292,620A  
;; FILING DATE: August 17, 1994

```
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1715:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1715

Query Match          5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      44 CCACCTCCCGACT 57
      |||||:|||||:
DB      3 CCACCCGCCACCU 16

RESULT 70
US-08-292-620A-1918
Sequence 1918, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
```

```
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1918:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1918

Query Match          5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      44 CCACCTCCCGACT 57
      |||||:|||||:
DB      3 CCACCCGCCACCU 16

RESULT 71
US-08-292-620A-1952
Sequence 1952, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
```

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1952:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1952

Query Match      5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      44 CCACCTCCCGAGCT 57
Db      3 CCACUCCCCACCU 16

RESULT 72
US-09-071-845-1715
; Sequence 1715, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
US-09-071-845-1715

Query Match      5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      44 CCACCTCCCGAGCT 57
Db      3 CCACUCCCCACCU 16

RESULT 73
US-09-071-845-1918
; Sequence 1918, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1918:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1918

Query Match      5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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OY 44 CCACCTCCCGACT 57  
Db 3 CCACCTCCCGACT 16

## RESULT 74

US-09-071-845-1952  
Sequence 1952, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwigen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071.845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292.620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008.895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989.849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1952:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1952

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 78.6%; Pred. No. 30;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 44 CCACCTCCCGACT 57  
Db 3 CCACCTCCCGACT 16

## RESULT 75

US-08-834-497A-49

Sequence 49, Application US/08834497A  
Patent No. 6140305

GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
APPLICANT: Drayna, Dennis T.  
APPLICANT: Feder, John N.  
APPLICANT: Gritke, Andreas  
APPLICANT: Ruddy, David  
APPLICANT: Tsuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834.497A  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/652.265  
FILING DATE: 23-MAY-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/632.673  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630.912  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0056-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-834-497A-49

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 36 TGGAGCTCCGACT 49  
Db 1 TGGAGCTCCGACT 14

## RESULT 76

US-08-834-497A-50  
Sequence 50, Application US/08834497A  
Patent No. 6140305  
GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
APPLICANT: Drayna, Dennis T.

```

; APPLICANT: Feder, John N.
; APPLICANT: Guirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-497A-50

Query Match      5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      36 TGGAGCTCCACCT 49
Db      1 TGGGTGCTCCACT 14

RESULT 77
; Sequence 5891, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

```

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5891
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5891

Query Match      5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      183 CCACCGTGTCTGTT 196
Db      2 CCACCGTGTCTGTT 15

RESULT 78
; Sequence 5892, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 5892  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-5892

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 183 CCACCGTCTGTT 196  
Db 1 CCACCGTCTGTT 14

RESULT 79  
US-10-156-306B-5820/C  
; Sequence 5820, Application US/10156306B  
; Patent No. 7022828  
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306B  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8014  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5820  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306B-5820

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 39 GAGCTCCACCTCCC 52  
Db 17 GTGCTCCACCTCCC 4

Search completed: October 2, 2006, 15:36:33  
Job time : 0.001 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:44:33 ; Search time 0.001 Seconds  
(without alignments)  
585.156 Million cell updates/sec

Title: US-10-642-946-6\_1967-2208  
Perfect score: 242  
Sequence: 1 ttcccagcagacagcagcga.....ccaactaaactgattcacc 242

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 58 seqs, 1209 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 58 summaries

Database : ngsdb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.6	7.7	25	1	127B probe for det
2	18.4	7.6	24	1	Parkinson syndrome
3	18.2	7.5	26	1	Microorganism tran
4	17.2	7.1	24	1	RFC-1 primer used
5	16.4	6.8	19	1	Microsatellite mar
6	16.2	6.7	21	1	Human gene single
7	16.2	6.7	22	1	Human G-protein co
8	16.2	6.7	22	1	Human GPCR9 revers
9	16.2	6.7	22	1	PCR related rever
10	16.2	6.7	22	1	NOV85 PCR primer,
11	16.2	6.7	22	1	DNA detection exte
12	16.2	6.7	23	1	DNA target sequenc
13	15.8	6.5	19	1	Intestinal epithel
14	15.8	6.5	21	1	ENPP3 target oligo
15	15.8	6.5	21	1	ENPP3 siRNA antisense
16	15.8	6.5	21	1	ENPP3 siRNA antisense
17	15.8	6.5	21	1	ENPP3 siRNA antisense
18	15.6	6.4	22	1	ENPP3 target oligo
19	15.6	6.4	22	1	Human promoter -14
20	15.4	6.3	18	1	Expression system
21	15.4	6.3	20	1	Human SRC-3 antisense
22	15.2	6.3	20	1	Primer for RT-PCR
23	15.2	6.3	20	1	T. gondii immunoge
24	15.2	6.3	20	1	T. gondii sequenci
25	15.2	6.3	20	1	Chimeric phosphoro
26	15.2	6.3	21	1	Human ABC1 gene in
27	15.2	6.3	21	1	NF-kappa-B inhibit
28	15.2	6.3	21	1	Human MAP kinase 8
29	15.2	6.3	21	1	ADW72412
30	15.2	6.3	21	1	ADW72414
31	15.2	6.3	21	1	ADW72416
32	15.2	6.3	21	1	ADW72418
33	15.2	6.3	21	1	ADW72420
34	15.2	6.3	21	1	ADW72422
35	15.2	6.3	21	1	ADW72424
36	15.2	6.3	21	1	ADW72426
37	15.2	6.3	21	1	ADW72428
38	15.2	6.3	21	1	ADW72430
39	15.2	6.3	21	1	ADW72432
40	15.2	6.3	21	1	ADW72434
41	15.2	6.3	21	1	ADW72436
42	15.2	6.3	21	1	ADW72438
43	15.2	6.3	21	1	ADW72440
44	15.2	6.3	21	1	ADW72442
45	15.2	6.3	21	1	ADW72444
46	15.2	6.3	21	1	ADW72446
47	15.2	6.3	21	1	ADW72448
48	15.2	6.3	21	1	ADW72450
49	15.2	6.3	21	1	ADW72452
50	15.2	6.3	21	1	ADW72454
51	15.2	6.3	21	1	ADW72456
52	15.2	6.3	21	1	ADW72458
53	15.2	6.3	21	1	ADW72460
54	15.2	6.3	21	1	ADW72462
55	15.2	6.3	21	1	ADW72464
56	15.2	6.3	21	1	ADW72466
57	15.2	6.3	21	1	ADW72468
58	15.2	6.3	21	1	ADW72470

## ALIGNMENTS

RESULT 1	AE890482	standard; DNA; 25 BP.
ID	AE890482	standard; DNA; 25 BP.
AC	AE890482	
DT	20-OCT-2005	(first entry)
XX		
DE	127B probe for detection of osteoarthritis gene, SEQ ID NO:1578.	
XX		
KW	osteoarthritis; antiarthritic; osteopathic; diagnosis; drug screening;	
XX	pharmaceutical; ss; probe.	
OS	Canis familiaris.	
XX		
PN	WO2005075685-A1.	
XX		
PD	18-AUG-2005.	
XX		
PF	02-FEB-2005; 2005WO-US003375.	
XX		
PR	02-FEB-2004; 2004US-0541346P.	
XX		
PA	(NEST ) NESTEC SA.	
XX		
P1	Middleton RP, Hannah SS;	
XX		
DR	WPI; 2005-564577/57.	
XX		
PT	Polynucleotides differentially expressed in canine osteoarthritis; useful	
PT	in diagnosing and prognosticating osteoarthritis in mammals; and in	
PT	identifying compounds useful for treating the disease.	
XX		
PS	Example 5; SEQ ID NO 1578; 170bp; English.	
XX		
CC	The present invention relates to degenerative joint diseases, such as	
CC	osteoarthritis and new compositions, devices and methods based on unique	
CC	profiles of gene expression associated with osteoarthritis. Specifically	
CC	claimed is a combination (A) comprising polynucleotide molecules (I),	
CC	where (I) are differentially expressed in an osteoarthritic or in a pre-	
CC	osteoarthritic subject compared to expression in subjects which are not	
CC	osteoarthritic or pre-osteoarthritic. Also given is a method of detecting	
CC	(M1) differential expression of nucleic acids in a sample; detecting (M2)	

PCR primer used to  
Chimeric phosphoro  
Chimeric phosphoro  
Human MD-1 RP105-a  
Human MD-1 RP105-a  
Solium glycosylase  
Human phosphodiester  
Human phosphodiester  
Skin permeabilizat  
Primer F2 for H. py  
Human Alstrom's sy  
FOH1 siRNA antisense  
FOH1 siRNA sense  
FOH1 target oligo  
FOH1 target oligo  
FOH1 siRNA antisense  
FOH1 siRNA sense  
ENPP3 siRNA sense  
FOH1 target oligo  
Mitochondrial poly  
Up-regulated renal  
Dog genomic marker  
Dog genomic marker  
Set 1 left PCR pri  
Melanoma associate

CC differential expression of polypeptides; measuring (M3) the effect of a  
 CC test compound on the expression of one or more genes differentially  
 CC expressed in osteoarthritis; diagnosing or prognosticating (M4)  
 CC osteoarthritis by measuring the production of transcription or  
 CC translation products of one or more genes comprising any of SEQ ID Nos 1-  
 CC 1558 in a sample from the subject; a kit for detecting osteoarthritis by  
 CC oligonucleotides of at least 10 consecutive bases comprising any of SEQ  
 CC ID Nos 1-1558 or their fragments; and modulating (M5) osteoarthritis-  
 CC arthritis associated gene expression in a cell by administering a  
 CC compound that affects the expression of at least one gene comprising a  
 CC sequence selected from SEQ ID Nos 1-1558. In M5 the compound is a vitamin  
 CC (preferably 1 alpha,25-dihydroxy vitamin D3 or 24R,25-dihydroxyvitamin  
 CC D3), mineral, nutraceutical, small molecule pharmaceutical, protein,  
 CC polypeptide, nucleic acid, fatty acid (preferably eicosapentaenoic acid  
 CC or arachidonic acid) or polysaccharide (glucosamine or chondroitin  
 CC sulfate). The present sequence is 127B probe for detection of an  
 CC osteoarthritis-related gene.

CC  
 XX Sequence 25 BP; 3 A; 13 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 7.7%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 7.3; Mismatches 0; Gaps 0;

Matches 21; Conservative 0; Indels 4; Gaps 0;

QY 43 TCCACCTCCCGAGCTGCTGCTCAC 67  
 DB 1 TCTATCTCCCGAGCTGCTGCTCAC 25

RESULT 2  
 ABL40677 standard; DNA; 24 BP.

AC ABL40677;

DT 17-JUN-2002 (first entry)

DE Parkinson syndrome associated protein 13.31 cDNA RT-PCR primer 1.

KM Parkinson syndrome associated protein 13.31; human; anti-Parkinson;  
 KW cerebral cortex function disorder; gene therapy; RT-PCR; primer; ss.

OS Homo sapiens.

PN CNJ328042-A.

PD 26-DEC-2001.

PF 14-JUN-2000; 2000CN-00116476.

PR 14-JUN-2000; 2000CN-00116476.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y; Xie Y;

DR WPI; 2002-242316/30.

PT Polypeptide-human Parkinson syndrome associated protein 13.31 and  
 PT polynucleotide encoding it.

PS Example 2; Page 18 (Disclosure); 34pp; Chinese.

CC The invention relates to a novel human Parkinson syndrome associated  
 CC protein 13.31. The protein can be expressed by standard DNA  
 CC recombination. The Parkinson syndrome associated protein 13.31 and  
 CC encoding polynucleotides are useful for treating diseases such as  
 CC cerebral cortex function disorder. The present sequence represents the  
 CC human Parkinson syndrome associated protein 13.31 cDNA isolating RT-PCR  
 CC primer

CC Sequence 24 BP; 3 A; 11 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 7.6%; Score 18.4; DB 1; Length 24;  
 Best Local Similarity 95.0%; Pred. No. 8;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 CCACCTCCCGAGCTGCTGCC 63  
 DB 5 CCACCTCCCGAGCTGCTGCC 24

RESULT 3

ADO23704 standard; DNA; 26 BP.

AC ADO23704;

DT 15-JUL-2004 (first entry)

DE Microorganism transformation/DNA preparation-related PCR primer - SEQ 49.

KM microorganism transformation; DNA fragment preparation; PCR; primer; ss.

OS Unidentified.

PN JP2004129654-A.

PD 30-APR-2004.

PF 10-SEP-2003; 2003JP-00317927.

PR 19-SEP-2002; 2002JP-00273747.

PA (MITU) MITSUBISHI CHEM CORP.

DR WPI; 2004-433769/41.

PT Preparing DNA fragment from microorganism transformation, by preparing  
 PT DNA units which have structure for connecting DNA fragment for homologous  
 PT recombination, connecting DNA units with DNA fragment, and producing DNA  
 PT fragment.

PS Example 2; SEQ ID NO 49; 27pp; Japanese.

CC The invention relates to a novel method for preparing a DNA fragment from  
 CC a microorganism transformation. The method comprises preparing DNA units  
 CC which have a structure enabling them to connect DNA fragments for  
 CC homologous recombination, connecting these DNA units with a DNA fragment  
 CC and producing a DNA fragment. The current sequence is that of a PCR  
 CC primer of the invention which is related to microorganism  
 CC transformation/DNA fragment preparation.

SQ Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 7.5%; Score 18.2; DB 1; Length 26;

Best Local Similarity 87.0%; Pred. No. 7.8; Mismatches 3; Indels 0; Gaps 0;

QY 129 TCCATCTCTTGGAGCAGCTCTC 151  
 DB 4 TCCATCTCTATGGAGCAGCAGCTCTGC 26

RESULT 4

AAD31117 standard; DNA; 24 BP.

AC AAD31117;

DT 21-AUG-2002 (first entry)

DE RFC-1 primer used in production of heterozygous mutant RFC mouse.

KW Reduced folate carrier; rfc; genetic modification; animal model; cancer;  
 KW neural tube defect; Parkinson's disease; Alzheimer's disease;

XX	cardiovascular disease; stroke; cleft palate; mouse; PCR primer; ss.
XX	
OS	Mus musculus.
XX	
PN	WO200224868-A2.
XX	
PD	28-MAR-2002.
XX	
PF	24-SEP-2001; 2001WO-US029966.
XX	
PR	22-SEP-2000; 2000US-0234853P.
XX	
PA	(ROOS-) ROOSEVELT INST ELEANOR.
XX	
PA	(OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX	
PI	(UWYO-) UNIV WESTERN ONTARIO.
XX	
PI	Patterson D, Brennan MB, Hochgeschwender U, Flintoff WF;
XX	
PI	Sadlish H, Underhill TM, Williams FMR;
XX	
DR	WPI; 2002-416280/44.
XX	
PT	Novel genetically modified non-human animal useful as model for defective
XX	
PT	folate transport comprises genetic modification resulting in decreased
XX	
PT	expression and/or biological activity of endogenous reduced folate
XX	
PT	carrier gene.
XX	
PS	Example 1; Page 32; 69pp; English.
XX	
CC	The invention relates to genetically modified non-human animal comprising
XX	
CC	modification in at least one allele of endogenous reduced folate carrier
XX	
CC	(rfc) gene in the animal, where genetic modification results in reduction
XX	
CC	in endogenous RFC expression or biological activity in animal. The non-
XX	
CC	human animal optionally is further modified by introduction into genome,
XX	
CC	a nucleic acid sequence encoding biologically active human RFC. The
XX	
CC	modified animal of the invention is useful for evaluating anti-folate
XX	
CC	compounds for treating cancer, for studying the molecular and biochemical
XX	
CC	events associated with folate transport and for identifying compounds
XX	
CC	useful for treating conditions associated with defective folate
XX	
CC	transport. Furthermore, a compound which binds to RFC with a higher
XX	
CC	affinity than the affinity of folate for human RFC may be useful for
XX	
CC	treating a neural tube defect, Parkinson's disease, Alzheimer's disease,
XX	
CC	cardiovascular disease, stroke, cleft palate. In the genetically modified,
XX	
CC	animal, expression level of human rfc can be varied, as desired, to
XX	
CC	provide a model system for testing various compounds. The present
XX	
CC	sequence is a PCR primer used in production of heterozygous mutant RFC
XX	
CC	mouse
XX	
SO	Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
XX	
Query Match	7.1%; Score 17.2; DB 1; Length 24;
XX	
Best Local Similarity	86.4%; Pred. No. 11;
XX	
Matches	19; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX	
Oy	14 CACTGGATTGGTCACCTGGC 35
XX	
Db	23 CAATGGATGCTGTCACCTGGC 2
XX	
RESULT 5	
XX	ID ADR46326 standard; DNA; 19 BP.
XX	
XX	ADR46326;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Microsatellite marker PCR primer 19-R.
XX	
XX	Microsatellite marker; Bex4; ovarian cancer; cytostatic; human;
XX	
KW	gene therapy; tumour suppressor protein; PCR; primer; ss.
XX	
OS	Homo sapiens.
XX	

```

PN WO2004072269-A2.
PD 26-AUG-2004.
PF 12-FEB-2004; 2004WO-US0004413.
PR 12-FEB-2003; 2003US-0446877P.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PI Shridhar V, Chien J;
PX WPI; 2004-625868/60.
PT New vector comprising an isolated nucleic acid encoding a Bex4
PT polypeptide, useful for treating cancer, e.g. ovarian, cervical, brain,
PT breast, prostate or liver cancer.
PS Example 1, SEQ ID NO 39; 47pp; English.
PX
XX
CC The present sequence is that of PCR primer 19-R for a microsatellite
CC marker within BAC CTR-B-470F8 on 19q14.3. PCR was performed on genomic
CC DNA from 15 early-stage and 18 late-stage ovarian tumours of different
CC histologies. LOH analysis was performed to identify potential candidate
CC tumour suppressor genes involved in ovarian carcinogenesis. The invention
CC is based on the discovery that Bex4 (or proapoptotic protein on
CC chromosome X (PAPX)) ADR46296 is down-regulated in cancer cells. Claimed
CC methods for killing a tumour cell comprise administering to the tumour
CC cell a nucleic acid that encodes a Bex4 polypeptide, a vector comprising
CC the nucleic acid, or a Bex4 polypeptide. The tumour cell is selected from
CC an ovarian, cervical, brain, breast, prostate and hepatic tumour cell.
CC Detection of a lower than normal level of Bex4 polypeptide in cells in a
CC sample indicates a predisposition of an individual to develop cancer. A
CC claimed method for detecting cancer recurrence in an individual diagnosed
CC with and treated for cancer comprises measuring the level of bex4 gene
CC methylation. The presence of hypermethylation indicates recurrence. The
CC cancer is ovarian, breast, prostate, cervical, brain or liver cancer.
CC
SQ Sequence 19 BP; 2 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
XX
QY Query Match 6.8%; Score 16.4; DB 1; Length 19;
DB Best Local Similarity 94.4%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
52 CCAGCTGCTGCTCACCT 69
|||||
1 CCAGCTGCTGCTCACCT 18
RESULT 6
AAF96003/c
ID AAF96003 standard; DNA; 21 BP.
AC AAF96003;
XX
XX 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #764.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX Key Location/Qualifiers
XX FT 11
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX

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PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
DR
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 101; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
CC
CC Revised record issued on 18-NOV-2004 : The variation feature was
CC incorrectly given a capital V
XX
SQ Sequence 21 BP; 5 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CTCGACGACGACTGATTT 23
Db 21 CTCGACGACGACTGCGCTAT 1
RESULT 7
ABSS59191
ID ABSS59191 standard; DNA; 22 BP.
XX
AC ABSS59191;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human G-protein coupled receptor, reverse primer #113.
XX
KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW primer; PCR; ss.
XX
OS Homo sapiens.
XX
PN WO200259313-A2.
XX
PD 01-AUG-2002.

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PF 18-DEC-2001; 2001WO-US049394.
XX
PR 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Ld L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CM, Shenoy SG, Guise V, Malayanekar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciore P, MacDougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX
XX WPI; 2002-599789/64.
DR
XX
XX New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
XX Claim 9; Page 586; 685pp; English.
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albritght hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABSS58747-ABSS59231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX
SQ Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 133 TCTCTTTGAGCAGCTCTCAC 153
Db 2 TCTCTTTAGAGCCCTTTGAC 22
RESULT 8
ABN89181
ID ABN89181 standard; DNA; 22 BP.
XX
AC ABN89181;
XX
DT 28-AUG-2002 (first entry)
XX

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DE Human GPCR9 reverse PCR primer SEQ ID NO:121.  
 XX  
 KW Human; GPCR; GPCRX; G protein-coupled receptor; antiatherosclerotic;  
 KW anorectic; antibacterial; fungicide; protozoacide; virocid; analgesic;  
 KW cyostatic; immunomodulator; metabolic; antiaesthetic; antiparkinsonian;  
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;  
 KW antifertility; neuroprotective; antiangiinal; cardiant; anticancer;  
 KW antiallergic; nootropic; tranquilizer; neuroleptic; antidepressant;  
 KW antianemic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;  
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;  
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;  
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;  
 KW autoimmune disorder; infectious disease; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200226985-A2.  
 XX  
 XX 04-APR-2002.  
 PD  
 XX  
 XX 28-SEP-2001; 2001WO-US030552.  
 PF  
 XX  
 XX 28-SEP-2000; 2000US-0236284P.  
 PR 28-SEP-2000; 2000US-0236286P.  
 PR 03-OCT-2000; 2000US-0237581P.  
 PR 06-OCT-2000; 2000US-0238735P.  
 PR 16-OCT-2000; 2000US-0240736P.  
 PR 05-JAN-2001; 2001US-0260013P.  
 PR 08-JAN-2001; 2001US-0260338P.  
 PR 17-JAN-2001; 2001US-0262158P.  
 PR 18-JAN-2001; 2001US-0262498P.  
 PR 19-JAN-2001; 2001US-0263133P.  
 PR 24-JAN-2001; 2001US-0263691P.  
 PR 02-FEB-2001; 2001US-0266109P.  
 PR 26-FEB-2001; 2001US-0271634P.  
 PR 27-SEP-2001; 2001US-00965422.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 PI Spytek KA, Casman S, Padigaru M, Dickson K, Vernet C;  
 PI Spaderna SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;  
 PI Macdougall JR, Smithson G, Li L, Malanker UM, Taylor S, Gunther E;  
 PI Tchernev VT;  
 PI  
 XX Tchernev VT;  
 XX  
 XX WPI; 2002-499868/53.  
 PS  
 XX Example 1; Page 198; 213pp; English.  
 CC ABN89112 to ABN89130 encoding the human G protein-coupled receptor  
 CC (GPCRX) proteins given in AB891440 to AB89158. GPCRX proteins can have  
 CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,  
 CC virocid, analgesic, cyostatic, immunomodulator, metabolic, hypotensive,  
 CC antiaesthetic, antiparkinsonian, hypertensive, osteopathic, hypotensive,  
 CC antiinflammatory, antifertility, neuroprotective, antiangiinal,  
 CC cardiant, anticancer, antiallergic, nootropic, tranquilizer, neuroleptic,  
 CC antidepressant, antianemic, anticonvulsant, haemostatic, hepatotropic,  
 CC immunosuppressive, cerebroprotective, dermatological, antiaddictive,  
 CC nephrotropic and gynaecological activities, and can be used in vaccines  
 CC and gene therapy. GPCRX proteins and polynucleotides can be used for  
 CC treating or preventing a GPCRX-associated disorder such as  
 CC cardiomyopathy, atherosclerosis, a disorder related to cell signal  
 CC processing and metabolic pathway modulation, in a human. GPCRX proteins  
 CC and polynucleotides can also be used in the manufacture of a medicament  
 CC for preventing or treating disorders or syndromes including developmental  
 CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative  
 CC disorders, autoimmune disorders, infectious diseases and diabetes.  
 CC ABN89131 to ABN89187 represent PCR primers and probes used in the

CC exemplification of the present invention  
 XX  
 SQ Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;  
 Query Match 6.7%; Score 16.2; DB 1; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 133 TCTCTTTGAGACCACTCTTCAC 153  
 Db 2 TCTCTTTAGACCCCTTTTCAC 22  
 RESULT 9  
 ABT05734  
 ID ABT05734 standard; DNA; 22 BP.  
 XX  
 AC ABT05734;  
 XX  
 XX 16-OCT-2002 (first entry)  
 DT  
 XX  
 XX GPCR related reverse PCR primer SEQ ID No 187.  
 DE  
 XX  
 XX Antidiabetic; cyostatic; anorectic; nootropic; neuroprotective; GPCRX;  
 KW antiparkinsonian; cardiant; antiatherosclerotic; immunosuppressive;  
 KW hypotensive; haemostatic; antifertility; antiaesthetic; antiinflammatory;  
 KW anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;  
 KW diabetes; metabolic disorder; diabetes; obesity; infectious disease;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;  
 KW Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;  
 KW metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;  
 KW congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;  
 KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
 KW prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;  
 KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;  
 KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;  
 KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;  
 KW gene therapy; transgenic animal; PCR; primer; ss.  
 KW  
 XX Unidentified.  
 XX  
 OS  
 XX WO200246229-A2.  
 XX  
 XX 13-JUN-2002.  
 PD  
 XX  
 XX 05-DEC-2001; 2001WO-US046530.  
 PF  
 XX  
 XX 05-DEC-2000; 2000US-0251459P.  
 PR 29-DEC-2000; 2000US-0259007P.  
 PR 04-DEC-2001; 2001US-00005041.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX  
 XX Casman SJ, Padigaru M, Burgess CE, Shinkets RA, Spytek KA;  
 PI Gilbert JH, Mayotte JE, Baumgartner JC, Mishra V, Vernet CM;  
 PI Dickinson KS, Ballinger RA, Wolenc AR;  
 PI  
 XX WPI; 2002-537559/57.  
 PS  
 XX Example 2; Page 226; 264pp; English.  
 CC The invention relates to a novel isolated G-protein coupled receptor X  
 CC (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide  
 CC and the antibody of the isolated protein is useful for treating or  
 CC preventing a GPCRX-associated disorder in a subject, preferably human,  
 CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The  
 CC isolated protein, its encoding polynucleotide and the antibody of the  
 CC isolated protein is useful for treating or preventing metabolic  
 CC disorders, diabetes, obesity, infectious disease, anorexia,

CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,  
 CC immune disorders, haematopoietic disorders, and various dyslipidaemias,  
 CC metabolic disturbances associated with obesity, the metabolic syndrome X,  
 CC wasting disorders associated with chronic diseases, and cancer. The  
 CC disorders also include cardiomyopathy, atherosclerosis, hypertension,  
 CC congenital heart defects, aortic stenosis, subaortic stenosis,  
 CC transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,  
 CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,  
 CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic  
 CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial  
 CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,  
 CC its encoding polynucleotide and the antibody of the isolated protein is  
 CC useful in screening assays, detection assays (e.g., chromosomal mapping,  
 CC tissue typing, forensic biology). The isolated polynucleotide is useful  
 CC in gene therapy, to express the isolated protein, to detect GPCR mRNA or  
 CC a genetic lesion in a GPCR gene, and to modulate GPCR activity. The  
 CC cell of the invention is useful for producing non-human transgenic  
 CC animals. This polynucleotide sequence represents a reverse PCR primer of  
 CC a GPCR protein of the invention  
 CC  
 SQ Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 133 TCTCTTGAGGACCTCTCAG 153  
 Db 2 TCTCTTGAGGACCTCTCAG 22

RESULT 10  
 ID ADH49242 standard; DNA; 22 BP.

XX ADH49242;

XX 25-MAR-2004 (first entry)

XX NOV85 PCR primer, SEQ ID 526.

XX Human, NOVA; atherosclerosis; hypertension; obesity; cancer; cytostatic;  
 KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV85; PCR;  
 XX primer; ss.

OS Homo sapiens.

XX WO200268652-A2.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005910.

XX 26-FEB-2001; 2001US-0271646P.

XX 27-FEB-2001; 2001US-0271840P.

XX 28-FEB-2001; 2001US-0272404P.

XX 28-FEB-2001; 2001US-0272405P.

XX 28-FEB-2001; 2001US-0272410P.

XX 02-MAR-2001; 2001US-0272787P.

XX 02-MAR-2001; 2001US-0272922P.

XX 02-MAR-2001; 2001US-0273048P.

XX 16-MAR-2001; 2001US-0276401P.

XX 20-MAR-2001; 2001US-0277324P.

XX 30-MAR-2001; 2001US-0280339P.

XX 02-APR-2001; 2001US-0280818P.

XX 12-APR-2001; 2001US-0283443P.

XX 23-APR-2001; 2001US-0285754P.

XX 24-APR-2001; 2001US-0286096P.

XX 03-MAY-2001; 2001US-0288353P.

PR 17-MAY-2001; 2001US-0291703P.  
 PR 31-MAY-2001; 2001US-0294834P.  
 PR 20-JUN-2001; 2001US-0296959P.  
 PR 21-JUN-2001; 2001US-0299845P.  
 PR 05-JUL-2001; 2001US-0303422P.  
 PR 13-AUG-2001; 2001US-0311981P.  
 PR 16-AUG-2001; 2001US-0312858P.  
 PR 17-AUG-2001; 2001US-0313280P.  
 PR 29-AUG-2001; 2001US-0315614P.  
 PR 17-SEP-2001; 2001US-0322818P.  
 PR 25-FEB-2002; 2002US-00322818.

XX (CURA-) CURAGEN CORP.

PA Alsobrook JP, Anderson DM, Ballinger RA, Boldog FL, Burgess CE;  
 PI Casman ST, Ellerman KE, Gangoli EA, Gerlach VL, Gilbert JA;  
 PI Gorman L, Guo X, Guev VY, Kekuda R, Li L, Liu X, Maityankar UM,  
 PI Miller CE, Millet I, Padigaru M, Patutajan M, Pena CE, Peyman JA;  
 PI Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ,  
 PI Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;  
 XX WPI; 2002-698672/75.

XX New NOVA polypeptides or polynucleotides, useful for preventing or  
 PT treating disorders or syndromes e.g., atherosclerosis, hypertension,  
 PT obesity or cancer.

XX Example 2; Page 882; 923pp; English.

XX The present invention relates to novel human NOVA proteins, where X is  
 CC any number from 1 to 91 and their coding sequences (see ADH48717-  
 CC ADH48930). The proteins and coding sequences are useful for preventing or  
 CC treating disorders or syndromes e.g., atherosclerosis, hypertension,  
 CC obesity or cancer. The present sequence was used in an example from the  
 CC invention.

XX Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 133 TCTCTTGAGGACCTCTCAG 153  
 Db 2 TCTCTTGAGGACCTCTCAG 22

RESULT 11

ID ADX84073 standard; DNA; 22 BP.

XX ADX84073;

XX 05-MAY-2005 (first entry)

XX DNA detection extension primer #48.

XX Analysis; mass spectroscopy; PCR; primer; ss.

XX Synthetic.

XX WO2005014850-A2.

XX 17-FEB-2005.

XX 06-AUG-2004; 2004WO-US025526.

XX 06-AUG-2003; 2003US-0493238P.

XX 07-MAY-2004; 2004US-0568958P.

XX (UYMA-) UNIV MASSACHUSETTS.

XX Gims EI, Galdzicka M;

XX WPI; 2005-195764/20.  
DR Clinical assay system for assaying sample, has central controller, sample  
XX transfer module, nucleic acid extraction and measurement module,  
PT thermocycling module, primer extension module, mass spectrometry module  
PT analyzing sample.  
XX  
PS Claim 6; SEQ ID NO 144; 207bp; English.  
XX  
CC The invention relates to a system for performing an assay on a biological  
CC sample, comprising a central controller programmed to exchange  
CC information about the biological sample with an outside system or  
CC database and exchange information about the biological sample with one or  
CC more modules of the system, a sample transfer module for transferring a  
CC portion of the sample to a first container, a nucleic acid extraction  
CC module for extracting nucleic acids from cells within the portion and for  
CC transferring the portion from the first container to a second container,  
CC a nucleic acid measurement module for measuring the concentration of  
CC nucleic acids in the portion, a PCR preparation module for adding PCR  
CC reaction materials to the portion, a thermocycling module for amplifying  
CC a target sequence and extending a primer in the portion, a primer  
CC extension preparation module for adding primer extension reaction  
CC materials to the portion, a mass spectrometry preparation module for  
CC removing a sample of the portion from the second container to a support  
CC for analysis by mass spectrometry and a mass spectrometry module for  
CC analyzing the sample. The invention also relates to an automated method  
CC for detecting mutations in a target gene. The diagnostic assay is an  
CC assay for detecting a pathogen in the sample. The pathogen is a virus,  
CC bacterium or fungus. The virus is a virus of the family Herpesviridae,  
CC preferably Cytomegalovirus (CMV). The system enables high accurate assays  
CC on nucleic acid sequences (e.g. clinically relevant nucleic acid  
CC sequences) using mass spectrometry. This sequence represents a DNA  
CC detection extension primer used in the scope of the invention.  
XX  
SQ Sequence 22 BP; 5 A; 5 C; 3 G; 9 T; 0 U; 0 Other;  
XX  
Query March 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 126 GTTTCATCTCTTGGAGCAC 146  
Db 1 GTTTCATCTATTGGTACAC 21  
XX  
RESULT 12  
ADL24990 standard; DNA; 23 BP.  
XX  
AC ADL24990;  
XX  
DT 05-MAY-2005 (first entry)  
XX  
DE DNA target sequence #56.  
XX  
KM Analysis; mass spectroscopy; ss.  
XX  
OS Synthetic.  
XX  
PN WO2005014850-A2.  
XX  
PD 17-FEB-2005.  
XX  
PF 06-AUG-2004; 2004WO-US025526.  
XX  
PR 06-AUG-2003; 2003US-0493238P.  
XX  
PR 07-MAY-2004; 2004US-0568958P.  
XX  
PA (UTMA-) UNIV MASSACHUSETTS.  
XX  
PI Glina EI, Galdzicka M;  
XX

DR WPI; 2005-195764/20.  
XX  
XX Clinical assay system for assaying sample, has central controller, sample  
PT transfer module, nucleic acid extraction and measurement module,  
PT thermocycling module, primer extension module, mass spectrometry module  
PT analyzing sample.  
XX  
PS Disclosure; SEQ ID NO 562; 207bp; English.  
XX  
CC The invention relates to a system for performing an assay on a biological  
CC sample, comprising a central controller programmed to exchange  
CC information about the biological sample with an outside system or  
CC database and exchange information about the biological sample with one or  
CC more modules of the system, a sample transfer module for transferring a  
CC portion of the sample to a first container, a nucleic acid extraction  
CC module for extracting nucleic acids from cells within the portion and for  
CC transferring the portion from the first container to a second container,  
CC a nucleic acid measurement module for measuring the concentration of  
CC nucleic acids in the portion, a PCR preparation module for adding PCR  
CC reaction materials to the portion, a thermocycling module for amplifying  
CC a target sequence and extending a primer in the portion, a primer  
CC extension preparation module for adding primer extension reaction  
CC materials to the portion, a mass spectrometry preparation module for  
CC removing a sample of the portion from the second container to a support  
CC for analysis by mass spectrometry and a mass spectrometry module for  
CC analyzing the sample. The invention also relates to an automated method  
CC for detecting mutations in a target gene. The diagnostic assay is an  
CC assay for detecting a pathogen in the sample. The pathogen is a virus,  
CC bacterium or fungus. The virus is a virus of the family Herpesviridae,  
CC preferably Cytomegalovirus (CMV). The system enables high accurate assays  
CC on nucleic acid sequences (e.g. clinically relevant nucleic acid  
CC sequences) using mass spectrometry. This sequence represents a DNA target  
CC sequence used in the scope of the invention.  
XX  
SQ Sequence 23 BP; 5 A; 6 C; 3 G; 9 T; 0 U; 0 Other;  
XX  
Query March 6.7%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 126 GTTTCATCTCTTGGAGCAC 146  
Db 1 GTTTCATCTATTGGTACAC 21  
XX  
RESULT 13  
ADL24990/C  
ID ADL24990 standard; DNA; 19 BP.  
XX  
AC ADL24990;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Intestinal epithelium/geyer's patch M cell-associated PCR primer #135.  
XX  
KM Intestinal epithelium cell development; peyer's patch M cell development;  
KM inflammatory bowel disease; glutenenteropathy; infectious disease;  
KM autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;  
KM Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
KM immune system disorder; hypersensitivity; anaphylaxis;  
KM blood group incompatibility; ss; human; PCR; primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200280852-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 04-APR-2002; 2002WO-US010873.  
XX  
PR 04-APR-2001; 2001US-0281416P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX





CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX  
SQ Sequence 21 BP; 3 A; 4 C; 4 G; 0 T; 10 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 18; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGCAGCTGTTAAG 181  
Db 20 AACGGAACACCTGTTAAG 2

RESULT 16  
ACLA6620/c  
ID ACLA6620 standard; RNA; 21 BP.

XX ACLA6620;

XX 24-MAR-2005 (first entry)

XX ENPP3 siRNA antisense sequence, SEQ ID 7692.

XX Cyrostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
XX short interfering RNA; gene silencing.

XX Synthetic.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABCG4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

PS Claim 3; SEQ ID NO 7692; 113bp; English.

CC The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCG4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX Sequence 21 BP; 3 A; 4 C; 4 G; 0 T; 10 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 18;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGCAGCTGTTAAG 181  
Db 21 AACGGAACACCTGTTAAG 3

RESULT 17  
ACLA6978  
ID ACLA6978 standard; DNA; 21 BP.

XX ACLA6978;

XX 24-MAR-2005 (first entry)

XX ENPP3 target oligonucleotide, SEQ ID 8050.

XX Cyrostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.

XX Homo sapiens.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABCG4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

PS Claim 3; SEQ ID NO 8050; 113bp; English.

CC The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCG4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 18;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGCAGCTGTTAAG 181  
Db 2 AACGGAACACCTGTTAAG 20

RESULT 18

```

AAD45780
ID AAD45780 standard; DNA; 22 BP.
XX
AC AAD45780;
XX
XX 27-DEC-2002 (first entry)
XX
DE Human promoter -147 CYP4503A5 specific probe #1.
XX
KM Human, cytochrome P450, CYP3A4; CYP3A5; glucathione S-transferase;
KM polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent;
KM drug-drug interaction; drug adverse effect; anti-cancer agent; enzyme;
KM probe; promoter; ss.
XX
OS Homo sapiens.
XX
FN WO200268448-A1.
XX
PD 06-SEP-2002.
XX
PF 26-FEB-2002; 2002WO-US006135.
XX
PR 26-FEB-2001; 2001US-0271630P.
XX
PA (DNAS-) DNA SCI INC.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Guida M, Hall J, Petros WP, Vredenburg JJ, Colvin OM, Marks JR,
XX
DR WPI; 2002-691652/74.
XX
PT New nucleic acid molecule useful for identifying polymorphisms associated
PT with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer
PT treatments, comprises at least one base variation from human CYP3A4 or
PT CYP3A5 sequence.
XX
PS Example 3; Page 27; 41pp; English.
XX
CC The invention relates to a nucleic acid molecule comprising at least one
CC base variation from human cytochrome P450 (CYP) 3A4 or CYP3A5 sequence.
CC Nucleic acid molecules of the invention are useful for identifying
CC polymorphisms associated with CYP3A4, CYP3A5 or glucathione S-transferase
CC (GST) M1 substrates which influence breast cancer treatments. They are
CC also useful in diagnostic purposes to identify individuals having a
CC polymorphic genotype which influence the outcome of breast cancer
CC treatments and the selection of chemotherapeutic agents used to treat
CC breast cancer. The polymorphisms detected are used to screen altered
CC metabolism of CYP3A4, CYP3A5 or GSTM1 substrates, potential drug-drug
CC interactions, drug adverse effects, likelihood of successful clinical
CC outcome following treatment with anti-cancer agents such as cisplatin,
CC cyclophosphamide and/or BCNU. The present sequence is human promoter -147
CC CYP4503A5 specific probe
XX
SQ Sequence 22 BP; 2 A; 13 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 56 CTGCTGCTCCTACCTGCTTTCC 77
||| ||| ||| ||| ||| |||
DB 1 CTGCAGCCGCCACCTCTCTCC 22

```

```

XX
KM anti-HIV; cytostatic; vaccine; expression; cell culture;
KM acquired immune deficiency syndrome; immune disorder; cancer; neoplasm;
KM protein production; antibody production; PCR; primer; ss.
XX
OS Unidentified.
XX
FN WO2005054467-A1.
XX
PD 16-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-JP018006.
XX
PR 03-DEC-2003; 2003JP-00405269.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Teunoda H, Habu K;
XX
DR WPI; 2005-425413/43.
XX
PT Novel DNA construct comprising mammalian beta actin promoter being
PT functionally coupled to enhancer, useful for producing protein e.g.
PT antibody or treating AIDS or cancer.
XX
PS Example 1; SEQ ID NO 33; 48pp; Japanese.
XX
CC The invention describes a DNA construct (I) comprising a mammalian beta
CC actin promoter being functionally coupled to the enhancer. Also described
CC are: a vector (II) comprising (I); a cell (III) comprising (II); a
CC transgenic non-human animal comprising (II); a totipotent cell comprising
CC (II); and increasing (M1) an expression of a DNA, comprising integrating
CC beta actin promoter to the upstream of the DNA, where the promoter is
CC obtained from a host cell, in which the DNA exist. (II) is useful for
CC expressing a DNA in a host cell such as mammalian cell e.g. rodent cell.
CC (III) is useful for producing protein which involves culturing (II) in a
CC culture medium and recovering protein from the culture and medium. (I) or
CC (II) is useful for producing protein e.g. antibody or treating AIDS or
CC cancer. (I) enables to produce large quantities of protein e.g. antibody.
CC This sequence represents a DNA construct associated primer.
XX
SQ Sequence 22 BP; 4 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 110 GTGCCACTAGCGCTCTGTTCC 131
||| ||| ||| ||| ||| |||
DB 1 GTGCACACGACGCCACGTTGCC 22

```

```

RESULT 19
AEA33500
ID AEA33500 standard; DNA; 22 BP.
XX
AC AEA33500;
XX
XX 25-AUG-2005 (first entry)
XX
DE Expression system associated primer SEQ ID NO 33.

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```

RESULT 20
AAF26513
ID AAF26513 standard; DNA; 18 BP.
XX
AC AAF26513;
XX
XX 27-MAR-2001 (first entry)
XX
DE Human SRC-3 antisense oligonucleotide #17.
XX
KM Steroid receptor coactivator-3; SRC-3; antisense; infection;
KM inflammation; tumour; cancer; ss.
XX
OS Homo sapiens.
XX
FN US6156571-A.
XX
PD 05-DEC-2000.
XX
PF 15-NOV-1999; 99US-00440612.
XX

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PR 15-NOV-1999; 99US-00440612.  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Coweart LM;  
XX  
DR WPI; 2001-079549/09.  
XX  
PT Novel antisense compound useful to prevent or delay infection,  
PT inflammation or tumor formation, specifically hybridizes with, and  
PT inhibits the expression of human steroid receptor coactivator-3.  
XX  
PS Claim 1; Col 40; 36pp; English.  
XX  
CC The present invention relates to an antisense oligonucleotide, targeted  
CC to a nucleic acid molecule encoding human steroid receptor coactivator-3  
CC (SRC-3). The invention is useful for inhibiting the expression of SRC-3  
CC in human cells or tissues in vitro. It is useful for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits. It is useful  
CC prophylactically, to prevent or delay infection, inflammation or tumor  
CC formation  
XX  
SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 6.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 14 CACTGGATTGGTCAC 30  
Db 1 CACTGGATTGGTCGC 17  
XX  
RESULT 21  
AAX91393  
ID AAX91393 standard; DNA; 20 BP.  
XX  
AC AAX91393;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
XX Primer for RT-PCR analysis of T. gondii immunogenic protein DNA.  
XX  
KM Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;  
KM T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;  
KM Toxoplasma oocyst; RT-PCR primer; ss.  
XX  
OS Synthetic.  
OS Toxoplasma gondii.  
XX  
PN WO9932633-A1.  
XX  
PD 01-JUL-1999.  
XX  
PF 18-DEC-1998; 98WO-US027137.  
XX  
PR 19-DEC-1997; 97US-00994825.  
XX  
PA (HESKA-) HESKA CORP.  
XX  
PI Milhausen MJ, Lutz SB, Ng RK;  
XX  
DR WPI; 1999-418930/35.  
XX  
PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat  
PT infection caused by this microorganism.  
XX  
PS Example 2; Page 69; 381pp; English.  
XX  
CC The invention provides isolated Toxoplasma gondii nucleic acids that  
CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,  
CC immunogenic proteins and antibodies to the proteins can be used to  
CC inhibit T. gondii oocyst shedding in a cat due to infection with T.

CC gondii. They can be used for preventing T. gondii infection and for  
CC preventing the spread of T. gondii infection. They can also be used for  
CC detecting T. gondii infection. The detection method can be used to detect  
CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts  
CC such as Cryptosporidium oocysts and Toxoplasma oocysts. Sequences  
CC AAX91276-395 primers used in RT-PCR analysis of nucleic acid sequences  
CC encoding immunogenic T. gondii proteins  
XX  
SQ Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;  
Query Match 6.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 23;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 189 TGTCTTAGGCTGTCTAG 208  
Db 1 TGGCTGTTGGTGTCTCG 20  
XX  
RESULT 22  
AAS42716  
ID AAS42716 standard; DNA; 20 BP.  
XX  
AC AAS42716;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
XX T. gondii immunogenic protein PCR primer nTG78 #2.  
XX  
XX Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;  
KM Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;  
KM oocyte shedding; PCR primer.  
XX  
OS Toxoplasma gondii.  
OS  
PN US2001014447-A1.  
XX  
PD 16-AUG-2001.  
XX  
PF 18-DEC-1998; 98US-00216393.  
XX  
PR 19-DEC-1997; 97US-00994825.  
XX  
PA (MILH/) MILHAUSEN M J.  
XX  
PI Milhausen MJ;  
XX  
DR WPI; 2001-529100/58.  
XX  
PT Detecting parasite oocysts or cysts in feces, comprises eluting DNA from  
PT sample into aqueous solution by heating, amplifying DNA with primers  
PT specific for oocysts or cysts being detected, and detecting amplification  
PT product.  
XX  
PS Example 2; Page 25; 188pp; English.  
XX  
XX The invention relates to detection of parasite oocysts or cysts in a  
XX faeces sample comprising contacting the sample with a solid support,  
XX drying and then washing the sample with an aqueous wash solution, adding  
XX an aqueous elution solution and eluting DNA from the sample by heating  
XX and amplifying by PCR oocyst/cyst-specific DNA and detecting the  
XX amplification products. The method is useful for detecting parasite  
XX oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts  
XX or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia  
XX cysts. The method is also useful for developing vaccines to prevent  
XX oocyte shedding in cats. The present sequence is a PCR primer used to  
XX isolate DNAs encoding immunogenic proteins from Toxoplasma gondii  
SQ  
Query Match 6.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 23;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY      189 TGTCTGTAGGTTGTCTAG 208
XX      |||||||
XX      1 TGGCTGTTGGGTTGTCTGG 20

RESULT 23
ADG17312
ID      ADG17312 standard; DNA; 20 BP.
XX
XX      ADG17312;
AC
XX      26-FEB-2004 (first entry)
XX
DE      T. gondii sequencing primer #118.
XX
XX      Toxoplasma gondii; oocyst shedding; genetic vaccine; vaccine; ss; primer.
XX
XX      Toxoplasma gondii.
OS
XX      US2003194393-A1.
XX
XX      16-OCT-2003.
XX
XX      17-DEC-2002; 2002US-00321856.
XX
XX      19-DEC-1997; 97US-00994825.
XX      18-DEC-1998; 98US-00216393.
XX
XX      (MILH/) MILHAUSEN M J.
XX
XX      Milhausen MJ;
PI
XX      WPI; 2003-899768/82.
XX
XX      Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst
XX      shedding by cats infected with Toxoplasma gondii.
XX
XX      Example 2; SEQ ID NO 262; 198pp; English.
XX
XX      The invention relates to an isolated Toxoplasma gondii protein. The
XX      CC protein is useful for inhibit oocyst shedding by cats infected with
XX      CC Toxoplasma gondii. The protein is useful for preventing or ameliorating
XX      CC diseases caused by infection with T. gondii. The nucleic acid can be used
XX      CC as genetic vaccine which encodes the protein. The protein and the nucleic
XX      CC acid are used as diagnostic reagents for detection of T. gondii
XX      CC infection. The present sequence is used in the exemplification of the
XX      CC invention.
XX
SQ      Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
XX
Query Match      6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      189 TGTCTGTAGGTTGTCTAG 208
XX      |||||||
XX      1 TGGCTGTTGGGTTGTCTGG 20
Db

RESULT 24
ADP78412
ID      ADP78412 standard; DNA; 20 BP.
XX
XX      ADP78412;
AC
XX      12-AUG-2004 (first entry)
XX
XX      Chimeric phosphorothioate oligonucleotide #2211.
XX
XX      GFAT; Antidiabetic; Cardiant;
XX      KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
XX      KW reperfusion; ss.

```

```

XX      XX
XX      OS      Synthetic.
XX      FH      Key
XX      FT      modified_base
XX      FT      1..4
XX      FT      /*tag= a
XX      FT      /mod_base= other
XX      FT      /note= "2-methoxyethyl wing"
XX      FT      modified_base
XX      FT      17..20
XX      FT      /*tag= b
XX      FT      /mod_base= other
XX      FT      /note= "2-methoxyethyl wing"
XX      PN      WO2004035763-A2.
XX      PD      29-APR-2004.
XX      XX      02-OCT-2003; 2003WO-US033332.
XX      PF      17-OCT-2002; 2002US-0419268P.
XX      PR      (PHAA ) PHARMACIA CORP.
XX      XX      (PHAA ) PHARMACIA CORP.
XX      PA      Broschat KO, Crosby SD;
XX      XX      WPI; 2004-348453/32.
XX      DR      17-OCT-2002; 2002US-0419268P.
XX      XX
XX      PT      New compounds, particularly antisense oligonucleotides targeted to a
XX      PT      nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX      PT      (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX      PT      ischemia/reperfusion injury.
XX      XX
XX      PS      Claim 4; SEQ ID NO 2211; 175pp; English.
XX
XX      The present invention relates to a compound which specifically hybridizes
XX      CC with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX      CC of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX      CC modulating the expression of GFAT, and which comprise any of the 1063
XX      CC sequences of 20 base pairs, given in the specification. The compound,
XX      CC composition and methods are useful for treating a disease or condition
XX      CC associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX      CC cardiovascular or neurological disorder, ischemia/reperfusion injury.
XX      CC They are also useful in research and diagnostics for modulating the
XX      CC expression of GFAT. The present sequence represents a chimeric
XX      CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
XX      CC oligonucleotides inhibit human GFAT expression.
XX
SQ      Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match      6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      54 AGCTGCTGCTCACCCTGCTT 73
XX      |||||||
XX      1 ATCTGCTGCTCACCCTGATT 20
Db

RESULT 25
AAC69341
ID      AAC69341 standard; DNA; 21 BP.
XX
XX      AAC69341;
AC
XX      29-JAN-2001 (first entry)
XX
XX      Human ABC1 gene intron 14 polymorphic site, SEQ ID NO:240.
XX
XX      Human ABC1 cholesterol transporter; chromosome 9q31;
XX      KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
XX      KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;
XX      KW cardiovascular disease; coronary artery disease; coronary restenosis;
XX      KW cerebrovascular disease; peripheral vascular disease;

```

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.  
 OS Homo sapiens.  
 XX MO200055318-A2.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-IB000532.  
 XX  
 XX 15-MAR-1999; 99US-0124702P.  
 XX 08-JUN-1999; 99US-0138048P.  
 XX 17-JUN-1999; 99US-0139600P.  
 XX 01-SEP-1999; 99US-0151977P.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 XX WPI; 2000-587528/55.  
 XX  
 XX New ABC1 polypeptide is useful for treating diseases associated with ABC1  
 PT biological activity, e.g. Alzheimer's disease, Huntington's disease and  
 PT cancer.  
 XX  
 XX Example; Fig 11; 229pp; English.  
 PS  
 XX  
 XX The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds. It  
 CC further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or  
 CC prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as Genbank Accession No: AJ012376.1. The  
 CC present sequence represents a polymorphic site of the human ABC1 gene  
 XX  
 XX Sequence 21 BP; 2 A; 12 C; 3 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 6.3%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 22;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 58 GCTGCTCACCCTGCTTCC 77  
 ||||||||| ||| |||

DB 1 GCAGCTCACCCTGCTTCC 20  
 RESULT 26  
 AAH62254/C  
 ID AAH62254 standard; DNA; 21 BP.  
 XX  
 XX AAH62254;  
 XX  
 XX 09-SEP-2004 (revised)  
 DT 12-SEP-2001 (first entry)  
 XX  
 XX NF-kappa-B inhibitor polymorphism containing DNA fragment #155.  
 DE  
 XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
 KW heart disease; paternity testing; forensic science; ds.  
 XX  
 XX Homo sapiens.  
 OS Unidentified.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 11  
 FT variation  
 FT /tag=a  
 FT /standard\_name="single nucleotide polymorphism"  
 XX  
 XX MO200138576-A2.  
 XX  
 XX 31-MAY-2001.  
 PD  
 PD 17-NOV-2000; 2000WO-US031639.  
 XX  
 XX 24-NOV-1999; 99US-0167334P.  
 XX  
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 XX Cargill M, Ireland JS, Lander ES;  
 PI WPI; 2001-367705/38.  
 XX  
 XX New nucleic acid segments of the human genome, particularly from genes  
 PT including polymorphic sites, for phenotype correlation, forensics,  
 PT paternity testing, medicine and genetic analysis.  
 XX  
 XX Claim 1; Page 42; 80pp; English.  
 PS  
 XX  
 XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
 CC contain single nucleotide polymorphisms (SNPs). A method is included in  
 CC the invention for analysing a nucleic acid sample, which consists of  
 CC determining the base occupying any one of the polymorphic sites given in  
 CC the SNP containing sequences. The nucleotide sequences can be used in the  
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
 CC diseases, diseases of the cardiovascular system, and infection by  
 CC microorganisms. The oligonucleotides are also useful in the manufacture  
 CC of a medicament for the treatment or prophylaxis of the diseases, and as  
 CC a pharmaceutical. SNP containing oligonucleotides are useful in  
 CC applications such as phenotype correlation, forensics, paternity testing,  
 CC medicine and genetic analysis  
 CC  
 CC Revised record issued on 09-SEP-2004: Correction to Feature Table Key  
 CC  
 XX  
 XX Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 6.3%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 22;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 37 GCGAGCTCCACCTCCGAGC 56  
 ||||||||| ||| |||  
 DB 21 GAGAGCTCCACCTCGCGGC 2  
 ||||||||| ||| |||  
 RESULT 27  
 ADU66202

ID	ADU66202	standard; RNA; 21 BP.
XX		
AC	ADU66202;	
XX		
DT	27-JAN-2005	(first entry)
XX		
DE	Human MAP kinase 8/JNK1 modified siRNA #27.	
XX		
KW	RNA interference; mitogen activated protein kinase inhibitor; disease; inflammation; immunosuppressive; immune disorder; autoimmune disease; allergy; antiallergic; cytostatic; neoplasm; cancer; ss; siRNA;	
KW	gene silencing; small interfering RNA; MAP kinase inhibitor.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004097020-A2.	
XX		
PD	11-NOV-2004.	
XX		
PF	23-APR-2004; 2004WO-US012517.	
XX		
PR	25-APR-2003; 2003US-00424339.	
PR	30-APR-2003; 2003US-00427160.	
PR	23-MAY-2003; 2003US-00444853.	
PR	23-OCT-2003; 2003US-00693059.	
PR	24-NOV-2003; 2003US-00720448.	
XX	14-JAN-2004; 2004US-00757803.	
XX		
PA	(SIRN-) SIRNA THERAPEUTICS INC.	
XX		
PI	Meswigen J, Beigelman L, Ueman N, Haeblerli P, Chowrira B;	
PI	Polisky B;	
XX		
DR	WPI, 2005-012649/01.	
XX		
PT	Novel short interfering nucleic acid molecule useful for inhibiting	
PT	mitogen activated protein kinase gene expression e.g., c-JUN associated	
PT	with diseases e.g., inflammatory disease or autoimmune disease.	
XX		
PS	Disclosure; SEQ ID NO 1705; 322pp; English.	
XX		
CC	The invention relates to a chemically synthesized double stranded short	
CC	interfering nucleic acid (siNA) molecule (I) that directs cleavage of a c	
CC	-JUN RNA through RNA interference (RNAi), where one strand of the siNA	
CC	molecule comprises nucleotide sequence having sufficient complementarity	
CC	to the c-JUN RNA for the siNA molecule to direct cleavage of the c-JUN	
CC	RNA through RNA interference. (I) is useful for inhibiting mitogen	
CC	activated protein kinase gene (e.g., c-JUN, JNK1, JNK2, p38, ERK1 or	
CC	ERK2) expression associated with diseases e.g., inflammatory disease,	
CC	autoimmune disease, allergy, cancer. (I) exhibits improved RNA	
CC	interference activity and nuclease resistance. The present sequence	
CC	represents a human MAP kinase 8/JNK1 modified siRNA.	
XX		
QO	Sequence 21 BP; 5 A; 3 C; 5 G; 2 T; 6 U; 0 Other;	
XX		
Query Match	6.3%; Score 15.2; DB 1; Length 21;	
Best Local Similarity	55.0%; Pred. No. 22;	
Matches	11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;	
OY	196 TAGGTTGCTTAGGCTGAT 215	
DB	1 UACAGUUGUCUAGCUGAAT 20	
XX		
RESULT 28		
ID	ADW72412/c	
XX		
AC	ADW72412 standard; DNA; 21 BP.	
XX		
ADW72412;		
XX		
DT	24-MAR-2005 (first entry)	
XX		
DE	Mitochondrial polymerase PolG target DNA #59.	

XX Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;  
KW carnitine deficiency; pyruvate carboxylase deficiency;  
KW mitochondrial cytopathy; mitochondrial DNA depletion;  
KW mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;  
KW retinitis pigmentosa; pyruvate dehydrogenase deficiency;  
KW Alzheimer's disease; Parkinson's disease; diabetes; aging; heart disease;  
KW mitochondrial polymerase; Polg; muscular-gen.; ophthalmological;  
KW cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;  
KW neuroprotective; cardiovascular-gen.; antidiabetic; ds.  
XX  
OS Synthetic.  
XX  
XX WO200501062-A2.  
XX  
XX PD 06-JAN-2005.  
XX  
XX PF 25-JUN-2004; 2004MO-US020454.  
XX  
XX PR 25-JUN-2003; 2003US-0482603P.  
PA (GENC-) GENCIA CORP.  
XX  
PI Khan S;  
XX  
DR WPI; 2005-075550/08.  
PT New polynucleotide encoding a polypeptide having an organelle or  
PT chloroplast localization signal, and a protein transduction domain,  
PT useful for treating diseases with defective mitochondrial function.  
PS Claim 96; SEQ ID NO 370; 98pp; English.

The invention relates to a polynucleotide encoding a recombinant polypeptide comprising an organelle and/or chloroplast localization signal and a protein transduction domain. The invention also relates to a recombinant viral vector comprising the polynucleotide, a cell comprising a modified organelle comprising a bacteriophage, a method of transfecting a cell comprising contacting the cell with a vector operably linked to a polypeptide having a protein transduction domain and an organelle targeting signal, a method of modifying an organelle comprising transfecting the cell with a recombinant lambda phage, the recombinant lambda phage comprising a polynucleotide encoding an organelle localization signal operably linked to a bacteriophage lambda surface protein, where the organelle localization signal is displayed on a surface of the recombinant lambda phage and directs the recombinant lambda phage to the organelle, and where the recombinant lambda phage introduces a polynucleotide into the organelle, a composition comprising a recombinant polypeptide comprising an organelle localization signal operably linked to a protein transduction domain, where the recombinant polypeptide is operably linked to a polynucleotide, a method for modifying the metabolism of a cell comprising contacting the cell with a recombinant vector displaying a recombinant polypeptide comprising a mitochondrial localization signal operably linked to a protein transduction domain, the recombinant vector comprising a polynucleotide encoding a functional respiratory chain component, where the functional respiratory chain component compensates for the at least one defective respiratory chain component when expressed by the cell, a method for modifying cytochrome oxidase activity in a cell, and a method of treating a mitochondrial disease in a host, comprising contacting a host's cell with a recombinant vector displaying a recombinant polypeptide comprising a mitochondrial localization signal operably linked to a protein transduction domain, the recombinant vector encoding a functional mitochondrial polypeptide, where the recombinant vector transfects at least one of the host's mitochondria enabling the host's cell to express the functional mitochondrial polypeptide in the at least one transfected mitochondrion. The methods and compositions are useful for transfecting cells and organelle DNA in living cells directly, in particular for transfecting mitochondria and chloroplasts, and for treating diseases related to organelle dysfunction, such as Alpers Disease, carnitine deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy, mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate

CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,  
CC diabetes, aging and heart disease. This sequence represents mitochondrial  
CC polymerase Polg target DNA used in the scope of the invention.

XX Sequence 21 BP; 8 A; 4 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 6.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 22;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 53 CAGCTGCTGCTCCTCAGCTGCT 72  
Db 20 CAGCTGCTGCTCCTCCTGTT 1

RESULT 29  
ADW72414  
ID ADW72414 standard; RNA; 21 BP.

XX ADW72414;

XX 24-MAR-2005 (first entry)

XX Mitochondrial polymerase Polg siRNA strand #118.

XX Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;  
XX carnitine deficiency; pyruvate carboxylase deficiency;  
XX mitochondrial cytopathy; mitochondrial DNA depletion;  
XX mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;  
XX retinitis pigmentosa; pyruvate dehydrogenase deficiency;  
XX Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease;  
XX mitochondrial polymerase; Polg; muscular-gen.; ophthalmological;  
XX cerebropolymerase; anticonvulsant; antiparkinsonian; nootropic;  
XX neuroprotective; cardiovascular-gen.; antidiabetic; ss;  
XX short interfering RNA; siRNA; RNA interference; gene silencing.

XX Synthetic.

OS WO2005001062-A2.

XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-US020454.

XX 25-JUN-2003; 2003US-0482603P.

XX (GENC-) GENCIA CORP.

XX Khan S;

XX WPI; 2005-075550/08.

XX New polynucleotide encoding a polypeptide having an organelle or  
PT chloroplast localization signal, and a protein transduction domain,  
PT useful for treating diseases with defective mitochondrial function.

XX Claim 96; SEQ ID NO 372; 98pp; English.

XX The invention relates to a polynucleotide encoding a recombinant  
CC polypeptide comprising an organelle and/or chloroplast localization  
CC signal and a protein transduction domain. The invention also relates to a  
CC recombinant viral vector comprising the polynucleotide, a cell comprising  
CC a modified organelle comprising a bacteriophage, a method of transfecting  
CC a cell comprising contacting the cell with a vector operably linked to a  
CC polypeptide having a protein transduction domain and an organelle  
CC targeting signal, a method of modifying an organelle comprising  
CC transfecting the cell with a recombinant lambda phage, the recombinant  
CC lambda phage comprising a polynucleotide encoding an organelle  
CC localization signal operably linked to a bacteriophage lambda surface  
CC protein, where the organelle localization signal is displayed on a  
CC surface of the recombinant lambda phage and directs the recombinant  
CC lambda phage to the organelle, and where the recombinant lambda phage  
CC introduces a polynucleotide into the organelle, a composition comprising

CC a recombinant polypeptide comprising an organelle localization signal  
CC operably linked to a protein transduction domain, where the recombinant  
CC polypeptide is operably linked to a polynucleotide, a method for  
CC modifying the metabolism of a cell comprising contacting the cell with a  
CC recombinant vector displaying a recombinant polypeptide comprising a  
CC mitochondrial localization signal operably linked to a protein  
CC transduction domain, the recombinant vector comprising a polynucleotide  
CC encoding a functional respiratory chain component, where the functional  
CC respiratory chain component compensates for the at least one defective  
CC respiratory chain component when expressed by the cell, a method for  
CC modifying cytochrome oxidase activity in a cell, and a method of treating  
CC a mitochondrial disease in a host, comprising contacting a host's cell  
CC with a recombinant vector displaying a recombinant polypeptide comprising  
CC a mitochondrial localization signal operably linked to a protein  
CC transduction domain, the recombinant vector encoding a functional  
CC mitochondrial polypeptide, where the recombinant vector transfects at  
CC least one of the host's mitochondria enabling the host's cell to express  
CC the functional mitochondrial polypeptide in the at least one transfected  
CC mitochondrion. The methods and compositions are useful for transfecting  
CC cells and organelle DNA in living cells directly, in particular for  
CC transfecting mitochondria and chloroplasts, and for treating diseases  
CC related to organelle dysfunction, such as Alpers Disease, carnitine  
CC deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy,  
CC mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial  
CC myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate  
CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,  
CC diabetes, aging and heart disease. This sequence represents mitochondrial  
CC polymerase Polg siRNA used in the scope of the invention.

XX Sequence 21 BP; 1 A; 8 C; 4 G; 2 T; 6 U; 0 Other;

Query Match 6.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 65.0%; Pred. No. 22;  
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 53 CAGCTGCTGCTCCTCAGCTGCT 72  
Db 2 CAGCTGCTGCTCCTCCTGTT 21

RESULT 30  
AEC03076/C

XX ID AEC03076 standard; DNA; 21 BP.

XX AEC03076;

XX 03-NOV-2005 (first entry)

XX Human IGE short interfering nucleic acid SEQ ID NO 679.

XX antiallergic; antiinflammatory; antiasthmatic; dermatological;  
XX immunosuppressive; expression; RNA interference; allergy;  
XX atopic dermatitis; urticaria; dermatological disease;  
XX immediate type hypersensitivity; immunosuppressive; asthma;  
XX antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;  
XX ear, nose, throat disease; inflammation; respiratory disease;  
XX immune disorder; IGE; short interfering nucleic acid; siRNA;  
XX gene silencing; ss.

XX Homo sapiens.

XX WO2005080410-A1.

XX 01-SEP-2005.

XX 21-FEB-2005; 2005WO-NZ000021.

XX 20-FEB-2004; 2004US-0546434P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Murlison GJ, Grigor MR, Havukkala JU, Munro G,  
PI Abernethy N, Webster G;

```

XX DR WPI; 2005-591970/60.
XX
XX PT New composition comprises small interfering nucleic acid molecule (siNA)
XX PT capable of reducing expression of a target gene that is active in a IGE-
XX PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
XX PT dermatitis.
XX
XX PS Example 2; SEQ ID NO 679; 178bp; English.
XX
XX CC The invention describes a composition comprising a small interfering
XX CC nucleic acid molecule (siNA) capable of reducing expression of a target
XX CC gene that is active in a IGE-mediated disorder, a genetic construct that
XX CC expresses the siNA, and a binding agent that specifically binds to a
XX CC target antigen expressed on the surface of the cell. Also described are:
XX CC a method for the treatment of an IGE-mediated disorder in a patient;
XX CC prevention of IGE-mediated disorder in a patient; reduction of
XX CC eosinophilia in a patient; modulating an IGE-mediated immune response to
XX CC of an immune response to a specific antigen in a patient. The composition
XX CC is useful in the preparation of a medicament useful for the treatment of
XX CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,
XX CC urticaria, atopic dermatitis, food allergies, diseases that benefit from
XX CC the reduction of eosinophilia in the tissues of the respiratory system,
XX CC or disorders having hypersensitivity immune reaction. This sequence
XX CC represents a siNA for suppression of human IGE expression.
XX
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 142 AGCACCCTCTCAGCGAGCT 161
Db 21 AGTACTTCTCAGCGAGCT 2

RESULT 31
AAV13327
ID AAV13327 standard; DNA; 18 BP.
XX
XX AC AAV13327;
XX
XX DT 14-MAY-1998 (first entry)
XX
XX DE Sense primer Exon 9 for human 5-lipoxygenase gene.
XX
XX KM Inflammatory disease; polymorphism; 5-lipoxygenase; asthma;
XX KM ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis;
XX KM arthritis; diagnosis; treatment; PCR primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9742347-A2.
XX
XX PD 13-NOV-1997.
XX
XX PF 29-APR-1997; 97WO-US007137.
XX
XX PR 06-MAY-1996; 96US-0016890P.
XX PR 25-APR-1997; 97US-00846020.
XX
XX PA (BGMH ) BRIGHAM & WOMENS HOSPITAL.
XX
XX PI Drazen JM, In K, Asano K, Beier D, Grobholz J;
XX
XX DR WPI; 1997-558997/51.
XX
XX PT Classifying patients with inflammatory disease, specifically asthma -
XX PT according to polymorphisms in 5-lipoxygenase gene regulatory region, e.g.
XX PT to identify candidates for lipoxygenase inhibitor treatment.

```

```

XX PS Example 1; Page 19; 56bp; English.
XX
XX CC The present sequence was used in the development of a novel method for
XX CC classifying patients suffering from an inflammatory disease. The method
XX CC comprises identifying in DNA from at least 1 patient a sequence
XX CC polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene
XX CC (AA88431), in a 5-LOX regulatory gene sequence. The method can be
XX CC applied to subjects with asthma, ulcerative colitis, bronchitis,
XX CC sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or
XX CC rheumatoid arthritis. Specifically it can be used to diagnose asthma or
XX CC susceptibility to disease, identify treatments suitable for individual
XX CC patients or assess the likely success of treatment
XX
SQ Sequence 18 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match      6.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 CCTCCCGAGCTGCTG 61
Db 2 CCTCCCGAGCTGCTG 16

RESULT 32
ADJ95475
ID ADJ95475 standard; DNA; 18 BP.
XX
XX AC ADJ95475;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Equine herpesvirus type 1-related PCR primer #2.
XX
XX KM virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;
XX KM Equine herpesvirus type 4; genetic marker; ORF30-ml region marker;
XX KM virucide; vaccine; EHV-1 strain V592 polymerase ORF30-ml region;
XX KM neurovirulence; herpesvirus disease; PCR; primer; ss.
XX
XX OS Equine herpesvirus 1.
XX
XX PN WO2004011677-A2.
XX
XX PD 05-FEB-2004.
XX
XX PF 23-JUL-2003; 2003WO-GB003279.
XX
XX PR 26-JUL-2002; 2002US-0398576P.
XX
XX PA (ANIM-) ANIMAL HEALTH TRUST.
XX
XX PI Davis Poynter N, Nugent J, Birch-Machin I, Allen G;
XX
XX DR WPI; 2004-143877/14.
XX
XX PT Assessing the virulence of a herpesvirus isolate, useful in preventing or
XX PT treating herpesvirus infection, by using virulence marker corresponding
XX PT to an ORF30-ml region.
XX
XX PS Claim 24; Page 60; 63bp; English.
XX
XX CC This invention relates to a novel method of assessing the virulence of a
XX CC herpesvirus isolate, for example Equine herpesvirus type 1 (EHV-1) or
XX CC type 4 (EHV-4), which comprises using a genetic marker, especially an
XX CC ORF30-ml region marker. The invention may be useful for the production of
XX CC compounds with a virucide activity or for the development of a vaccine.
XX CC The method, kit and sequence of the EHV-1 strain V592 polymerase ORF30-ml
XX CC region are useful for assessing the virulence of a herpesvirus or
XX CC neurovirulence. The vaccine is useful for immunising a host against a
XX CC herpesvirus disease and for treating disease. The present sequence is
XX CC that of a PCR primer which was used in the exemplification of the
XX CC invention.

```



XX SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 6.1%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCTCAGCAGCA 15  
1 TTTCTCAGCAGCA 15  
DB 1 TTCTCAGCAGCA 15  
RESULT 33  
AEE10387/C  
ID AEE10387 standard; DNA; 18 BP.  
XX AC AEE10387;  
XX DT 26-JAN-2006 (first entry)  
XX DE Maize gamma-zein PCR primer SEQ ID NO:2.  
XX KW ss; PCR; primer; gamma-zein; transgenic plant; mucopolysaccharidosis;  
XX KW metabolic; metabolic disorder.  
XX OS Zea mays.  
XX FN WO2005113775-A1.  
XX PD 01-DEC-2005.  
XX PF 19-MAY-2005; 2005WO-CA000762.  
XX PR 21-MAY-2004; 2004US-0573777P.  
XX PR 04-AUG-2004; 2004US-0598428P.  
XX PA (UFRP-) UNIV FRASER SIMON.  
XX PI Kermode AR, He X, Clarke L;  
XX DR WPI; 2005-812257/82.  
XX PT New nucleotide sequence comprising a first nucleic acid sequence encoding  
PT a gamma-zein signal peptide; a second nucleic acid sequence encoding the  
PT protein of interest; and a regulatory element, useful for producing  
PT transgenic plants.  
XX PS Example 2; SEQ ID NO 2; 53pp; English.  
XX CC The invention relates to a new nucleotide sequence which comprises: a  
CC first nucleic acid sequence encoding a signal peptide that localizes a  
CC protein of interest fused to the signal peptide to an endoplasmic  
CC reticulum-derived protein body within a cell; a second nucleic acid  
CC sequence encoding the protein of interest; and a regulatory element  
CC operatively linked with the first nucleotide sequence, where one or more  
CC than one of the first nucleic acid, the second nucleic acid and the  
CC regulatory element, is heterologous with respect to one or more than one  
CC of first nucleic acid, the second nucleic acid and the regulatory  
CC element. Also described are: a nucleotide sequence comprising, a gamma-  
CC zein regulatory element operatively linked with a nucleic acid sequence  
CC encoding a gamma-zein signal peptide fused to a heterologous protein of  
CC interest, and a gamma-zein 3' UTR operatively linked to the nucleic acid  
CC sequence; a vector comprising the nucleotide sequence; a plant comprising  
CC the nucleotide sequence; a plant cell comprising the nucleotide sequence;  
CC a seed comprising the nucleotide sequence; a method of producing a  
CC protein of interest comprising providing a plant comprising the  
CC nucleotide sequence; and expressing the protein of interest; and an  
CC expression construct comprising the following operatively linked elements  
CC P-35'-UTR-GSP-X-33'-UTR. The nucleotide sequence is useful for producing  
CC transgenic plants and seeds having heterologous protein, such as gamma-  
CC zein peptide, localized to the endoplasmic reticulum protein bodies in  
CC the transgenic plant. The produced proteins are useful in treatment of,  
CC e.g., lysosomal diseases such as mucopolysaccharidosis. The present

CC CC Sequence represents a PCR primer used with primer ABE10386 to amplify and  
CC clone the 5'UTR and signal peptide-encoding sequences of gamma-zein.  
XX SQ Sequence 18 BP; 2 A; 5 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 28;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 34 GCTGGAGCTTCACCTCC 51  
18 GCTGGAGCTTCACCTCC 1  
DB 18 GCTGGAGCTTCACCTCC 1  
RESULT 34  
ADG31596/C  
ID ADG31596 standard; DNA; 20 BP.  
XX AC ADG31596;  
XX DT 26-FEB-2004 (first entry)  
XX DE PCR primer used to amplify human PKHD1 exon 57 for mutation analysis.  
XX KW PCR; ss; polycystic kidney and hepatic disease 1; PKHD1;  
XX KW autosomal recessive polycystic kidney disease; ARPKD;  
XX KW congenital hepatic fibrosis; human; nephrotropic; cell proliferation;  
XX KW cellular adhesion; repulsion; primer.  
XX OS Homo sapiens.  
XX FN WO2003085088-A2.  
XX PN 16-OCT-2003.  
XX PD 03-FEB-2003; 2003WO-US003410.  
XX PF 01-FEB-2002; 2002US-0353472P.  
XX PR (UABR-) UAB RES FOUND.  
XX PA Germine GG, Onuchic LF, Nagasawa Y, Guay-Woodford LM, Somolo S;  
XX PI Furu VM;  
XX DR WPI; 2003-877030/81.  
XX PT New polycystic kidney and hepatic disease 1 polynucleotides and  
PT polypeptides, useful in diagnostic testing and for developing targeted  
PT therapeutic interventions for patients with autosomal recessive  
PT polycystic kidney disease.  
XX PS Disclosure; Page 40; 41pp; English.  
XX CC This invention relates to a novel nucleic acid that encodes the  
CC polycystic kidney and hepatic disease 1 (PKHD1) polypeptide. It has been  
CC identified that a mutation in the PKHD1 gene is associated with autosomal  
CC recessive polycystic kidney disease (ARPKD), which is characterised by  
CC enlarged kidneys and congenital hepatic fibrosis, and is most commonly  
CC observed in children and infants. The present invention describes the  
CC identification of the PKHD1 gene, mapped to human chromosome 6p21.1-p12,  
CC and splice variants thereof. The PKHD1 polynucleotides and polypeptides  
CC are useful in diagnostic testing and for developing targeted therapeutic  
CC interventions for patients with ARPKD. Furthermore, they exhibit  
CC nephrotropic activity and are involved in the regulation of cell  
CC proliferation, cellular adhesion and repulsion. This oligonucleotide  
CC sequence is a PCR primer used to amplify human PKHD1 exons for mutation  
CC analysis, in an exemplification of the invention.  
XX SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
OY      22  TTGTGTCACCTGCTGGG 39
Db      20  TTGTGTAACCTAGCTGGG 3

RESULT 35
ID      ADP78946 standard; DNA; 20 BP.
XX
AC      ADP78946;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide #2745.
XX
KM      GFAT; Antidiabetic; Cardiant;
KW      Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
reperfusion; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..4
FT      /*tag= a
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
FT      modified_base 17..20
FT      /*tag= b
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
XX
PN      WO2004035763-A2.
XX
PD      29-APR-2004.
XX
PF      02-OCT-2003; 2003WO-US033332.
XX
PR      17-OCT-2002; 2002US-0419268P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Broschat KO, Crosby SD;
XX
DR      WPI; 2004-348453/32.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT      (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT      ischemia/reperfusion injury.
XX
PS      Claim 4; SEQ ID NO 2745; 175pp; English.
XX
CC      The present invention relates to a compound which specifically hybridizes
CC      with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC      of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC      modulating the expression of GFAT, and which comprise any of the 3063
CC      sequences of 20 base pairs, given in the specification. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC      cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC      They are also useful in research and diagnostics for modulating the
CC      expression of GFAT. The present sequence represents a chimeric
CC      phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC      oligonucleotides inhibit human GFAT expression.
XX
SQ      Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match      6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      56  CTGCTGCTCACCCTGCTT 73
```

```
Db      1  CTGCTGCTCACCCTGATT 18

RESULT 36
ID      ADP78939 standard; DNA; 20 BP.
XX
AC      ADP78939;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide #2738.
XX
KM      GFAT; Antidiabetic; Cardiant;
KW      Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
reperfusion; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..4
FT      /*tag= a
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
FT      modified_base 17..20
FT      /*tag= b
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
XX
PN      WO2004035763-A2.
XX
PD      29-APR-2004.
XX
PF      02-OCT-2003; 2003WO-US033332.
XX
PR      17-OCT-2002; 2002US-0419268P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Broschat KO, Crosby SD;
XX
DR      WPI; 2004-348453/32.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT      (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT      ischemia/reperfusion injury.
XX
PS      Claim 4; SEQ ID NO 2738; 175pp; English.
XX
CC      The present invention relates to a compound which specifically hybridizes
CC      with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC      of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC      modulating the expression of GFAT, and which comprise any of the 3063
CC      sequences of 20 base pairs, given in the specification. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC      cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC      They are also useful in research and diagnostics for modulating the
CC      expression of GFAT. The present sequence represents a chimeric
CC      phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC      oligonucleotides inhibit human GFAT expression.
XX
SQ      Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
Query Match      6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      56  CTGCTGCTCACCCTGCTT 73
Db      2  CTGCTGCTCACCCTGATT 19
```

```
RESULT 37
ADP81801/C
ID ADP81801 standard; DNA; 20 BP.
XX
XX AC ADP81801;
XX
XX DT 26-AUG-2004 (first entry)
XX
DE Human MD-1 RP105-associated antisense oligo, ISIS 260183.
XX
XX MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
XX human; antisense; phosphorochioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key modified_base Location/Qualifiers
XX FT 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorochioate backbone in which all cytidine
XX residues are 5-methylcytidines"
XX modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) bases"
XX modified_base 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) bases"
XX
XX US2004110146-A1.
XX
XX 10-JUN-2004.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Doile KW;
XX
XX WPI; 2004-440335/41.
XX
XX New oligonucleotide compound that inhibits expression of MD-1 RP105-
XX associated, useful for preparing a composition for treating autoimmune
XX disorder.
XX
XX Example 15; SEQ ID NO 40; 63pp; English.
XX
XX The invention relates to compounds, compositions and methods for
XX modulating the expression of MD-1 RP105-associated (also called as MD-1
XX and MD1) DNA. The composition comprise antisense oligonucleotides
XX targeted to MD-1 RP105-associated DNA. The compound is useful for
XX preparing a composition for treating autoimmune disorder. It is also
XX useful in gene therapy. The present sequence is an antisense
XX oligonucleotide targeted to human MD-1 RP105-associated DNA. This
XX sequence is used to illustrate the method of the invention.
XX
XX Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 CTGCTCAGCTGCTTTTC 76
DB 18 CAGACTCAGCTGCTTTTC 1
```

```
RESULT 38
ADP81821
ID ADP81821 standard; DNA; 20 BP.
XX
XX AC ADP81821;
XX
XX DT 26-AUG-2004 (first entry)
XX
DE Human MD-1 RP105-associated DNA target region #11.
XX
XX MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
XX human; ds.
XX
OS Homo sapiens.
XX
XX US2004110146-A1.
XX
XX 10-JUN-2004.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Doile KW;
XX
XX WPI; 2004-440335/41.
XX
XX New oligonucleotide compound that inhibits expression of MD-1 RP105-
XX associated, useful for preparing a composition for treating autoimmune
XX disorder.
XX
XX Example 15; SEQ ID NO 60; 63pp; English.
XX
XX The invention relates to compounds, compositions and methods for
XX modulating the expression of MD-1 RP105-associated (also called as MD-1
XX and MD1) DNA. The composition comprise antisense oligonucleotides
XX targeted to MD-1 RP105-associated DNA. The compound is useful for
XX preparing a composition for treating autoimmune disorder. It is also
XX useful in gene therapy. The present sequence is human MD-1 RP105-
XX associated DNA target region. This sequence is used to illustrate the
XX method of the invention.
XX
XX Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 CTGCTCAGCTGCTTTTC 76
DB 3 CAGACTCAGCTGCTTTTC 20
XX
RESULT 39
ADR70686/C
ID ADR70686 standard; DNA; 20 BP.
XX
XX ADR70686;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX Solanum glycosylase related PCR primer SEQ ID NO:23.
XX
XX glycosylase; enzyme; saccharide; pharmaceutical; food additive;
XX industrial raw material; PCR; primer; ss; plant.
XX
XX Solanum.
XX
XX Synthetic.
XX
XX WO2004078979-A1.
XX
```

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PD 16-SEP-2004.
XX
PF 03-MAR-2004; 2004WO-JP002675.
XX
PR 03-MAR-2003; 2003JP-00055468.
XX
PR 31-MAR-2003; 2003JP-00093642.
XX
PA (RIKE ) RIKEN KK.
XX
PI Muranaka T, Kohara A;
XX
DR WPI; 2004-662429/64.
XX
PT New glycosylase protein derived from Solanaceae plant, useful for
XX manufacturing pharmaceuticals and food additive.
XX
PS Example 5; SEQ ID NO 23; 61pp; Japanese.
XX
CC The present invention describes a glycosylase protein (I) having a
CC sequence of SEQ ID NO:1, 3, 7, 9 or 11 (S1) (ADR70664, ADR70666,
CC ADR70670, ADR70672 or ADR70674), a sequence comprising (S1) in which one
CC or more amino acids are deleted, substituted and/or added, or a sequence
CC exhibiting 70% or more homology with (S1), where the amino acid sequence
CC exhibits glycosylase activity. Also described: (1) a gene (II) encoding
CC host (1) a recombinant vector (III) containing: (1) a gene (II) encoding
CC host (IV) comprising (II) or (III); and (4) producing (I), using (IV).
CC (I) is useful for combining a saccharide with a substrate, which involves
CC reacting saccharide and a substrate in the presence of (I). (I) can be
CC used in manufacturing pharmaceuticals, food additive or as industrial raw
CC material. (I) has high substrate specificity. The present sequence
CC represents a PCR primer for a Solanum glycosylase protein, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 38 GGAGCTCCAGCTCCCGAG 55
DB 19 GGAGCTCAACATCCCCAG 2
XX
RESULT 40
ADZ47085
ID ADZ47085 standard; DNA; 20 BP.
XX
AC ADZ47085;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human phosphodiesterase 4B antisense oligo target site SEQ ID NO:113.
XX
KW ss; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
XX expression; autoimmune disease; immune disorder.
XX
OS Homo sapiens.
XX
PN US2005101000-A1.
XX
PD 12-MAY-2005.
XX
PF 11-DEC-2002; 2002US-00317869.
XX
PR 11-DEC-2002; 2002US-00317869.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KM;
XX
DR WPI; 2005-345404/35.
XX

```

```

PT New compound 8-80 nucleobases in length targeted to a nucleic acid
PT molecule encoding phosphodiesterase 4B, useful for diagnosing or treating
PT disease associated with expression of phosphodiesterase 4B, e.g.
PT autoimmune disease.
XX
PS Example 15; SEQ ID NO 113; 25pp; English.
XX
CC The invention relates to a novel compound 8-80 nucleotides in length
CC targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where
CC the compound specifically hybridizes with the nucleic acid molecule
CC encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of
CC phosphodiesterase 4B. A compound of the invention has immunosuppressive
CC activity. The compound is useful for modulating the expression of
CC phosphodiesterase 4B. It is useful for diagnosing or treating diseases
CC associated with expression of phosphodiesterase 4B, including autoimmune
CC disease. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 61 GCCTCAGCTGCTTTTCCA 78
DB 1 GCCTCAGCTGCTTTTCCA 18
XX
RESULT 41
ADZ47045/c
ID ADZ47045 standard; DNA; 20 BP.
XX
AC ADZ47045;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human phosphodiesterase 4B antisense oligonucleotide SEQ ID NO:73.
XX
KW ss; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
XX expression; autoimmune disease; immune disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="OTHER=phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note="2-methoxyethyl nucleotides"
FT 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note="2-methoxyethyl nucleotides"
XX
PN US2005101000-A1.
XX
PD 12-MAY-2005.
XX
PF 11-DEC-2002; 2002US-00317869.
XX
PR 11-DEC-2002; 2002US-00317869.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KM;
XX
DR WPI; 2005-345404/35.
XX

```

PT New compound 8-80 nucleobases in length targeted to a nucleic acid  
PT molecule encoding phosphodiesterase 4B, useful for diagnosing or treating  
PT diseases associated with expression of phosphodiesterase 4B, e.g.  
PT autoimmune disease.  
XX  
PS Example 15; SEQ ID NO 73; 25pp; English.  
XX  
CC The invention relates to a novel compound 8-80 nucleotides in length  
CC targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where  
CC the compound specifically hybridizes with the nucleic acid molecule  
CC encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of  
CC phosphodiesterase 4B. A compound of the invention has immunosuppressive  
CC activity. The compound is useful for modulating the expression of  
CC phosphodiesterase 4B. It is useful for diagnosing or treating diseases  
CC associated with expression of phosphodiesterase 4B, including autoimmune  
CC disease. The present sequence is used in the exemplification of the  
CC invention.  
CC  
XX  
SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 6.1%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 61 GCCTCAGCTGCTTTCCA 78  
DB 20 GCCTCAGCTGCTTTCTTA 3  
XX  
RESULT 42  
AEC80212/C  
ID AEC80212 standard; DNA; 20 BP.  
XX  
AC AEC80212;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE Skin permeabilization associated mouse gene RT-PCR primer SEQ ID NO 63.  
XX  
KW drug delivery; permeabilization; reverse transcriptase PCR; RT-PCR; PCR;  
KW primer; ss.  
XX  
OS Mus sp.  
XX  
PN WO200508299-A1.  
XX  
PD 22-SEP-2005.  
XX  
PF 10-SEP-2004; 2004WO-JP013219.  
XX  
PR 10-MAR-2004; 2004JP-00068249.  
XX  
PS 10-MAR-2004; 2004JP-00068249.  
XX  
PA (HISA-) HISAMITSU MEDICAL CO LTD.  
XX  
PI (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.  
XX  
PI Tsuji A, Kato M, Sai Y, Li Q;  
XX  
DR WPI; 2005-676484/69.  
XX  
PT Estimation of percutaneous drug permeability, involves pouring drug  
PT solution into chamber having subcutaneous tissue side and epidermal side,  
PT injecting specific solution, and measuring permeability mediated by  
PT transporter.  
XX  
PS Example 1; SEQ ID NO 63; 37pp; Japanese.  
XX  
CC The invention describes permeability of a percutaneous drug is assayed by  
CC pouring a solution containing percutaneous drug into a chamber having  
CC subcutaneous tissue side and epidermal side, injecting polyhydric alcohol  
CC -containing solution into the epidermal side, and measuring the degree of  
CC permeability mediated by a dermal transporter. Also described is a  
CC method of secreting for an inhibitory substance, which involves  
CC performing comparative evaluation showing the extent of skin

CC permeability. The method is useful for assaying permeability of  
CC percutaneous drugs e.g. indomethacin. The skin permeability of a  
CC percutaneous drug can be assayed more efficiently. This sequence  
CC represents a mouse gene specific primer associated with skin permeability  
CC to a percutaneous drug. Note: This sequence is also available in  
CC electronic format directly from wipo at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 6.1%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 212 GTATCAGTATACCACTA 229  
DB 19 GTATCAGTATACCACTA 2  
XX  
RESULT 43  
AAV25273/C  
ID AAV25273 standard; DNA; 21 BP.  
XX  
AC AAV25273;  
XX  
DT 11-JUN-1998 (first entry)  
XX  
DE Primer F2 for H.pylori gly gene.  
XX  
KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;  
KW identification; binding compound; bacteria; life cycle; activator;  
KW inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;  
KW PCR primer; ss.  
XX  
XX  
OS Synthetic.  
XX  
OS Helicobacter pylori.  
XX  
PN WO9737044-A1.  
XX  
PD 09-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-US005223.  
XX  
PR 29-MAR-1996; 96US-00625811.  
PR 02-APR-1996; 96US-00758731.  
PR 25-OCT-1996; 96US-00736905.  
PR 28-OCT-1996; 96US-00738859.  
PR 06-DEC-1996; 96US-00761318.  
XX  
PA (ASTR ) ASTRA AB.  
XX  
PI Smith D, Alm RA;  
XX  
DR WPI; 1997-503122/46.  
XX  
PT Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) -  
PT useful in vaccines to treat or prevent H. pylori infection and for  
PT diagnosis of H. pylori infection.  
XX  
PS Example; Page 108; 1145pp; English.  
XX  
CC This sequence represents a primer for the H.pylori gly gene. The  
CC amplified sequence was used to compare homology of the coding sequences  
CC of the invention with other known proteins. The protein encoded by the  
CC DNA of the invention may be used in a vaccine to prevent or treat  
CC H. pylori infection or to identify H.pylori polypeptide binding compounds,  
CC useful as potential H.pylori life cycle activators or inhibitors. The DNA  
CC and probes derived from it may be used for the identification of H.pylori  
CC in a sample and the diagnosis of H.pylori infection. Nucleic acid  
CC sequences complementary to the DNA act as antisense sequences and can be  
CC used to prevent the translation of H.pylori mRNA. Antibodies against the  
CC protein can be used in immunoassays to evaluate the abundance and  
CC distribution of H.pylori-specific antigens. The genomic sequence of

```
CC H.pylori (ATCC 55679) was determined from overlapping contigs generated
CC by mechanically shearing the bacterial DNA. The sequences were analysed
CC for ORF of at least 180 nucleotides, and the predicted coding regions
CC defined by computer evaluation. To identify likely H.pylori antigens for
CC vaccine development, the amino acid sequences predicted from various ORF
CC were analysed for significant homology to other known or exported
CC membrane proteins. Having identified and determined the sequences of
CC interest, particular regions can be isolated from H.pylori by PCR
CC amplification for recombinant polypeptide production, e.g. in E. coli
CC hosts
XX
SQ Sequence 21 BP; 4 A; 2 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 TCACCTGCTTTCCCAAC 81
DB 19 TCACGAGATTTCACAC 2
RESULT 44
ADH77769/C
ID ADH77769 standard; DNA; 21 BP.
XX
AC ADH77769;
XX
DT 22-APR-2004 (first entry)
XX
DE Human Alstrom's syndrome-related gene (ALMS1) PCR primer #10.
XX
KW human; ALMS1; Alstrom's syndrome; PCR; ss; primer.
XX
OS Homo sapiens.
XX
PN FR2832420-A1.
XX
PD 23-MAY-2003.
XX
PF 12-NOV-2002; 2002FR-00014097.
XX
PR 09-NOV-2001; 2001US-0345883P.
XX
PA (HOPE) HOFPMANN LA ROCHE & CO AG F.
XX (JACK-) JACKSON LAB.
XX
PI Collin GB, Marshall J, Martin ML, Nagger JK, Nishina MP, Sow V;
XX WPI; 2003-610292/58.
XX
DR WPI; 2003-610292/58.
XX
PT New DNA associated with Alstrom syndrome, useful for diagnosis and
PT identification of carriers, also related polypeptides, antibodies and
PT transgenic animals.
XX
PS Example; SEQ ID NO 12; 71bp; French.
XX
CC The invention comprises the amino acid and coding sequence of the human
CC protein ALMS1 which is associated with Alstrom's syndrome. The DNA and
CC protein sequences of the invention are useful in the diagnosis of
CC Alstrom's syndrome. The present DNA sequence represents a PCR primer for
CC the human ALMS1 gene.
XX
SQ Sequence 21 BP; 7 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 GCACCTGAGTTTGGTCAC 30
DB 21 GCACCTGAGCTTTGTCAC 4
```

```
RESULT 45
ACL48195
ID ACL48195 standard; RNA; 21 BP.
XX
AC ACL48195;
XX
DT 24-MAR-2005 (first entry)
XX
DE FOLH1 siRNA antisense sequence, SEQ ID 9267.
XX
KW Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
OS Synthetic.
XX
PN WO2005001092-A2.
XX
PD 06-JAN-2005.
XX
PF 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
PA (AMHP) WYETH.
XX
PI Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
DR WPI; 2005-075568/08.
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX Claim 3; SEQ ID NO 9267; 113bp; English.
XX
PS The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTCTCCGACGACGACATG 18
DB 1 TTCTCCGACGACGACGATG 18
DB 1 TTCTCCGACGACGACGATG 18
RESULT 46
ACL48194/C
ID ACL48194 standard; RNA; 21 BP.
XX
AC ACL48194;
XX
DT 24-MAR-2005 (first entry)
```

DE FOLH1 siRNA sense sequence, SEQ ID 9266.  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
KW short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI, 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 9266; 113pp; English.  
XX  
XX The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 0 T; 6 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTCTCCAGCAGCAGCTG 18  
DB 19 TTCTCCAGCAGCAGCTG 2  
RESULT 47  
ACL48196/c  
ID ACL48196 standard; DNA; 21 BP.  
XX  
XX ACL48196;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX FOLH1 target oligonucleotide, SEQ ID 9268.  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.

XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
KW short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI, 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 9268; 113pp; English.  
XX  
XX The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC target oligonucleotide from one such CRTP for which short interfering  
CC RNAs (siRNA) were produced. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTCTCCAGCAGCAGCTG 18  
DB 20 TTCTCCAGCAGCAGCTG 3  
RESULT 48  
ACL48430/c  
ID ACL48430 standard; DNA; 21 BP.  
XX  
XX ACL48430;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX FOLH1 target oligonucleotide, SEQ ID 9502.  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX

DR	WP1; 2005-075568/08.
XX	
PT	Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT	activated by the polypeptide or antibody, and a carrier, useful for
PT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 9502; 113pp; English.
XX	
CC	The present invention relates to a novel pharmaceutical composition
CC	comprising: (a) an agent capable of modulating an expression level or
CC	protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC	, an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC	FLJ11866, GPR84, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRTP for which short interfering
CC	RNA (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pat_sequences
XX	
SQ	Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
Query Match:	6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity	88.9%; Pred. No. 24;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	1 TTCTCAGCACAGCACTG 18                Db 18 TTCTCACCACAGCACTG 1
RESULT 49	
ACL48198	
ID	ACL48198 standard; RNA; 21 BP.
XX	
AC	ACT48198;
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	FOLH1 siRNA antisense sequence, SEQ ID 9270.
XX	
KW	Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW	short interfering RNA; gene silencing.
XX	
OS	Synthetic.
XX	
PX	WO2005001092-A2.
PN	
PD	06-JAN-2005.
XX	
PF	19-MAY-2004; 2004MO-US015645.
XX	
PR	20-MAY-2003; 2003US-0471723P.
XX	
PA	(AMHP ) WYETH.
XX	
PI	Be X, Wei L, Slonim DK, Howes SH;
XX	
DR	WP1; 2005-075568/08.
XX	
PT	Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT	activated by the polypeptide or antibody, and a carrier, useful for
PT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 9270; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRP) or gene  
CC ; an antibody specific for a CRP, or a T cell activated by a CRP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRP by RNA interference or an antisense mechanism. The CRPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0.

Oy 1 TTCTCGAGCACGACTG 18  
Db ::::| | | | | | | :  
2 UUCUCCACGACGACGUG 19

RESULT 50  
ACLA8197/C  
ID ACL48197 standard; RNA; 21 BP.  
XX  
XX AC ACL48197;  
XX  
XX 24-MAR-2005 (first entry)  
DT  
DE FOLH1 siRNA sense sequence, SEQ ID 9269.  
XX  
XX FOLH1 siRNA sense sequence, SEQ ID 9269.  
XX  
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;  
KM short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
OS  
XX WO2005001092-A2.  
PN  
PD 06-JAN-2005.  
PF  
PR 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
PA (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
PI  
XX WPI; 2005-075568/08.  
DR  
XX  
PT Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
PS  
XX Claim 3; SEQ ID NO 9269; 113pp; English.

The present invention relates to a novel pharmaceutical composition  
comprising: (a) an agent capable of modulating an expression level or  
protein activity of a cancer-related transmembrane protein (CRP) or gene  
; an antibody specific for a CRP, or a T cell activated by a CRP; and  
(b) a carrier. The pharmaceutical composition may also comprise a  
polynucleotide capable of inhibiting or decreasing the expression of the  
CRP by RNA interference or an antisense mechanism. The CRPs of the  
invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
pharmaceutical composition is useful for treating cancer, e.g. colon  
cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CRP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0.

Oy 1 TTCTCGAGCACGACTG 18  
Db ::::| | | | | | | :  
2 UUCUCCACGACGACGUG 19

RESULT 50  
ACLA8197/C  
ID ACL48197 standard; RNA; 21 BP.  
XX  
XX AC ACL48197;  
XX  
XX 24-MAR-2005 (first entry)  
DT  
DE FOLH1 siRNA sense sequence, SEQ ID 9269.  
XX  
XX FOLH1 siRNA sense sequence, SEQ ID 9269.  
XX  
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;  
KM short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
OS  
XX WO2005001092-A2.  
PN  
PD 06-JAN-2005.  
PF  
PR 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
PA (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
PI  
XX WPI; 2005-075568/08.  
DR  
XX  
PT Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
PS  
XX Claim 3; SEQ ID NO 9269; 113pp; English.



CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 0 T; 6 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TTCTCAGACAGCAGCTG 18  
Db 18 TTCTCAGACAGCAGCTG 1  
RESULT 51  
ACL46979 standard; RNA; 21 BP.  
XX  
XX ACL46979;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX ENPP3 siRNA sense sequence, SEQ ID 8051.  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
XX short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 8051; 113bp; English.  
XX  
XX  
XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRP) or gene  
XX (b) an antibody specific for a CRP, or a T cell activated by a CRP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRP by RNA interference or an antisense mechanism. The CRPs of the  
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 21 BP; 8 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 72.2%; Pred. No. 24;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 164 ACAGAACGACCGTAAAG 181  
Db 1 ACAGAACGACCGTAAAG 181  
RESULT 52  
ACL48193/C  
ID ACL48193 standard; DNA; 21 BP.  
XX  
XX ACL48193;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX FOLH1 target oligonucleotide, SEQ ID 9265.  
XX  
XX  
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 9265; 113bp; English.  
XX  
XX  
XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRP) or gene  
XX (b) an antibody specific for a CRP, or a T cell activated by a CRP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRP by RNA interference or an antisense mechanism. The CRPs of the  
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX target oligonucleotide from one such CRP for which short interfering  
XX RNA (siRNA) were produced. Note: The sequence data for this patent did  
XX not form part of the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
XX Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TTCTCAGACAGCAGCTG 18  
Db 21 TTCTCAGACAGCAGCTG 4

RESULT 53  
ADW72413/C  
ID ADW72413 standard; RNA; 21 BP.  
XX  
AC ADW72413;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Mitochondrial polymerase Polg siRNA strand #117.  
XX  
XX Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;  
KM carnitine deficiency; pyruvate carboxylase deficiency;  
KM mitochondrial cytopathy; mitochondrial DNA depletion;  
KM mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;  
KM retinitis pigmentosa; pyruvate dehydrogenase deficiency;  
KM Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease;  
KM mitochondrial polymerase; Polg; muscular-gen.; ophthalmological;  
KM cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;  
KM neuroprotective; cardiovascular-gen.; antidiabetic; ss;  
KM short interfering RNA; siRNA; RNA interference; gene silencing.  
XX  
OS Synthetic.  
XX  
PN WO200501062-A2.  
XX  
PD 06-JAN-2005.  
XX  
PF 25-JUN-2004; 2004WO-US020454.  
XX  
PR 25-JUN-2003; 2003US-0482603P.  
XX  
PA (GENC-) GENCIA CORP.  
XX  
PI Khan S;  
XX  
PI WPI; 2005-075550/08.  
XX  
PT New polynucleotide encoding a polypeptide having an organelle or  
PT chloroplast localization signal, and a protein transduction domain,  
PT useful for treating diseases with defective mitochondrial function.  
XX  
PS Claim 96; SEQ ID NO 371; 98bp; English.  
XX  
XX The invention relates to a polynucleotide encoding a recombinant  
CC polypeptide comprising an organelle and/or chloroplast localization  
CC signal and a protein transduction domain. The invention also relates to a  
CC recombinant viral vector comprising the polynucleotide, a cell comprising  
CC a modified organelle comprising a bacteriophage, a method of transfecting  
CC a cell comprising contacting the cell with a vector operably linked to a  
CC polypeptide having a protein transduction domain and an organelle  
CC targeting signal, a method of modifying an organelle comprising  
CC transfecting the cell with a recombinant lambda phage, the recombinant  
CC lambda phage comprising a polynucleotide encoding an organelle  
CC localization signal operably linked to a bacteriophage lambda surface  
CC protein, where the organelle localization signal is displayed on a  
CC surface of the recombinant lambda phage and directs the recombinant  
CC lambda phage to the organelle, and where the recombinant lambda phage  
CC introduces a polynucleotide into the organelle, a composition comprising  
CC a recombinant polypeptide comprising an organelle localization signal  
CC operably linked to a protein transduction domain, where the recombinant  
CC polypeptide is operably linked to a polynucleotide, a method for  
CC modifying the metabolism of a cell comprising contacting the cell with a  
CC recombinant vector displaying a recombinant polypeptide comprising a  
CC mitochondrial localization signal operably linked to a protein  
CC transduction domain, the recombinant vector comprising a polynucleotide  
CC encoding a functional respiratory chain component, where the functional  
CC respiratory chain component compensates for the at least one defective  
CC respiratory chain component when expressed by the cell, a method for  
CC modifying cytochrome oxidase activity in a cell, and a method of treating  
CC a mitochondrial disease in a host, comprising contacting a host's cell  
CC with a recombinant vector displaying a recombinant polypeptide comprising

CC a mitochondrial localization signal operably linked to a protein  
CC transduction domain, the recombinant vector encoding a functional  
CC mitochondrial polypeptide, where the recombinant vector transfects at  
CC least one of the host's mitochondria enabling the host's cell to express  
CC the functional mitochondrial polypeptide in the at least one transfected  
CC mitochondrion. The methods and compositions are useful for transfecting  
CC cells and organelle DNA in living cells directly, in particular for  
CC transfecting mitochondria and chloroplasts, and for treating diseases  
CC related to organelle dysfunction, such as Alpers Disease, carnitine  
CC deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy,  
CC mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial  
CC myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate  
CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,  
CC diabetes, aging and heart disease. This sequence represents mitochondrial  
CC polymerase Polg siRNA used in the scope of the invention.  
XX  
SQ Sequence 21 BP; 6 A; 4 C; 8 G; 2 T; 1 U; 0 Other;  
XX  
Query Match 6.1%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 53 CAGCTGCTGCTCACCCTG 70  
Db 18 CAGCTGCTGCTCCTCCCTG 1  
XX  
RESULT 54  
ADY33887/C  
ID ADY33887 standard; DNA; 21 BP.  
XX  
AC ADY33887;  
XX  
DT 19-MAY-2005 (first entry)  
XX  
DE Up-regulated renal cell carcinoma gene, RT-PCR primer SEQ ID No:54.  
XX  
XX diagnosis; renal cell carcinoma; gene expression; gene silencing;  
KM RNA interference; vaccine; cytostatic; reverse transcriptase-PCR; RT-PCR;  
KM primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2005019475-A2.  
XX  
PD 03-MAR-2005.  
XX  
PF 20-AUG-2004; 2004WO-JP012411.  
XX  
PR 20-AUG-2003; 2003US-0496552P.  
PR 27-FEB-2004; 2004US-0548201P.  
XX  
PA (ONCO-) ONCOTHERAPY SCI INC.  
PA (UITY ) UNIV TOKYO.  
XX  
PI Nakamura Y, Katagiri T;  
XX  
PI WPI; 2005-202667/21.  
XX  
DR WPI; 2005-202667/21.  
XX  
PT Diagnosing renal cell carcinoma (RCC), comprises determining an increased  
PT expression level of an RCC-associated gene, in a biological sample  
PT derived from a subject, compared to a normal control level of the gene.  
XX  
PS Example 1; SEQ ID NO 54; 122bp; English.  
XX  
XX The invention relates to a method (M1) of diagnosing renal cell carcinoma  
CC (RCC) or a predisposition for developing RCC in a subject. The method  
CC comprises determining in a biological sample derived from a subject, an  
CC expression level of an RCC-associated gene chosen from genes of RCCX 1-  
CC 32, where an increase in the level as compared to a normal control level  
CC of the gene indicates that the subject suffers from or is at risk of  
CC developing RCC. Also described are (1) an RCC reference expression  
CC profile, comprising a pattern of gene expression of two or more genes



```

XX Dog; genome; genomic marker; radiation hybrid map; identification;
KM chromosome location; gene marker; polymorphic microsatellite marker;
KM phenotype; behaviour; pedigree; ss.
XX Canis familiaris.
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX
XX 15-NOV-1999; 99WO-IB001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 70; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AA66139 to AA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be
CC useful for isolating corresponding human gene sequences e.g. genes
CC involved in genetic diseases
XX
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 149 CTCACGTCGAGCTGAA 164
Db 1 CTCACGTCGAGCTGAA 16

```

```

RESULT 57
ADP10727/C
ID ADP10727 standard; DNA; 20 BP.
XX
XX ADP10727;
XX
XX 12-AUG-2004 (first entry)
XX
XX Set 1 left PCR primer for marker probe #72.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR

```

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PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 58; SEQ ID NO 736; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection, in an
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
CC of allograft rejection and other disorders.
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
SQ

```

```

Query Match 6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 76 CCAAACCCACCTGT 91
Db 20 CCAAACCCACCTGT 5

```

```

RESULT 58
ADX81409/C
ID ADX81409 standard; DNA; 20 BP.
XX
XX ADX81409;
XX
XX 05-MAY-2005 (first entry)
XX
XX Melanoma associated SNP allelotyping primer, #636.
XX
XX melanoma; DNA polymorphism; SNP detection; cytostatic; gene therapy; PCR;
KM primer; ss.
XX
XX Homo sapiens.
XX
XX WO2005017176-A2.
XX
XX 24-FEB-2005.
XX
XX 05-MAY-2004; 2004WO-US014238.
XX
XX 23-JUL-2003; 2003US-0489703P.
XX
XX 06-NOV-2003; 2003US-00703789.
XX
XX 06-NOV-2003; 2003US-00703817.
XX
XX 06-NOV-2003; 2003US-00704513.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Kammerer SM, Braun A, Hoyal-Wrightson CR;
XX WPI; 2005-182387/19.
DR

```

XX Identifying a subject at risk of melanoma by detecting presence or  
PT absence of a polymorphic variation associated with melanoma, where the  
PT presence of polymorphic variations is indicative of the subject being at  
PT risk of melanoma.

Example 7; Page 119; 418bp; English.

XX The invention relates to a novel method for identifying a subject at risk  
CC of melanoma. The method comprises detecting the presence or absence of a  
CC polymorphic variation associated with melanoma, where the presence of the  
CC one or more polymorphic variations is indicative of the subject being at  
CC risk of melanoma. The invention further comprises: a method for  
CC identifying a polymorphic variation associated with melanoma proximal to  
CC an incident polymorphic variation associated with melanoma; an isolated  
CC nucleic acid which comprises a portion of or all of a nucleotide sequence  
CC comprising fully defined 68400-21300 base pairs sequences (SEQ ID NO. 3,  
CC 4, 5, 6, and/or 7) given in the specification, and comprises one or more  
CC polymorphic variations; an oligonucleotide comprising a nucleotide  
CC sequence complementary to a portion of the nucleotide sequence above,  
CC where the 3' end of the oligonucleotide is adjacent to a polymorphic  
CC variation; a microarray comprising the isolated nucleic acid linked to a  
CC solid support; an isolated polypeptide encoded by the isolated nucleic  
CC acid sequence; genotyping a nucleic acid; a method for identifying a  
CC candidate molecule that modulates cell proliferation; treating melanoma  
CC in a subject; and treating melanoma in a subject or preventing melanoma  
CC in a subject. The methods and sequences have cytostatic activity. The  
CC polynucleotides may be used in gene therapy. The methods are useful for  
CC identifying a subject at risk of melanoma, treating melanoma in a  
CC subject, or preventing melanoma in a subject. This polynucleotide  
CC sequence represents a primer used in the exemplification of the  
CC invention.

XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 6.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 28;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

147 CTCTACGCTGAGCTG 162

Db 16 CTCTACGCTGAGCTG 1

Search completed: October 2, 2006, 15:44:33  
Job time : 0.001 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:41:58 ; Search time 0.001 Seconds  
(without alignments)  
1309.220 Million cell updates/sec

Title: US-10-642-946-6\_1967-2208

Perfect score: 242

Sequence: 1 ttccacagacacacacgcga.....ccaactaacgtgattcac 242

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 124 seqs, 2705 residues

Total number of hits satisfying chosen parameters: 248

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 124 summaries

Database : pubmaindb1:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.8	8.2	25	1 US-11-036-317-967319	Sequence 987319,
2	18.2	7.5	25	1 US-10-310-914A-116991	Sequence 116991,
3	18.2	7.5	25	1 US-10-809-189-18892	Sequence 18892, A
4	18.2	7.5	25	1 US-11-036-317-87349	Sequence 87349, A
5	18.2	7.5	25	1 US-11-036-317-392205	Sequence 392205,
6	18.2	7.5	25	1 US-11-036-317-957321	Sequence 957321,
7	17.8	7.4	25	1 US-10-310-914A-1204416	Sequence 1204416,
8	17.8	7.4	25	1 US-11-036-317-915497	Sequence 915497,
9	17.8	7.4	25	1 US-11-060-756-162607	Sequence 162607,
10	17.8	7.4	25	1 US-11-060-756-165160	Sequence 165160,
11	17.8	7.4	25	1 US-11-060-756-272361	Sequence 272361,
12	17.8	7.4	25	1 US-11-060-756-272361	Sequence 272361,
13	17.8	7.4	25	1 US-11-060-756-272361	Sequence 272361,
14	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
15	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
16	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
17	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
18	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
19	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
20	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
21	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
22	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
23	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
24	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
25	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
26	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
27	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
28	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
29	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
30	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
31	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385,
32	16.8	6.9	20	1 US-10-310-914A-1180613	Sequence 1180613,
33	16.8	6.9	21	1 US-10-310-914A-178653	Sequence 178653,

*Published Application - NA - Main*

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c 107 15.8 6.5 21 1 US-10-831-997-768 Sequence 768, App
108 15.8 6.5 21 1 US-10-310-914A-117008 Sequence 117008,
109 15.8 6.5 21 1 US-10-310-914A-227677 Sequence 227677,
c 110 15.8 6.5 21 1 US-10-310-914A-593921 Sequence 593921,
c 111 15.8 6.5 21 1 US-10-310-914A-800173 Sequence 800173,
c 112 15.8 6.5 22 1 US-10-708-204-288 Sequence 288, App
c 113 15.8 6.5 22 1 US-10-708-204-2661 Sequence 2661, App
114 15.8 6.5 22 1 US-10-310-914A-160067 Sequence 160067,
115 15.8 6.5 22 1 US-10-310-914A-802509 Sequence 802509,
c 116 15.8 6.5 22 1 US-10-310-914A-978748 Sequence 978748,
c 117 15.8 6.5 22 1 US-10-310-914A-1115299 Sequence 1115299,
118 15.6 6.4 22 1 US-10-310-914A-45234 Sequence 45234, A
c 119 15.6 6.4 22 1 US-10-310-914A-419337 Sequence 419337,
c 120 15.6 6.4 22 1 US-10-310-914A-877383 Sequence 877383,
121 15.6 6.4 22 1 US-10-310-914A-955140 Sequence 955140,
c 122 15.6 6.4 22 1 US-10-310-914A-993524 Sequence 993524,
c 123 15.6 6.4 22 1 US-10-310-914A-1134411 Sequence 1134411,
c 124 15.6 6.4 22 1 US-10-310-914A-1326011 Sequence 1326011,

```

## ALIGNMENTS

```

RESULT 1
US-11-036-317-987319
; Sequence 987319, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 987319
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987319

```

```

Query Match      8.2%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No.13;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 TTCTCCAGCAGCAGCTGATTT 23
Db      1 TTCTCCAGAACAGCAATGATTT 23

```

```

RESULT 2
US-10-310-914A-116991
; Sequence 116991, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazai
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116991
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116991

```

```

Query Match      7.5%; Score 18.2; DB 1; Length 24;
Best Local Similarity 73.9%; Pred. No. 21;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      45 CACCTCCAGCTGCTGCTTAC 67
Db      1 CCCCUCGCCAGCAGCUCGCC 23

```

```

RESULT 3
US-10-809-189-18892
; Sequence 18892, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18892

```

```

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 TTCTCCAGCAGCAGCTGATTT 23
Db      3 TTCTCCAGAACAGCTATGATTT 25

```

```

RESULT 4
US-11-036-317-87349/C
; Sequence 87349, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87349
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-87349

```

```

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      124 TCGTTCCATCTCTTTGAGAC 146
Db      25 TCCTGCCATCTCTTTGAGAC 3

```



```
RESULT 5
US-11-036-317-392205
; Sequence 392205, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 392205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-392205

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TTCTCCAGACAGCAGCTGATTT 23
Db 1 TTCTCCAGACAGCAGCTGATTT 23

RESULT 6
US-11-036-317-987321
; Sequence 987321, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 987321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987321

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TTCTCCAGACAGCAGCTGATTT 23
Db 1 TTCTCCAGACAGCAGCTGATTT 23

RESULT 7
US-10-310-914A-1204416
; Sequence 1204416, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1204416
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1204416

Query Match      7.4%; Score 17.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 27;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GGCTGGAGCTCCACCTCCCC 53
Db 1 GGCGGAGGCTCCACCTCC 21

RESULT 8
US-11-036-317-915497
; Sequence 915497, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 915497
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-915497

Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 CTCGACAGCAGCAGCTGATTT 23
Db 1 CTCGACAGCAGCAGCTGATTT 21

RESULT 9
US-11-060-756-146184
; Sequence 146184, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146184

Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 144 CACCTTCACGTGAGCTGAA 164
Db 2 CACCTATCAGCTGAGCTCAA 22
```

```
RESULT 10
US-11-060-756-162607
; Sequence 162607, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162607
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-162607
```

```
Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      144 CACCTTCAGCTGAGCTGAA 164
Db      3 CACCTATCAGCTGAGCTCAA 23
```

```
RESULT 11
US-11-060-756-165160
; Sequence 165160, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-165160
```

```
Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      144 CACCTTCAGCTGAGCTGAA 164
Db      1 CACCTATCAGCTGAGCTCAA 21
```

```
RESULT 12
US-11-060-756-272361
; Sequence 272361, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 272361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-272361
```

```
Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      144 CACCTTCAGCTGAGCTGAA 164
Db      5 CACCTATCAGCTGAGCTCAA 25
```

```
RESULT 13
US-11-121-849-3059
; Sequence 3059, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3059
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-3059
```

```
Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      57 TGCTGCTCAGCTGCTTTTCC 77
Db      4 TGCTGCTTACCTGCTTTTGC 24
```

```
RESULT 14
US-10-719-900-615502/c
; Sequence 615502, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 615502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-615502
```

```
Query Match      7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      5 CCAGCAGCAGCTGATTTTGGTC 28
Db      25 CCAGCAGCAGCTGATGATGGGC 2
```

```
RESULT 15
US-10-719-900-729485
; Sequence 729485, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 729485
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-729485

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 128 TTCCATCTCTTGGAGCAGCTCTC 151
Db 2 TTCTAGGCTTTGGAGCAGCAGCTC 25

RESULT 16
US-10-719-900-767611
; Sequence 767611, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 767611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-767611

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 57 TCGTCCCTCAGCTGCTTTCCAA 80
Db 1 TACTGACGAGCTGCTTTCCAA 24

RESULT 17
US-10-932-182A-49117
; Sequence 49117, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKITO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
```

```
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-49117

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 97 GTAACATCTTTGGCCCACTAC 120
Db 1 GAAGTACATTGGGCCCACTAC 24

RESULT 18
US-10-933-982-210405
; Sequence 210405, Application US/10933982
; Publication No. US20060051769A1
; GENERAL INFORMATION:
; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-210405

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TTCTCCAGCAGCAGCTGATTTT 24
Db 2 TTCTCCGCGCAGCAGGCTGATATT 25

RESULT 19
US-11-036-317-651088/c
; Sequence 651088, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 651088
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-651088

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 37 GGGAGCTTCACCTCCAGCTGCT 60
Db 25 GGGAGCTACAGCTCAAGCTTCT 2
```

```
RESULT 20
US-11-036-317-678385
; Sequence 678385, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 678385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-678385
```

```
Query Match 7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 121 GCCGCTTCCATCTCTTGAGC 144
Db 1 GCATCGTTCCATCTGTTGAGC 24
```

```
RESULT 21
US-10-310-914A-938357
; Sequence 938357, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938357
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-938357
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 22;
Best Local Similarity 78.9%; Pred. No. 28;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 74 TTCGAACCCACCCCTGTA 92
Db 2 UCCGAACCCACCCCTGTA 20
```

```
RESULT 22
US-10-310-914A-529952/c
; Sequence 529952, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
```

```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 529952
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-529952
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 45 CACCTCCCAAGCTGCTGCC 63
Db 23 CACCTCCTCAGCTGCTGCC 5
```

```
RESULT 23
US-10-310-914A-938303
; Sequence 938303, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938303
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-938303
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 27;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 74 TTCGAACCCACCCCTGTA 92
Db 5 UCCGAACCCACCCCTGTA 23
```

```
RESULT 24
US-10-310-914A-59879
; Sequence 59879, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59879
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-59879
```

```
Query Match 7.1%; Score 17.2; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 47 CCTCCCAAGCTGCTGCTCACC 68
Db 1 CCCUCCAGCUCUCCUCCACC 22
```

```

RESULT 25
US-10-310-914A-565232
; Sequence 565232, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 565232
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-565232

Query Match          7.1%; Score 17.2; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy      56  CGCTGCTCACCTGCTTTTC 77
Db      1  CUGCUGCCUGCUGCUGUCC 22

RESULT 26
US-10-084-839-3863/C
; Sequence 3863, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hattim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Barsholomay, Luanne
; APPLICANT: Cheneak, Luanne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eib, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: IP, Hon S.
; APPLICANT: Ul, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowski, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lyamicheva, Natalie E.
; APPLICANT: Ma, Wupo
; APPLICANT: Neel, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedral, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3863
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3863

```

```

Query Match          7.1%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      120  GCCTCGTTTCATCTCTTGG 141
Db      23  GCCTCGTTCTATCTCTTGG 2

RESULT 27
US-09-962-290-9/C
; Sequence 9, Application US/09962290
; Patent No. US20020092034A1
; GENERAL INFORMATION:
; APPLICANT: Paterson, David
; APPLICANT: Brennan, Miles
; APPLICANT: Hochgeschwender, Ute
; APPLICANT: Flintoff, Wayne
; APPLICANT: Sadlish, Heather
; APPLICANT: Underhill, T. Michael
; APPLICANT: Williams, Frederick
; TITLE OF INVENTION: No. US20020092034A1-Human Model of Gestational and Adult Folate D.
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 3718-8
; CURRENT APPLICATION NUMBER: US/09/962,290
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/234,853
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(24)
; OTHER INFORMATION: primer
US-09-962-290-9

Query Match          7.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14  CACTGATTTGTGCACCTGCG 35
Db      23  CAATGATGTGTGCACCTGCG 2

RESULT 28
US-10-310-914A-392849
; Sequence 392849, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392849
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-392849

Query Match          7.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 27;
Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

OY 66 ACCTGCTTTCCAAACCCACC 87  
 ||:||||:|||||  
 Db 1 AACUGCUUCGCAACACACC 22

RESULT 29  
 US-10-310-914A-471177  
 ; Sequence 471177, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 471177  
 ; LENGTH: 24  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-471177

Query Match 7.1%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 68.2%; Pred. No. 27;  
 Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 31 CTGCGCTGGAGAGCTCCACTCCC 52  
 ||:||||:|||||  
 Db 1 CUCACUGGAGCUCACCUCC 22

RESULT 30  
 US-10-310-914A-382552  
 ; Sequence 382552, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 382552  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-382552

Query Match 7.0%; Score 17; DB 1; Length 19;  
 Best Local Similarity 64.7%; Pred. No. 37;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 62 CCTCAGCTGCTTTTCCA 78  
 ||:||||:|||||  
 Db 1 CCUCACCGCUCUCCCA 17

RESULT 31  
 US-10-310-914A-1324851/C  
 ; Sequence 1324851, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1324851  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-1324851

FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1324851  
 ; LENGTH: 20  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-1324851

Query Match 7.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 CCTCAGCTGCTTTTCCA 78  
 ||:||||:|||||  
 Db 20 CCTCAGCTGCTTTTCCA 4

RESULT 32  
 US-10-310-914A-1180613  
 ; Sequence 1180613, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1180613  
 ; LENGTH: 20  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-1180613

Query Match 6.9%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 70.0%; Pred. No. 37;  
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCCAGCAGCAGCTGGA 20  
 ::|||:||||:|  
 Db 1 UUCUCCAGCAAGCAGCUGCA 20

RESULT 33  
 US-10-310-914A-178653/C  
 ; Sequence 178653, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 178653  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-178653

Query Match 6.9%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 35;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 44 CCACCTCCAGCTGCTGCC 63  
|||  
DB 20 CCACCAACCCAGCTGCTGCC 1

RESULT 34  
US-10-310-914A-185040/c  
; Sequence 185040, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 185040  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-185040

Query Match 6.9%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CAGCAGCAGCTGATTTTG 25  
|||  
DB 20 CAGCAGCAGCTGATTTCTG 1

RESULT 35  
US-10-310-914A-1124039/c  
; Sequence 1124039, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 1124039  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1124039

Query Match 6.9%; Score 16.8; DB 1; Length 23;  
Best Local Similarity 90.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 CCTCCAGCTGCTGCTCA 66  
|||  
DB 20 CCACCCAGCTGCTGCTCA 1

RESULT 36  
US-10-310-914A-931759  
; Sequence 931759, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 931759  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-931759

Query Match 6.9%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 75.0%; Pred. No. 30;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 49 TCCACAGCTGCTGCTCACC 68  
|||  
DB 1 UCCACAGCAGCACCACC 20

RESULT 37  
US-10-084-839-3864  
; Sequence 3864, Application US/10084839  
; Publication No. US20030186238A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Argue, Brad T.  
; APPLICANT: Bartholomay, Christian T.  
; APPLICANT: Chehak, LuAnne  
; APPLICANT: Curtis, Michelle L.  
; APPLICANT: Eis, Peggy S.  
; APPLICANT: Hall, Jeff G.  
; APPLICANT: IP, Hon S.  
; APPLICANT: Ji, Lin  
; APPLICANT: Kaiser, Michael  
; APPLICANT: Kwiatkowski, Jr., Robert W.  
; APPLICANT: Lukowiak, Andrew A.  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Lyamicheva, Natalie E.  
; APPLICANT: Ma, Wupo  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Olson, Sarah M.  
; APPLICANT: Olson-Munoz, Marilyn C.  
; APPLICANT: Schaefer, James J.  
; APPLICANT: Skrzypczynski, Zdzigniew  
; APPLICANT: Takova, Tsetaka Y.  
; APPLICANT: Thompson, Lisa C.  
; APPLICANT: Vedvik, Kevin L.  
; TITLE OF INVENTION: RNA Detection Assays  
; FILE REFERENCE: FORS-0666  
; CURRENT APPLICATION NUMBER: US/10/084,839  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 4004  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 3864  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-084-839-3864

Query Match 6.9%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 34;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 114 CCACTAGCCTGCTTCATCTC 136  
|||  
DB 1 CCGTACGCTGCTTCATCTC 23

RESULT 38  
US-10-310-914A-970522

```
; Sequence 970522, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970522
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-970522
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 TTCGACGACGACTGAT 21
Db 1 UCCAGCACACUGGAV 18
```

## RESULT 39

```
US-11-083-784-1493132/c
; Sequence 1493132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714.333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1493132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1493132
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTCTCCAGCAGCACTG 18
Db 19 TTCTCCAGCAAGCACTG 2
```

## RESULT 40

```
US-11-101-244-1493132/c
; Sequence 1493132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1493132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1493132
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTCTCCAGCAGCACTG 18
Db 19 TTCTCCAGCAAGCACTG 2
```

## RESULT 41

```
US-10-310-914A-970523
; Sequence 970523, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970523
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-970523
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 TTCGACGACGACTGAT 21
Db 1 UCCAGCACACUGGAV 18
```

## RESULT 42

```
US-10-310-914A-853027
; Sequence 853027, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 853027
; LENGTH: 21
```



```
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-853027

Query Match
Best Local Similarity 6.8%; Score 16.4; DB 1; Length 21;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 44 CCACTCCCGAGCTGCTG 61
Db 1 CCACCCUCCCGACGACGUG 18

RESULT 43
US-10-310-914A-560231
; Sequence 560231, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 560231
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-560231

Query Match
Best Local Similarity 6.8%; Score 16.4; DB 1; Length 22;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 48 CTCGCCAGCTGCTGCTC 65
Db 1 CUCCCCAGCUCGCGCUC 18

RESULT 44
US-10-310-914A-998415
; Sequence 998415, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 998415
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-998415

Query Match
Best Local Similarity 6.8%; Score 16.4; DB 1; Length 22;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 43 TCACCTCCCGAGCTGCT 60
Db 1 UCCACCTCCCGACGACU 18

RESULT 45
US-10-310-914A-1111010

; Sequence 1111010, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1111010
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1111010

Query Match
Best Local Similarity 6.8%; Score 16.4; DB 1; Length 23;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 55 GCTGCTGCTCAGCTGCT 72
Db 3 GCUCGCGCCUCCAUCCGU 20

RESULT 46
US-10-310-914A-1111016
; Sequence 1111016, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1111016
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1111016

Query Match
Best Local Similarity 6.8%; Score 16.4; DB 1; Length 23;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 55 GCTGCTGCTCAGCTGCT 72
Db 4 GCUCGCGCCUCCAUCCGU 21

RESULT 47
US-10-310-914A-1256042/c
; Sequence 1256042, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1256042
; LENGTH: 23
; TYPE: RNA
```

```
; ORGANISM: Human
US-10-310-914A-1256042

Query Match      6.8%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      179 AAGCCACCGTGTCTGTT 196
      |||||
Db      19 AAGCCACCGTGTCTGTT 2

RESULT 48
US-10-310-914A-126098/c
; Sequence 126098, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126098
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-126098

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      44 CCACCTCCCGACGCTGCTCT 64
      |||||
Db      21 CCACCTCCCGAAGCTCTGCT 1

RESULT 49
US-10-310-914A-204775
; Sequence 204775, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 204775
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-204775

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY      34 GCTGGAGCTTCACCTCCCA 54
      |||||
Db      1 GCTGGAGCTTCACCTCCCA 21

RESULT 50
US-10-310-914A-306631/c
; Sequence 306631, Application US/10310914A

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 306631
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-306631

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      70 GCTTTCCAAACCCACCCCTG 90
      |||||
Db      21 GCTTTCCGAGCCCACTCTG 1

RESULT 51
US-10-310-914A-565231
; Sequence 565231, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 565231
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-565231

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 52.4%; Pred. No. 41;
Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY      56 CTGCTGCTTCACCTGCTTTC 76
      |||||
Db      1 CUGCUGCTCUCGUCGUCUC 21

RESULT 52
US-10-310-914A-1148315
; Sequence 1148315, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1148315
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
```

US-10-310-914A-1148315

Query Match 6.7%; Score 16.2; DB 1; Length 21;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 65 CACGCTGTTTCCAAACCCCA 85

DB 1 CACGCGCUCUCCCAUCCCA 21

RESULT 53

US-09-965-422-121

; Sequence 121, Application US/09965422

; Publication No. US20030216545A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Casman, Stacie

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Dickson, Kevin

; APPLICANT: Vernet, Corine

; APPLICANT: Spaderna, Steven K

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glenda

; APPLICANT: Li, Li

; APPLICANT: Malpankar, Urial M

; APPLICANT: Taylor, Sarah

; APPLICANT: Gunther, Erik

; APPLICANT: Tchernev, Velizar T

; TITLE OF INVENTION: No. US20030216545A1

; FILE REFERENCE: 21401-132 Proteins and Nucleic Acids Encoding Same

; CURRENT FILING DATE: 2001-09-27

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

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; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 2000-09-28

Query Match 6.7%; Score 16.2; DB 1; Length 22;

Best Local Similarity 85.7%; Pred. No. 39;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 TCTCTTGAGACACCTCTAC 153

DB 2 TCTCTTGAGACCCCTTTCAC 22

RESULT 54

US-10-005-041A-187

; Sequence 187, Application US/10005041A

; Publication No. US2003023231A1

; GENERAL INFORMATION:

; APPLICANT: Casman, Stacie J

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Burgess, Catherine E

; APPLICANT: Shinkens, Richard A

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Gilbert, Jennifer A

; APPLICANT: Mayotte, Jane E

; APPLICANT: Baumgartner, Jason C

; APPLICANT: Mishra, Vishnu

; APPLICANT: Vernet, Corine AM

; APPLICANT: Dickinson, Kevin S

; APPLICANT: Ballinger, Robert A

; APPLICANT: Wolenc, Adam R

; APPLICANT: Edinger, Shlomit R

; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glenda

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David J

; APPLICANT: Gunther, Erik

; APPLICANT: Gerlach, Valerie

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-215

; CURRENT FILING DATE: 2001-12-04

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

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; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

; PRIOR FILING DATE: 2000-12-05

RESULT 55

US-10-085-198-526

; Sequence 526, Application US/10085198

; Publication No. US2004009907A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-279

; CURRENT FILING DATE: 2002-02-25

; CURRENT FILING DATE: 2002-02-25

```
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27,324
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20,614
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 526
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-085-198-526
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 133 TCTCTTGAGCAGCCTCTAC 153  
|||||  
Db 2 TCTCTTAGAGCCCTTTCAC 22

```
RESULT 56
US-10-913-280-144
; Sequence 144, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Gimms, Edward I.
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-913-280-144
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 126 GTTTCATCTCTTGAGCAGC 146  
|||||  
|||||

```
Db 1 GTTTCATCTATTTGGTAGAC 21
RESULT 57
US-10-708-204-401/c
; Sequence 401, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 401
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-401
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 52 CCAGCTGCTGCTCCACCTGCT 72  
|||||  
Db 22 CCTGCTGCTGCTCCACCTGCT 2

```
RESULT 58
US-10-708-204-668/c
; Sequence 668, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-668
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 52 CCAGCTGCTGCTCCACCTGCT 72  
|||||  
Db 22 CCTGCTGCTGCTCCACCTGCT 2

```
RESULT 59
US-10-708-204-1098/c
; Sequence 1098, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
```

NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1098  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-1098

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 60  
US-10-708-204-1209/c  
Sequence 1209, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1209  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-1209

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 61  
US-10-708-204-1976/c  
Sequence 1976, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1976  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-1976

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 62  
US-10-708-204-1991/c  
Sequence 1991, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1991  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-1991

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 63  
US-10-708-204-2118/c  
Sequence 2118, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2118  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-2118

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 64  
US-10-708-204-2334/c  
Sequence 2334, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2334  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 65  
US-10-708-204-2334/c  
Sequence 2334, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2334  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 66  
US-10-708-204-2334/c  
Sequence 2334, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2334  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

RESULT 67  
US-10-708-204-2334/c  
Sequence 2334, Application US/10708204  
Publication No. US20050222399A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
FILE REFERENCE: 55033  
CURRENT APPLICATION NUMBER: US/10/708,204  
CURRENT FILING DATE: 2004-02-16  
NUMBER OF SEQ ID NOS: 7351  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2334  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo Sapiens  
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72  
DB 22 CTTGCTGCTGCCCACTCCT 2

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2334
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2334

Query Match
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCCTCCTCT 72
DB 22 CCGTCTGCTGCTGCTGCTCCTCT 2

RESULT 65
US-10-708-204-2487/c
; Sequence 2487, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2487
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2487

Query Match
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCCTCCTCT 72
DB 22 CCGTCTGCTGCTGCTGCTCCTCT 2

RESULT 66
US-10-310-914A-222541/c
; Sequence 222541, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222541
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-222541

Query Match
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 ACCGCCGAGCTGCTGCTCA 66
DB 22 ACTTCCCGAGCTTGTGCCCA 2

RESULT 67
US-10-310-914A-653245/c
; Sequence 653245, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 653245
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-653245

Query Match
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GGCTGGAGCTCCACCTCCC 53
DB 21 GACTGAGAGTCCACCTCCC 1

RESULT 68
US-10-310-914A-853475/c
; Sequence 853475, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 853475
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-853475

Query Match
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 32 TGGCTGGAGCTCCACCTCCC 52
DB 22 TTGCTGGAGCTCCCTGCC 2

RESULT 69
US-10-310-914A-1084017/c
; Sequence 1084017, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 1084017
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-914A-1084017
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      33 GGCTGGAGCTCCACCTCCCC 53
      ||||| ||||| ||||| |||||
DB      21 GACTGGAAGATCCACCTCCCC 1
```

```
RESULT 70
US-10-310-914A-1084697/c
; Sequence 1084697, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1084697
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1084697
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      33 GGCTGGAGCTCCACCTCCCC 53
      ||||| ||||| ||||| |||||
DB      21 GACTGGAAGATCCACCTCCCC 1
```

```
RESULT 71
US-10-310-914A-1084916/c
; Sequence 1084916, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1084916
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1084916
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      33 GGCTGGAGCTCCACCTCCCC 53
      ||||| ||||| ||||| |||||
DB      21 GACTGGAAGATCCACCTCCCC 1
```

```
RESULT 72
US-10-310-914A-1215444/c
; Sequence 1215444, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1215444
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1215444
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      33 GGCTGGAGCTCCACCTCCCC 53
      ||||| ||||| ||||| |||||
DB      21 GACTGGAAGATCCACCTCCCC 1
```

```
RESULT 73
US-10-310-914A-1215686/c
; Sequence 1215686, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1215686
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1215686
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      33 GGCTGGAGCTCCACCTCCCC 53
      ||||| ||||| ||||| |||||
DB      21 GACTGGAAGATCCACCTCCCC 1
```

```
RESULT 74
US-10-310-914A-1217123/c
; Sequence 1217123, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1217123
```

LENGTH: 22  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1217123

Query Match  
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53  
DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 75

US-10-310-914A-1263320/c  
Sequence 1263320, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1263320  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1263320

Query Match  
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53  
DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 76

US-10-310-914A-1287830/c  
Sequence 1287830, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1287830  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1287830

Query Match  
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53  
DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 77

US-10-913-280-562  
Sequence 562, Application US/10913280  
Publication No. US20050089894A1  
GENERAL INFORMATION:  
APPLICANT: Ginn, Edward I.  
APPLICANT: Galdick, Marzena  
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING  
FILE REFERENCE: 07917-238001  
CURRENT APPLICATION NUMBER: US/10/913.280  
CURRENT FILING DATE: 2004-08-06  
PRIOR APPLICATION NUMBER: US 60/493,238  
PRIOR FILING DATE: 2003-08-06  
PRIOR APPLICATION NUMBER: US 60/568,958  
PRIOR FILING DATE: 2004-05-07  
NUMBER OF SEQ ID NOS: 920  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 562  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Primer  
US-10-913-280-562

Query Match  
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 23;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 126 GTTCCATCTCTTGGAGCAGC 146  
DB 1 GTTCCATCTATTGGTACAC 21

RESULT 78

US-10-310-914A-126107/c  
Sequence 126107, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 126107  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-126107

Query Match  
Best Local Similarity 85.7%; Score 16.2; DB 1; Length 23;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 44 CCACCTCCCAAGCTGCTGCT 64  
DB 22 CCACCTCCCAACTCTGCT 2

RESULT 79

US-10-310-914A-445725  
Sequence 445725, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01



```

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 445725
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-445725

Query Match
Best Local Similarity 66.7%; Pred. No. 37;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CAGCACGACACTGATTTTGG 26
Db 1 CAGCACGACACUGGAAUUCUG 21

RESULT 80
US-10-310-914A-1335478
; Sequence 1335478, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Benclwich, Isaac
; APPLICANT: Shiller, Kynzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200, CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1335478
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1335478

Query Match
Best Local Similarity 61.9%; Pred. No. 37;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCGACGACGACGATTTT 23
Db 1 CUCCAGACGACCCUGGAUU 21

RESULT 81
US-11-083-784-1311431/C
; Sequence 1311431, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311431
; LENGTH: 19
```

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1311431

Query Match
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCTCCAGCACGAC 16
Db 16 TTCTCCAGCACGAC 1

RESULT 82
US-11-083-784-1488626
; Sequence 1488626, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1488626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1488626

Query Match
Best Local Similarity 81.2%; Pred. No. 47;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CACCTGCTGGGAGCT 43
Db 2 CACCTGCTGGGAGCT 17

RESULT 83
US-11-101-244-1311431/C
; Sequence 1311431, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311431
```

```
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1311431
```

```
Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTCTCCAGCAGCAGC 16
Db 16 TTCTCCAGCAGCAGC 1
```

RESULT 84

```
US-11-101-244-1488626
Sequence 1488626, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
PRIOR FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
NUMBER OF SEQ ID NOS: 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 1488626
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1488626
```

```
Query Match
Best Local Similarity 81.2%; Score 16; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 28 CACCTGGCTGGGAGCT 43
Db 2 CACCTGGCTGGGAGCT 17
```

RESULT 85

```
US-10-310-914A-178568/C
Sequence 178568, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentln version 3.3
SEQ ID NO 178568
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-178568
```

```
Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 42 CTCACCTCCCGAGCTGCT 60
Db 19 CCCACCCACCCCGAGCTGCT 1
```

RESULT 86

```
US-10-310-914A-178650/C
Sequence 178650, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentln version 3.3
SEQ ID NO 178650
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-178650
```

```
Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 44 CCACCTCCCGAGCTGCTGC 62
Db 19 CCACCTCCCGAGCTGCTGC 1
```

RESULT 87

```
US-10-310-914A-370776/C
Sequence 370776, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentln version 3.3
SEQ ID NO 370776
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-370776
```

```
Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 35 CTGGAGCTCCAGCTCTCCC 53
Db 19 CTGGAGCTCCAGCTCTCCC 1
```

RESULT 88

```
US-10-310-914A-851035/C
Sequence 851035, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
```

```
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent version 3.3
SEQ ID NO 851035
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-851035

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 75 TCCAAACCCACCTGTAA 93
Db 19 TCCAAACCCACCTGTAA 1

RESULT 89
US-10-310-914A-115160/c
Sequence 115160, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biomedically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent version 3.3
SEQ ID NO 115160
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-115160

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 50 CCCAGCTGCTGCTGACC 68
Db 19 CCTCAGCTGCTGCTGACC 1

RESULT 90
US-11-083-784-207366
Sequence 207366, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 207366
```

```
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-207366

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 146 CCTCTCAGCTGAGCTGAA 164
Db 1 CCUAVCAGCUCGAGCUCAA 19

RESULT 91
US-11-083-784-207502
Sequence 207502, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714.333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 207502
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-207502

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CAGCAGCACTGATTTT 24
Db 1 CAGCAGCAGCUCGAGCUCU 19

RESULT 92
US-11-083-784-675126
Sequence 675126, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 675126
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 675126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-675126
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 50;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      55 GCTGCTGCTCCTCCTCTCTCT 73
      ||:|||||:|||||:|||||:
Db      1 GCUCUCUCUCUUAUCUCUCU 19
```

RESULT 93

```
US-11-083-784-1246640
; Sequence 1246640, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1246640
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1246640
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 CAGCAGACACTGGATT 24
      |||||:|||||:|||||:
Db      1 CAGCAAGCAGCUGGAUU 19
```

RESULT 94

```
US-11-083-784-1358279/c
; Sequence 1358279, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1358279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1358279
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      133 TCTCTTGAGCAGCTCTC 151
      |||||:|||||:|||||:
Db      19 TCTCTTGAGCTCTCTC 1
```

RESULT 95

```
US-11-101-244-207366
; Sequence 207366, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 207366
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-207366
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      146 CCTTCACGCGAGCTGAA 164
      ||:|||||:|||||:
Db      1 CCUACGCGGAGCUCUA 19
```

RESULT 96

```
US-11-101-244-207502
; Sequence 207502, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```

RESULT 100
US-10-310-914A-178569/c
: Sequence 178569, Application US/10310914A
: Publication No. US2006000322A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Isaac
: APPLICANT: Shlier, Krusat
: TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
: TITLE OF INVENTION: uses thereof
: FILE REFERENCE: 06087.0200.CPUS01
: CURRENT APPLICATION NUMBER: US/10/310.914A
: CURRENT FILING DATE: 2002-12-06
: NUMBER OF SEQ ID NOS: 1388402
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 178569
: LENGTH: 20
: TYPE: RNA
: ORGANISM: Human
: US-10-310-914A-178569

```

```
Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      42 CTCGACCTCCCGACCTGCT 60
      ||||| ||||| |||||
Db      19 CCCGACCAACCCCGACCTGCT 1

RESULT 101
US-10-310-914A-1139581
; Sequence 1139581, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1139581
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1139581

Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 47;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      35 CTGGAGCTCCACCTCCCG 53
      ||||| ||||| |||||
Db      2 CUGGAGCUCUCCACCCGCC 20

RESULT 102
US-10-310-914A-1204303
; Sequence 1204303, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1204303
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1204303

Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      33 GGCTGGAGCTCCACCTCC 51
      ||||| ||||| |||||
Db      2 GGCGGAGCUCUCCACCCUC 20

RESULT 103
US-10-847-918-7690
; Sequence 7690, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7690
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-7690

Query Match      6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      163 AACGAAACGACCTGTTAG 181
      ||||| ||||| |||||
Db      1 AACGAAACACCTGTTAG 19

RESULT 104
US-10-847-918-7692/c
; Sequence 7692, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7692
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-7692

Query Match      6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      163 AACGAAACGACCTGTTAG 181
      ||||| ||||| |||||
Db      21 AACGAAACACCTGTTAG 3

RESULT 105
US-10-847-918-8050
; Sequence 8050, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
```

```

; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8050
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-8050

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACGAGACGACCTGTTAAG 181
Db 2 AACGAGACGACCTGTTAAG 20

RESULT 106
US-10-847-918-8052/c
; Sequence 8052, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8052
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-8052

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACGAGACGACCTGTTAAG 181
Db 2 AACGAGACGACCTGTTAAG 20

RESULT 107
US-10-831-997-768/c
; Sequence 768, Application US/10831997
; Publication No. US20050244834A1
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolt, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/10/831,997
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
```

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; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 768
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-997-768

Query Match
Best Local Similarity 81.0%; Score 15.8; DB 1; Length 21;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCGACGACGACCTGATTT 23
Db 21 CTCGACGACCTGACCTGCTAT 1

RESULT 108
US-10-310-914A-117008
; Sequence 117008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117008
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-117008

Query Match
Best Local Similarity 73.7%; Score 15.8; DB 1; Length 21;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 49 TCCCGAGCTGCTGCCTCAC 67
Db 1 TCCCGAGCAGCUGCCTUCCC 19

RESULT 109
US-10-310-914A-227677
; Sequence 227677, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 227677
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-227677

Query Match
Best Local Similarity 57.9%; Score 15.8; DB 1; Length 21;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

QY 55 GCTGCTGCCTCACCCTGCTT 73  
||:|:|:|:|:|:|:|:|:|:  
Db 1 GCUGGUGGCGUCUCCTGCGCU 19

```

RESULT 110
US-10-310-914A--593921/C
; Sequence 593921, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 593921
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A--593921

```

```

RESULT 111
US-10-310-914A-800173
; Sequence 800173, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 800173
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-800173

```

RESULT 112  
US-10-708-204-288/C  
; Sequence 288, Application US/10708204  
; Publication No. US2005022399A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
; TITLE OF INVENTION: THEREOF

```

; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 228
; LENGTH: 228
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-288

```

```

RESULT 113
US-10-708-204-2661/c
; Sequence 2661, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL, REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708, 204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2661
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2661

```

```

RESULT 114
US-10-310-914A-160067
; Sequence 160067, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 160067
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-160067

```

Query Match	6.5%	Score 15.8	DB 1	Length 22
Best Local Similarity	63.2%	Pred. No. 43		
Matches 12; Conservative	5	Mismatches 2	Indels 0	Gaps 0



OY 67 CCGCTTTTCCAAACCCCA 85  
| : : : : :  
Db 1 CAUGUUUUCCAAACCCCA 19

## RESULT 115

US-10-310-914A-802509  
; Sequence 802509, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 802509  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-802509

Query Match 6.5%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 57.9%; Pred. No. 43;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 59 CTGCTCCTCAGCTGCTTTTCC 77  
| : : : : :  
Db 2 CUCCCUACACCGCUUCC 20

RESULT 116  
US-10-310-914A-978748/C  
; Sequence 978748, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 978748  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-978748

Query Match 6.5%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 41 GCTCCACTCTCCCAAGCTGC 59  
| : : : : :  
Db 22 GCTCCACTCTCCCAAGCTGC 4

RESULT 117  
US-10-310-914A-1115299/C  
; Sequence 1115299, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1115299  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1115299

## Query Match

Best Local Similarity 6.5%; Score 15.8; DB 1; Length 22;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 37 GCGAGCTCAGCTCCCGC 55  
| : : : : :  
Db 19 GAGAGCTACAGCTCCCGC 1

## RESULT 118

US-10-310-914A-45234  
; Sequence 45234, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45234  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-45234

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 72.7%; Pred. No. 45;  
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 149 CTCAGCTGAGCTGACAGAC 170  
| : : : : :  
Db 1 CACAGGAGAGCTGACAGAC 22

RESULT 119  
US-10-310-914A-419337/C  
; Sequence 419337, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 419337  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-419337

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 52 CCACTGCTGCTCAGCTGCTT 73

Db 22 CCAGCTCCAGCTCATTTGCTT 1

RESULT 120  
US-10-310-914A-877383/c  
; Sequence 877383, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 877383  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-877383

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 131 CATCTCTTTGAGCACTCTCA 152  
Db 22 CATCTCTCTCCAGCCCTCTCA 1

RESULT 121  
US-10-310-914A-955140  
; Sequence 955140, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 955140  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-955140

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 63.6%; Pred. No. 45;  
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 47 CTTCCAGCTCGGCTCACC 68  
Db 1 CCGGCCGCGCCGCGCCGCC 22

RESULT 122  
US-10-310-914A-993524/c  
; Sequence 993524, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 993524  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-993524

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 188 GTGCTGTTAGGTTGCTAGG 209  
Db 22 GTGCTGTTAGGTTGCTAGG 1

RESULT 123  
US-10-310-914A-1134411/c  
; Sequence 1134411, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 1134411  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1134411

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 186 CCGTGTCTGTTAGGTTGCTA 207  
Db 22 CTTGTTGTCAGGTTCTCTCA 1

RESULT 124  
US-10-310-914A-1326011/c  
; Sequence 1326011, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 1326011  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1326011

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 43 TCACCTCCAGCTGCTGCTT 64  
|||||

Db 22 TCAGCTCCCGACCTTGCT 1

Search completed: October 2, 2006, 15:41:59  
Job time : 1 secs

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APPLICANT: Fry, Kirk

```

; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 736
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-736

Query Match          6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      76 CCAAAACCCACCTGCT 91
Db      20 CCAAAACCCACCTGCT 5

RESULT 4
US-10-424-339-1303
; Sequence 1303, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Naasim
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowrira, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
```

```

; SEQ ID NO 1303
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-424-339-1303

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 5.9;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      112 GCCCAGTACGCTCGTTTC 130
Db      1  GCCCTCAAGCGCTCGTTC 19

RESULT 5
US-10-424-339-1484/c
; Sequence 1484, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Naasim
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowrira, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1484
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-424-339-1484

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      112 GCCCAGTACGCTCGTTTC 130
Db      19 GCCCTCAAGCGCTCGTTC 1
```

```

RESULT 6
US-11-293-697-5004
; Sequence 5004, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5004
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized F
US-11-293-697-5004

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      14 CACTGGATTTCCTGACCT 32
      |||||
DB      1 CACTGGATTTCCTGACCT 19

RESULT 7
US-11-217-936-1113
; Sequence 1113, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1113
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1113

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 5.9;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      141 GAGCAGCTCTCAGCGAG 159
      |||||
DB      1 GAGCAGCTCTCAGCGAG 19

RESULT 8
US-11-217-936-1582/c
; Sequence 1582, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.

```

```

; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1582

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      141 GAGCAGCTCTCAGCGAG 159
      |||||
DB      19 GAGCAGCTCTCAGCGAG 1

RESULT 9
US-11-221-332-141/c
; Sequence 141, Application US/11221332
; Publication No. US20060121498A1
; GENERAL INFORMATION:
; APPLICANT: EIRx Therapeutics
; TITLE OF INVENTION: Enzymes involved in apoptosis
; FILE REFERENCE: 8912/2042
; CURRENT APPLICATION NUMBER: US/11/221,332
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/00957
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: GB0305267.7
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: QPCR primer
US-11-221-332-141

Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.6;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      69 TGCTTTTCAACCCACC 87
      |||||
DB      19 TGCTTTTCAACCCACC 1

RESULT 10
US-11-370-584-6418/c
; Sequence 6418, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21

```

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; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6418
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11313 for SEQ 2484,
US-11-370-584-6418
```

```
Query Match          5.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 6.9;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      165 CAGACGACCTGTTAG 181
      |||||
Db       17 CATACGACCTGATAG 1
```

```
RESULT 11
US-11-255-139A-6888/c
; Sequence 6888, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6888
```

```
Query Match          5.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      38 GGAGCTCCACCTCCC 52
      |||||
Db       16 GGTGCTCCACCTCCC 2
```

```
RESULT 12
US-11-255-139A-6889/c
; Sequence 6889, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6889
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6889
```

```
Query Match          5.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      38 GGAGCTCCACCTCCC 52
      |||||
Db       15 GGTGCTCCACCTCCC 1
```

```
RESULT 13
US-11-327-689-17/c
; Sequence 17, Application US/11327689
; Publication No. US20060177854A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/327,689
; FILING DATE: 05-Jan-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/497,957
; FILING DATE: 04-FEB-2000
; APPLICATION NUMBER: US/08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
```



```
/note= "N = 5'-phosphorylated cytosine
(p-C)"
FEATURE:
NAME/KEY: modified_base
LOCATION: 18
OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-digoxigenin-conjugated
guanine (G-dig)"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-327-689-17

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 35 CTGGAGCTCCACCT 49
Db 17 CTGGGCTCTCCACCT 3

RESULT 14
US-11-217-936-1347
; Sequence 1347, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Vasant
; APPLICANT: Carroll, Joseph
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (sIN)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217, 936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1347

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 19;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CAGCAGTGGATTGTG 25
Db 5 CAGCCCGAUVUUG 19

RESULT 15
US-11-217-936-1816/C
; Sequence 1816, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Strina Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (sIN)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217, 936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1816
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
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/ FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1816

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 19;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CAGCAGTGGATTGTG 25
Db 15 CAGCCCTGGATTGTG 1

RESULT 16
US-10-517-441-1250/C
; Sequence 1250, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBEC, John
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517, 441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 1250
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for MGMT
US-10-517-441-1250

Query Match
Best Local Similarity 5.5%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 213 TATCAGATACCACTAA 230
Db 18 TACGACATACCAATAA 1

RESULT 17
US-11-184-215-43/C
; Sequence 43, Application US/11184215
; Publication No. US20060122790A1
; GENERAL INFORMATION:
; APPLICANT: Fowler, Craig A.
; APPLICANT: Menla, Vinod C.
; APPLICANT: Rosso, Thomas L.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ORDERING SYSTEM
; FILE REFERENCE: ILLINC.050A
; CURRENT APPLICATION NUMBER: US/11/184, 215
```

CURRENT FILING DATE: 2005-07-15  
PRIOR APPLICATION NUMBER: 60/634,164  
PRIOR FILING DATE: 2004-12-07  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 43  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Synthetically prepared nucleic acid sequence  
US-11-184-215-43

Query Match 5.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 128 TTCGATCTTTGGAGCA 145  
Db 18 TGGCATCTTTGGAGCA 1

RESULT 18  
US-11-255-139A-4949  
Sequence 4949, Application US/11255139A  
Publication No. US20060154271A1  
GENERAL INFORMATION:  
APPLICANT: Sirta Therapeutics, Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
FILE REFERENCE: MBH01-664-A (400/050)  
CURRENT APPLICATION NUMBER: US/11/255,139A  
CURRENT FILING DATE: 2005-10-20  
NUMBER OF SEQ ID NOS: 8014  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4949  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-255-139A-4949

Query Match 5.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 11;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 64 TCACCTGCTTTCCAA 79  
Db 1 UCACCAGCUCUCCAA 16

RESULT 19  
US-11-293-697-4928/C  
Sequence 4928, Application US/11293697  
Publication No. US20060105376A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: Novel full length CDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/11/293,697  
CURRENT FILING DATE: 2005-12-05  
PRIOR APPLICATION NUMBER: US/10/108,260  
PRIOR FILING DATE: 2002-03-28  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4928  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p  
US-11-293-697-4928

Query Match 5.3%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 10;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 74 TTCGAAACCCACCCT 89  
Db 17 TTCGAAACCCCAACAT 2

RESULT 20  
US-11-327-689-49  
Sequence 49, Application US/11327689  
Publication No. US20060177854A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
Drayna, Dennis T.  
Feder, John N.  
Gulirke, Andreas  
Ruddy, David  
Tsuchinashi, Zenta  
Wolff, Roger K.

TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2811

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/327,689  
FILING DATE: 05-Jan-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/497,957  
FILING DATE: 04-FEB-2000  
APPLICATION NUMBER: US/08/834,497  
FILING DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0056-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-11-327-689-49.

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 13;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TGGAGCTCCACCT 49

Db 1 TGGGTGCTCCACT 14

## RESULT 21

US-11-327-689-50  
; Sequence 50, Application US/11327689  
; Publication No. US20060177854A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; Drayna, Dennis T.  
; Feder, John N.  
; Galke, Andreas  
; Ruddy, David  
; Tsuchihashi, Zenta  
; Wolff, Roger K.  
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/327,689  
FILING DATE: 05-Jan-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/497,957  
FILING DATE: 04-FEB-2000  
APPLICATION NUMBER: US/08/834,497  
FILING DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Polissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0056-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-11-327-689-50

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 13;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TGGAGCTCCACT 49  
|||||  
Db 1 TGGGTGCTCCACT 14

## RESULT 22

US-11-361-627-55  
; Sequence 55, Application US/11361627  
; Publication No. US20060199208A1  
; GENERAL INFORMATION:  
; APPLICANT: Srinivasan, Subha  
; Bingham, Jonathan  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR POLYNUCLEOTIDE DETECTION  
; FILE REFERENCE: 37087-8002 US 01  
; CURRENT APPLICATION NUMBER: US/11/361,627  
; CURRENT FILING DATE: 2006-02-24  
; PRIOR APPLICATION NUMBER: US/10/272,461  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/343,298  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 55  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-361-627-55

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 13;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 53 CAGCTGCTGCTCA 66  
|||||  
Db 4 CAGCTGCTGCTCA 17

RESULT 23  
US-11-255-139A-5820/C  
; Sequence 5820, Application US/11255139A  
; Publication No. US20060154271A1  
; GENERAL INFORMATION:  
; APPLICANT: McSwigen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/11/255,139A  
; CURRENT FILING DATE: 2005-10-20  
; NUMBER OF SEQ ID NOS: 8014  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5820  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-255-139A-5820

Query Match 5.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 13;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 GAGCTCCACTCCC 52  
|||||  
Db 17 GTGCTCCACTCCC 4

RESULT 24  
US-10-524-432-606  
; Sequence 606, Application US/10524432  
; Publication No. US20060127902A1  
; GENERAL INFORMATION:  
; APPLICANT: Genzyme Corporation  
; TITLE OF INVENTION: BRAIN ENDOTHELIAL EXPRESSION PATTERNS  
; FILE REFERENCE: 003482.00010  
; CURRENT APPLICATION NUMBER: US/10/524,432  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: US 60/403,390  
; PRIOR FILING DATE: 2002-08-15

```

? PRIOR APPLICATION NUMBER: US 60/458,978
? PRIOR FILING DATE: 2003-04-01
? NUMBER OF SEQ ID NOS: 869
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 606
? LENGTH: 17
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-524-432-606

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```
Query Match      5.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```

Qy      40 AGCTCCACCTCCCCAGC 56
          |||||
Db      1  AGCTCCAGACCCCGAGC 17

```

```

RESULT 25
US-11-190-801-1/c
; Sequence 1, Application US/11190801
; Publication No. US2006014192A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, KEVIN R.
; APPLICANT: PAGERVOID, SONJA K.
; APPLICANT: MATTS, JOY E. M.
; APPLICANT: MAY, HAROLD D.
; TITLE OF INVENTION: GENE PROBES FOR THE SELECTIVE DETECTION OF MICROORGANISMS THAT
; TITLE OF INVENTION: REDUCTIVELY DECHLORINATED POLYCHLORINATED BIPHENYL COMPOUNDS
; FILE REFERENCE: 4115-206
; CURRENT APPLICATION NUMBER: US/11/190,801
; CURRENT FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: 60/591,514
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-190-801-1

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Query Match	5.0%;	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%;	Pred. No. 14;		
Matches 14;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy	49	TCCCCAGCTGCTGCCTC	65
Db	17	TTCCCTTGCTGCTGCCTC	1

```

RESULT 26
US-11-255-139A-4513
; Sequence 4513, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MAH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4513
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-4513

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Query Match	5.0%;	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	64.7%;	Pred. No. 14;		
Matches 11; Conservative	3;	Mismatches 3;	Indels 0;	Gaps 0;

```

QY      36 TGGGAGCTCCACCTCC 52
      :|||:|:|||
Db      1 UGGCAGCTCUCUCCUCC 17

```

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Search completed: October 2, 2006, 15:38:59
Job time : 0.001 secs
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QY 133 TCTCTTGAGACCTCTCAC 153  
 Db 2 TCTCTTGAGACCTCTTTCAC 22

RESULT 4  
 LOCUS AX554633  
 DEFINITION Sequence 187 from Patent WO0246229.  
 ACCESSION AX554633  
 VERSION AX554633.1 GI:25898300  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shinkets,R.A., Spytek,K.A., Gilbert,J.A., Mayoite,J.E., Baumgartner,J.C., Mishra,V., Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.  
 TITLE Novel proteins and nucleic acids encoding same  
 JOURNAL Patent: WO 0246229-A 187 13-JUN-2002;  
 Curagen Corporation (US)  
 FEATURES  
 source 1..22  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PCR Primer Sequence"

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 3;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 TCTCTTGAGACCTCTCAC 153  
 Db 2 TCTCTTGAGACCTCTTTCAC 22

RESULT 5  
 LOCUS AX703310  
 DEFINITION Sequence 539 from Patent WO0205913.  
 ACCESSION AX703310  
 VERSION AX703310.1 GI:29538356  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Li,L., Ballinger,R.A., Padigaru,M., Kexuda,R., Colman,S.D., Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Guev,V., Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J., Sioter,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K., Gangoli,E.A. and Millet,I.  
 TITLE G-protein coupled receptors and nucleic acids encoding same  
 JOURNAL Patent: WO 0205913-A 539 01-AUG-2002;  
 Curagen Corporation (US)  
 FEATURES  
 source 1..22  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PCR Primer Sequence"

Query Match 6.7%; Score 16.2; DB 1; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 3;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 6  
 LOCUS AR529565/c  
 DEFINITION Sequence 768 from patent US 6727063.  
 ACCESSION AR529565  
 VERSION AR529565.1 GI:53918002  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolik,S., Daley,G.Q. and McCarthy,J.J.  
 TITLE Single nucleotide polymorphisms in genes  
 JOURNAL Patent: US 6727063-A 768 27-APR-2004;  
 Millennium Pharmaceuticals, Inc. and Whitehead Institute for Biomedical Research; Cambridge, MA  
 FEATURES  
 source 1..21  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 6.5%; Score 15.8; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.5;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCACGACGACCTGATT 23  
 Db 21 CTCACGACGACCTGACTAT 1

RESULT 7  
 LOCUS AX095590/c  
 DEFINITION Sequence 768 from Patent WO0118250.  
 ACCESSION AX095590  
 VERSION AX095590.1 GI:13511793  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolik,S., Daley,G.Q. and McCarthy,J.J.  
 TITLE Single nucleotide polymorphisms in genes  
 JOURNAL Patent: WO 0118250-A 768 15-MAR-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)  
 FEATURES  
 source 1..21  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 6.5%; Score 15.8; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.5;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCACGACGACCTGATT 23  
 Db 21 CTCACGACGACCTGACTAT 1

RESULT 8  
 LOCUS DD173031  
 DEFINITION Expression systems using mammalian beta-Actin promoter.  
 ACCESSION DD173031  
 VERSION DD173031.1 GI:83967286  
 KEYWORDS WO 2005054467-A/31.

SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Teunoda,H. and Habu,K.  
TITLE Expression systems using mammalian beta-Acclin promoter  
JOURNAL Patent: WO 2005054467-A 31 16-JUN-2005;  
CHUGAI PHARMACEUTICAL CO LTD  
COMMENT OS Artificial  
PN WO 2005054467-A/31  
PD 16-JUN-2005  
PF 03-DEC-2004 WO 2004JP018006  
PR 03-DEC-2003 JP 2003-405269  
PI hiroyuki teunoda,kiyoshi habu  
CC Description of Artificial Sequence : Artificially Synthesized  
CC Primer  
CC Sequence  
FEATURES Location/Qualifiers.  
source 1..22  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.5;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 110 GTGCCACTACGCTGTTCC 131  
Db 1 GTGCACACGACGCGCTTGC 22

RESULT 9  
LOCUS AR704960 22 bp DNA linear PAT 20-SEP-2005  
DEFINITION Sequence 23 from patent US 6929912.  
ACCESSION AR704960  
VERSION AR704960.1 GI:75923278  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Guida,M., Hall,U., Petros,W.P., Vredenburg,J.J., Colvin,O.M. and Marks,J.R.  
TITLE Methods for evaluating the ability to metabolize pharmaceuticals  
JOURNAL Patent: US 6929912-A 23 16-AUG-2005;  
Genesee Pharmaceuticals, Inc. and Duke University; New Haven, CT  
FEATURES Location/Qualifiers  
source 1..22  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 6.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.5;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 56 CTGCTGCTCAGCTGCTTCC 77  
Db 1 CTGCAGCCCGCCTCTTCTCC 22

RESULT 10  
LOCUS AR279129 20 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 262 from patent US 6514694.  
ACCESSION AR279129  
VERSION AR279129.1 GI:29713772  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Milhausen,M.J.  
TITLE Methods for the detection of encysted parasites  
JOURNAL Patent: US 6514694-A 262 04-FEB-2003;  
Heeska Corporation; Fort Collins, CO  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 6.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 4.4;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 189 TGCTGTTAGGTTGCTAG 208  
Db 1 TGCTGTTAGGTTGCTAG 20

RESULT 11  
LOCUS AR393701 21 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 240 from patent US 6617122.  
ACCESSION AR393701  
VERSION AR393701.1 GI:40120515  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Hayden,M.R., Brooke-Wilson,A.R. and Pinstone,S.N.  
TITLE Process for identifying modulators of ABC1 activity  
JOURNAL Patent: US 6617122-A 240 09-SEP-2003;  
Xenon Genetics, Inc.; Burnaby; BC  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 6.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 4.1;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 58 GCTGCTCAGCTGCTTCC 77  
Db 1 GCAGCTCAGCTGCTTCC 20

Search completed: October 2, 2006, 15:34:16  
Job time : 0.001 secs

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```
US-08-765-340-30
; Sequence 30, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.,
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; TITLE OF INVENTION: COMPOUND
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version
; SOFTWARE: #1.30 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 145146/94
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311130/94
; FILING DATE: 21-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SERUNIAN, LESLIE
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 1452-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
;
US-08-765-340-30

Query Match          6.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      147 CCCTTCCTCTCTGCCAT 164
      ||| ||| ||| ||| ||| |||
Db      3 CCCTCTCTCTCTGCCAT 20

RESULT 2
US-09-702-251-85
; Sequence 85, Application US/09702251
; Patent No. 6372492
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0199
; CURRENT APPLICATION NUMBER: US/09/702,251
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85

US-09-574-779B-88/c
; Sequence 88, Application US/09574779B
; Patent No. 6767720
; GENERAL INFORMATION:
; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE
; TITLE OF INVENTION: No. 6767720el cDNAs encoding catenin-binding proteins with
; FILE REFERENCE: 2676-4415US
; CURRENT APPLICATION NUMBER: US/09/574,779B
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 99201543.8
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer FVR1479F
;
US-09-574-779B-88

Query Match          6.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      182 GACTTCACAGAGCA 198
      ||| ||| ||| ||| ||| |||
Db      17 GACTTCACAGAGCA 1

RESULT 4
US-09-593-711A-63
; Sequence 63, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
;
US-09-593-711A-63

Query Match          6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 133 GAGACACCTGCTCCCCCTTC 152  
Db 1 GCGACAGCTGCTCCACCTTC 20

RESULT 5  
 US-09-593-711A-180  
 Sequence 180, Application US/09593711A  
 Patent No. 6271030  
 GENERAL INFORMATION:  
 APPLICANT: Brett P. Montia  
 APPLICANT: Madeline M. Butler  
 TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION  
 FILE REFERENCE: RTS-0118  
 CURRENT APPLICATION NUMBER: US/09/593,711A  
 CURRENT FILING DATE: 2000-06-14  
 NUMBER OF SEQ ID NOS: 244  
 SEQ ID NO 180  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-593-711A-180

Query Match	6.4%	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%;	Pred. No. 16;		
Matches 17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

QY	136	ACACCTGCTCCCCCTTCTCC	155
Db	1	ACAGCTGCTCCACCTTCTTC	20

RESULT 6  
 US-09-295-593-9/c  
 ; Sequence 9, Application US/09295593  
 ; Patent No. 6417169  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WRIGHT, Jim A.  
 ; APPLICANT: YOUNG, Aiping H.  
 ; APPLICANT: LEE, Yoon S.  
 ; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE  
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL  
 ; TITLE OF INVENTION: GROWTH  
 ; FILE REFERENCE: 012396-046  
 ; CURRENT APPLICATION NUMBER: US/09/295,593  
 ; CURRENT FILING DATE: 1999-04-22  
 ; EARLIER APPLICATION NUMBER: US 60/082,791  
 ; EARLIER FILING DATE: 1998-04-23  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-295-593-9

Query Match	6.4%	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%;	Pred. No. 16;		
Matches 17;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0

QY	98	GGCCCCCTCTCATTTCTCTG	117
Db	20	GGCCCCCGCTCTTCTCCCG	1

RESULT 7  
US-09-484-629B-28/c  
; Sequence 28, Application US/09484629B  
; Patent No. 6998472  
; GENERAL INFORMATION:

```

1  TITLE OR INVENTION: Obesity gene
2  FILE REFERENCE: 18396/1140
3  CURRENT APPLICATION NUMBER: US/09/484,629
4  CURRANT FILING DATE: 2000-01-18
5  PRIOR APPLICATION NUMBER: PCT/GB99/02658
6  PRIOR FILING DATE: 1998-12-08
7  NUMBER OF SEQ. ID NOS: 37
8  SOFTWARE: PatentIn version 3.2
9  SEQ ID NO 28
10 LENGTH: 21
11 TYPE: DNA
12 ORGANISM: Artificial
13 FEATURE:
14 OTHER INFORMATION: synthetic primer
15 FEATURE:
16 NAME/KEY: misc feature
17 LOCATION: (1)..(21)
18 OTHER INFORMATION: synthetic primer
19 US-09-484-629B-28

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Query Match	6.4%	Score 15.2;	DB 1;	Length 21;
Best Local Similarity	85.0%	Pred. No. 15;		
Matches 17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

**QY**      139 CCTGCTCCCCCTTCTCCTTC 158  
          ||||| |  
**Db**      20 CCTGCTCCCGCTCCTCCTGC 1

RESULT 8  
 US-08-741-406-10/c  
 Sequence 10 Application US/08741406  
 Patent No. 572118  
 GENERAL INFORMATION:  
 APPLICANT: Schffler, Immo E.  
 TITLE OF INVENTION: Mammalian Artificial Chromosomes and  
 TITLE OF INVENTION: Methods of Using Same  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/741,406  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/550,717  
 FILING DATE: 31-OCT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-UD 2317  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-741-406-10

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Query Match      6.4%; Score 15; DB 1; Length 20
Best Local Similarity 100.0%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 0; Indels
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Qy	178	CAGGACTTCACAAG	192
Db	16	CAGGACTTCACAAG	2

RESULT 5  
US-09-02

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US-09-024-472-10/C
Sequence 10, Application US/09024472
Patent No. 6133503
GENERAL INFORMATION:
APPLICANT: Scheffler, Immo E.
TITLE OF INVENTION: Mammalian Artificial Chromosomes and
METHOD OF INVENTION: Methods of Using Same
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,472
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/741,406
FILING DATE:
APPLICATION NUMBER: US 08/550,717
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-024-472-10

Query Match          6.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY      178 CAGGACTTCACGANG 192
Db      16 CAGGACTTCACGANG 2
|||||
|||||

RESULT 10
US-09-517-467B-252
Sequence 252, Application US/09517467B
Patent No. 6451602
GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
FILE REFERENCE: RRS-0150
CURRENT APPLICATION NUMBER: US/09/517,467B

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; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345

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OTHER INFORMATION: Antisense Oligonucleotides  
US-09-517-467B-252

Qy	41	TGCCATCCCCCTGGTGAT	58
Db	1	TCCCATCCCCCTGGTGCT	18

Query March	6.3%	Score 14.8	DB 1	Length 20
Best Local Similarity	88.9%	Pred. No.18		
Matches 16, Conservative	0	Mismatches 2	Indels 0	Gaps 0

OY 70 CGTGAGAGCTGTTGTT 87  
|||||  
Db 20 CGTGAGAGCTGTTGTT 3

## RESULT 12

US-10-413-255-2/c  
Sequence 2, Application US/10413255  
Patent No. 6949637  
GENERAL INFORMATION:  
APPLICANT: Lilly, Craig M.  
Luster, Andrew D.  
Drazen, Jeffrey M.  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS, PREDICTION  
AND TREATMENT OF ASTHMA AND OTHER INFLAMMATORY CONDITIONS  
BASED ON EOTAXIN CODING SEQUENCE POLYMORPHISM  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/413,255  
FILING DATE: 14-Apr-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/076,259  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,720  
FILING DATE: 16-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Trevisan, Maria A.  
REGISTRATION NUMBER: 48,207  
REFERENCE/DOCKET NUMBER: B00801.70282. US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-413-255-2

Query Match 6.3%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 70 CGTGAGAGCTGTTGTT 87  
|||||  
Db 20 CGTGAGAGCTGTTGTT 3

RESULT 13  
US-08-117-952-294/c  
Sequence 294, Application US/08117952  
Patent No. 3851760  
GENERAL INFORMATION:  
APPLICANT: Evans, Glen A.  
APPLICANT: Smith, Michael W.  
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE

TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
NUMBER OF SEQUENCES: 797  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,952  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,471  
FILING DATE: 15-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
FILING DATE: 15-JUN-1993  
INFORMATION FOR SEQ ID NO: 294:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Oligonucleotide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-117-952-294

Query Match 6.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 17;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 74 AGAGCTGTTGTTGAA 91  
|||||  
Db 18 AAGCTGTTTGTGAA 1

RESULT 14  
US-09-825-923-6  
Sequence 6, Application US/09825923  
Patent No. 6696556  
GENERAL INFORMATION:  
APPLICANT: Snapir, Amir  
APPLICANT: Heinoonen, Paula  
APPLICANT: Alhopuro, Pia  
APPLICANT: Karvonen, Matti  
APPLICANT: Koskinen, Markku  
APPLICANT: Pesonen, Ullamari  
APPLICANT: Scheinin, Mika  
APPLICANT: Salonen, Jukka T  
APPLICANT: Tuomainen, Tomi-Pekka  
APPLICANT: Lakka, Timo A  
APPLICANT: Myrskanen, Kristina  
APPLICANT: Salonen, Riitta  
APPLICANT: Kaunonen, Jussi  
APPLICANT: Valkonen, Veli-Pekka  
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor  
FILE REFERENCE: Alpha-2B-AR variant  
CURRENT APPLICATION NUMBER: US/09/825,923  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 09/422,985

PRIOR FILING DATE: 2000-05-25  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PCR primer  
US-09-825-923-6

Query Match 6.1%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 143 CTCCTCTCTCTCTC 158  
Db 4 CTCCTCTCTCTCTC 19

RESULT 15  
US-10-077-870-6  
Sequence 6, Application US/10077870  
Patent No. 7029849  
GENERAL INFORMATION:  
APPLICANT: Salonen, Jukka T  
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof  
FILE REFERENCE: 0933-0183P  
CURRENT APPLICATION NUMBER: US/10/077, 870  
CURRENT FILING DATE: 2002-05-21  
PRIOR APPLICATION NUMBER: FI 20010323  
PRIOR FILING DATE: 2001-02-20  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 6  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PCR primer pair 1, directed  
US-10-077-870-6

Query Match 6.1%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 143 CTCCTCTCTCTCTC 158  
Db 4 CTCCTCTCTCTCTC 19

RESULT 16  
US-09-056-285A-41  
Sequence 41, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES: 43  
ADDRESSEE: FOLEY, HONG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-7000  
TELEFAX: 617-832-1000  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer".  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-056-285A-41

Query Match 6.1%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 21;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 CTTCTCTTCTGCGCAT 164  
Db 3 CATTCTCTTCTGCGCAT 18

RESULT 17  
US-09-952-464A-41  
Sequence 41, Application US/09952464A  
Patent No. 6956103  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
FILE REFERENCE: 21087.0017U1  
CURRENT APPLICATION NUMBER: US/09/952,464A  
CURRENT FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: 09/473,273  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 09/461,542  
PRIOR FILING DATE: 1999-12-15  
PRIOR APPLICATION NUMBER: 09/366,952  
PRIOR FILING DATE: 1999-08-04  
PRIOR APPLICATION NUMBER: 09/056,285  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: 08/822,999  
PRIOR FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 41  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6956103e =  
US-09-952-464A-41

Query Match 6.1%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 21;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 CTTCTCTTCTGCGCAT 164  
| | | | | | | | | | | | | | | | | | | | | |

Db 3 CATCTCTTGTGCAT 18

```
RESULT 18
US-09-422-978-10001/c
; Sequence 10001, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10001
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136, in compleme
US-09-422-978-10001
```

```
Query Match 6.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 209 CATGCTCTTGTGTCTCT 227
Db 19 CTTACTCTTGTGTGTCT 1
```

```
RESULT 19
US-08-850-993-10/c
; Sequence 10, Application US/08850993
; Patent No. 5955277
; GENERAL INFORMATION:
; APPLICANT: Hansen, Torben
; APPLICANT: Andersen, Carsten
; APPLICANT: Pedersen, Oluf B.
; TITLE OF INVENTION: Mutant cDNA Encoding The p53alpha
; TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase
; FILE REFERENCE: 4802.200-US
; CURRENT APPLICATION NUMBER: US/08/850,993
; CURRENT FILING DATE: 1997-05-05
; EARLIER APPLICATION NUMBER: 0539/96
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-08-850-993-10
```

```
Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 77 GCTGCTTTTGAAGAGC 95
Db 20 GCTGAGGTTTGAGAGC 2
```

```
RESULT 20
US-09-392-350-35/c
; Sequence 35, Application US/09392350
; Patent No. 6133032
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3 KINASE P110 BETA EXPRESSION
; FILE REFERENCE: RTS-0075
; CURRENT APPLICATION NUMBER: US/09/392,350
; CURRENT FILING DATE: 1999-09-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-350-35
```

```
Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 64 AGTTCAGTGAGAGCTGCT 82
Db 19 AGTTCATGTCAGGCTGCT 1
```

```
RESULT 21
US-09-283-011-35/c
; Sequence 35, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mosele, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Watburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
```

TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-283-011-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 GACTTCACAGAGCAAT 200  
Db 20 GTCTTCACAGAGCAAT 2

RESULT 22  
US-09-593-711A-62  
; Sequence 62, Application US/09593711A  
; Patent No. 6271030  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION  
; FILE REFERENCE: RFS-0118  
; CURRENT APPLICATION NUMBER: US/09/593, 711A  
; CURRENT FILING DATE: 2000-06-14  
; NUMBER OF SEQ ID NOS: 244  
; SEQ ID NO 62  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense oligonucleotide  
US-09-593-711A-62

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 138 ACCTGCTCCCTCTCTCT 156  
Db 1 AGCTGCTCCACTTCTTCT 19

RESULT 23  
US-09-422-978-11320  
; Sequence 11320, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET 020CPI  
; CURRENT APPLICATION NUMBER: US/09/422, 978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298, 850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109, 732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082, 614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 11320  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind

LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-4207 for SEQ 3455, in complement  
US-09-422-978-11320

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 CTCTCATTCCTCCCTCCC 122  
Db 2 CTCTCATTCCTCCCTCCC 20

RESULT 24  
US-09-033-936-35/C  
; Sequence 35, Application US/09033936  
; Patent No. 6632976  
; GENERAL INFORMATION:  
; APPLICANT: TOMIZUKA, KAZUMA  
; APPLICANT: YOSHIDA, HITOSHI  
; APPLICANT: HANAOKA, KAZUNORI  
; APPLICANT: OSHIMURA, MITSUO  
; APPLICANT: ISHIDA, ISAO  
; TITLE OF INVENTION: CHIMERIC ANIMAL AND METHOD FOR PRODUCING THE SAME  
; FILE REFERENCE: 081356/0114  
; CURRENT APPLICATION NUMBER: US/09/033, 936  
; CURRENT FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: PCT/JP96/02427  
; PRIOR FILING DATE: 1996-08-29  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-033-936-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 136 ACACCTGCTCCCTCTCTC 154  
Db 20 ACACCTGCTCTCTCTCAC 2

RESULT 25  
US-09-012-135A-35/C  
; Sequence 35, Application US/09012135A  
; Patent No. 6716575  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory  
; APPLICANT: Mosie, Kevin  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1  
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/09/012.135A  
FILING DATE: January 22, 1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,268  
FILING DATE: January 9, 1998  
APPLICATION NUMBER: 08/755,728  
FILING DATE: No. 6716575ember 25, 1996  
APPLICATION NUMBER: 60/023,943  
FILING DATE: August 14, 1996  
APPLICATION NUMBER: 60/008,809  
FILING DATE: December 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 231/282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-012-135A-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 182 GACTTCACAGAGCAAT 200  
Db 20 GTCTTCACAGAGCAAT 2

RESULT 26  
US-09-784-332-35/C  
Sequence 35, Application US/09784332  
Patent No. 6841579  
GENERAL INFORMATION:  
APPLICANT: Plozman, Gregory  
Mossle, Kevin  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ATR-1  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784.332  
FILING DATE: 16-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/283,011  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 09/012,135  
FILING DATE: January 22, 1998  
APPLICATION NUMBER: 08/755,728  
FILING DATE: No. 6841575ember 25, 1996  
APPLICATION NUMBER: 60/023,943

FILING DATE: August 14, 1996  
APPLICATION NUMBER: 60/008,809  
FILING DATE: December 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 231/282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-784-332-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 182 GACTTCACAGAGCAAT 200  
Db 20 GTCTTCACAGAGCAAT 2

RESULT 27  
US-08-765-340-29  
Sequence 29, Application US/08765340  
Patent No. 6150092  
GENERAL INFORMATION:  
APPLICANT: UCHIDA, K.  
APPLICANT: UCHIDA, T.  
APPLICANT: TANAKA, Y.  
APPLICANT: MATSUDA, Y.  
APPLICANT: KONDO, S.  
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID  
NUMBER OF SEQUENCES: 185  
TITLE OF INVENTION: COMPOUND  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version  
SOFTWARE: #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,340  
FILING DATE: 23-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 145146/94  
FILING DATE: 27-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 311130/94  
FILING DATE: 21-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SERUNIAN, LESLIE  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 1452-4005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-08-765-340-29

Query Match 5.9%; Score 14; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 CTCCTCTGCCATG 165  
Db 2 CTCCTCTGCCATG 15

## RESULT 28

US-08-373-124A-178  
Sequence 178, Application US/08373124A  
Patent No. 5646042

## GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-178

Query Match 5.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 31;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTCCTCCCCCTTCTCT 156  
Db 1 CTCCTCCCCCTTCTCT 17

## RESULT 29

US-08-373-124A-180

Sequence 180, Application US/08373124A  
Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 180:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-180

Query Match 5.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 31;

Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 143 CTCCTCTCTCTCTCT 159  
Db 1 CTCCTCTCTCTCTCT 17

RESULT 30

US-08-435-628-178  
; Sequence 178, Application US/08435628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwigen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Filth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 178:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-628-178  
Query Match 5.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 31;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
QY 140 CTGCTCCCTTCCTTCT 156  
DB 1 CUCCUCCUCCUCCUCCU 17  
RESULT 31  
US-08-435-628-180  
; Sequence 180, Application US/08435628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Filth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 180:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-628-180  
Query Match 5.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 31;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
QY 143 CTCCTCCCTTCCTTCT 159  
DB 1 CUCCUCCUCCUCCUCCU 17  
RESULT 32  
US-08-311-486C-1151  
; Sequence 1151, Application US/08311486C  
; Patent No. 5811300  
; GENERAL INFORMATION:  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth Draper  
; APPLICANT: Kevin Ksich  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwigen  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

; TITLE OF INVENTION: TNF-
; NUMBER OF SEQUENCES: 1157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,486C
; FILING DATE: September 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-486C-1151

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 29;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 91 AGAGCTGCCCCCTCT 107
Db 1 AGAGCCAGCCCCCUCU 17

RESULT 33
US-09-422-978-4193/c
; Sequence 4193, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Maria
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020Cp1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4193
; LENGTH: 18
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```

; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ 259,
US-09-422-978-4193

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 TTCTCCTGCTCCACATC 126
Db 17 TTCTCCTAATCCACATC 1

RESULT 34
PCT-US95-04094-3
; Sequence 3, Application PC/TUS9504094
; GENERAL INFORMATION:
; APPLICANT: ALMS, William
; APPLICANT: WHITE, Barbara
; TITLE OF INVENTION: HUMAN INTERLEUKIN VARIANTS GENERATED BY
; TITLE OF INVENTION: ALTERNATIVE SPLICING
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04094
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,010
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feuery, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 028754-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-04094-3

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 113 TTCTGCTCCACATCTTG 129
Db 1 TTCTGCTCAATCCATC 17

RESULT 35
US-08-502-185-9/c
; Sequence 9, Application US/08502185
```

```
Patent No. 5639736
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,185
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
FAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-502-185-9

Query Match 5.8%; Score 13.8; DB 1; length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 213 CTTCTGTTCTGTCGTC 229
Db 19 CGCTGTTCTGTCGTC 3

RESULT 36
US-08-398-945-9/c
Sequence 9, Application US/08398945
Patent No. 5639872
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,945
FILING DATE:
```

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
FAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-398-945-9

Query Match 5.8%; Score 13.8; DB 1; length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 213 CTTCTGTTCTGTCGTC 229
Db 19 CGCTGTTCTGTCGTC 3

RESULT 37
US-08-501-779-9/c
Sequence 9, Application US/08501779
Patent No. 5661135
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,779
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
FAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-501-779-9

Query Match 5.8%; Score 13.8; DB 1; length 19;
Best Local Similarity 88.2%; Pred. No. 27;
```

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGCTGC 229

Db 19 CGTCTGTCTGTGTC 3

## RESULT 38

US-08-501-713-9/C

Sequence 9, Application US/08501713

Patent No. 5710136

GENERAL INFORMATION:

APPLICANT: Robinson, Gregory S.

APPLICANT: Smith, Lois E.H.

TITLE OF INVENTION: Inhibition of

TITLE OF INVENTION: Neovascularization Using

TITLE OF INVENTION: VEGF-Specific

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/501,713

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-031DV2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-330-1300

TELEFAX: 617-330-1311

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-501-713-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 27;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGCTGC 229

Db 19 CGTCTGTCTGTGTC 3

## RESULT 39

US-08-378-860-9/C

Sequence 9, Application US/08378860

Patent No. 5731294

GENERAL INFORMATION:

APPLICANT: Robinson, Gregory S.

APPLICANT: Smith, Lois E.H.

TITLE OF INVENTION: Inhibition of

TITLE OF INVENTION: Neovascularization Using

TITLE OF INVENTION: VEGF-Specific

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lappin & Kusner

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,860

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-330-1300

TELEFAX: 617-330-1311

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-378-860-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 27;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGCTGC 229

Db 19 CGTCTGTCTGTGTC 3

## RESULT 40

US-08-501-626-9/C

Sequence 9, Application US/08501626

Patent No. 5801156

GENERAL INFORMATION:

APPLICANT: Robinson, Gregory S.

APPLICANT: Smith, Lois E.H.

TITLE OF INVENTION: Inhibition of

TITLE OF INVENTION: Neovascularization Using

TITLE OF INVENTION: VEGF-Specific

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/501,626

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031DV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-501-626-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 27;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 213 CTTCTGTTCTGCTGC 229  
Db 19 CGCTCTGTTCTGCTGC 3

RESULT 41  
US-08-501-356-9/c  
Sequence 9, Application US/08501356  
Patent No. 5814620  
GENERAL INFORMATION:  
APPLICANT: Robinson, Gregory S.  
APPLICANT: Smith, Lois E.H.  
TITLE OF INVENTION: Inhibition of  
TITLE OF INVENTION: Neovascularization Using  
TITLE OF INVENTION: VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusner  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/501,356  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031DV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1311  
TELEFAX: 617-330-1300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-501-356-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 27;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 213 CTTCTGTTCTGCTGC 229  
Db 19 CGCTCTGTTCTGCTGC 3

RESULT 42  
US-08-270-581-6  
Sequence 6, Application US/08270581  
Patent No. 5856168  
GENERAL INFORMATION:  
APPLICANT: Weigel, Paul H.  
APPLICANT: Deangelis, Paul L.  
TITLE OF INVENTION: Hyaluronate Synthase Gene and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/270,581  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSG:161\PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-270-581-6

Query Match 5.8%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 27;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 ATGGTTAGTCCCATCC 48  
Db 2 ATGGCTTAGTCCCATTC 18

RESULT 43  
US-09-146-893-6  
Sequence 6, Application US/09146893  
Patent No. 6453504  
GENERAL INFORMATION:  
APPLICANT: Weigel, Paul H.  
APPLICANT: Deangelis, Paul L.  
TITLE OF INVENTION: Hyaluronate Synthase Gene and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee

```

; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77101-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,893
; FILING DATE: 03-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/270,581
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: USG:161\PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-146-893-6

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 44
US-10-117-795-8
; Sequence 8, Application US/10117795
; Patent No. 6852514
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.073
; CURRENT APPLICATION NUMBER: US/10/117,795
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/559,793
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-10-117-795-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18
```

```

Db      2 ATGCTTAGTGCATTC 18

RESULT 45
US-10-124-222-8
; Sequence 8, Application US/10124222
; Patent No. 6855502
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/10/124,222
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-10-124-222-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 46
US-11-024-426-8
; Sequence 8, Application US/11024426
; Patent No. 7026159
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/11/024,426
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-11-024-426-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 47
US-10-156-306B-6881/C
; Sequence 6881, Application US/10156306B
; Patent No. 7022828
```



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; GENERAL INFORMATION:
; APPLICANT: MGSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6881
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306B-6881

Query Match      5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 35;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      148 CCTTCTCCTTCTGCC 162
Db      16  CCTGCTCCTTCTGCC 2

RESULT 48
US-10-156-306B-6882/C
; Sequence 6882, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MGSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6882
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306B-6882

Query Match      5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 35;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      148 CCTTCTCCTTCTGCC 162
Db      15  CCTGCTCCTTCTGCC 1

RESULT 49
US-09-358-972-204/C
; Sequence 204, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephardt, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
```

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; CURRENT APPLICATION NUMBER: US/09/358,972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; US-09-358-972-204

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGAG 65
Db      17  TTGGGATGAGTGAG 3

RESULT 50
US-09-406-064-70/C
; Sequence 70, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephardt, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; US-09-406-064-70

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGAG 65
Db      17  TTGGGATGAGTGAG 3

RESULT 51
```

```
US-09-430-615-40/c
; Sequence 40, Application US/09430615
; Patent No. 627578
; GENERAL INFORMATION:
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Andrews, Christine Ann
; APPLICANT: Hartnett, James Robert
; APPLICANT: Welch, Roy
; APPLICANT: Shultz, John William
; TITLE OF INVENTION: Method for Amplified Nucleic Acid Detection
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/430,615
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAN reverse
US-09-430-615-40

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 17 TTGGGATGAGTGTGAG 3

RESULT 52
US-09-406-065-45/c
; Sequence 45, Application US/09406065
; Patent No. 6312902
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Improved Nucleic Acid Detection
; FILE REFERENCE: Improved Nucleic Acid Detection
; CURRENT APPLICATION NUMBER: US/09/406,065
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAN reverse
; OTHER INFORMATION: probe
US-09-406-065-45

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 17 TTGGGATGAGTGTGAG 3

RESULT 53
US-09-250-609-48
; Sequence 48, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-250-609-48

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 2 TTGGTGTAGTGTGAG 16

RESULT 54
US-09-250-611-48
; Sequence 48, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Baaset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-250-611-48

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 2 TTGGTGTAGTGTGAG 16
```

```
RESULT 55
US-09-422-978-11764
; Sequence 11764, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in complemen
US-09-422-978-11764

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      113 TCCTGCTCCACTCT 127
Db      2 TCCTTCTCCACTCT 16

RESULT 56
US-09-788-847-70/c
; Sequence 70, Application US/09788847
; Patent No. 6653078
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lelepe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/788,847
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/406,064
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; OTHER INFORMATION: probe
```

```
US-09-788-847-70

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGG 65
Db      17 TTGGGATGAGTGG 3

RESULT 57
US-09-790-417-204/c
; Sequence 204, Application US/09790417
; Patent No. 6730479
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: PRO-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; OTHER INFORMATION: probe
US-09-790-417-204

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGG 65
Db      17 TTGGGATGAGTGG 3

RESULT 58
US-09-255-912-14
; Sequence 14, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Antisense Oligonucleotide  
US-09-255-912-14

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 CTCCTATTCCTGCTGCC 121  
Db 1 CTCCTCTCCGCTCTCC 18

## RESULT 59

US-08-413-740A-162  
; Sequence 162, Application US/08413740A  
; Patent No. 6171859  
; GENERAL INFORMATION:  
; APPLICANT: HERRNSTADT, CORINNA  
; APPLICANT: PARKER, WILLIAM D.  
; APPLICANT: DAVIS, ROBERT  
; APPLICANT: MILLER, SCOTT W.  
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial  
; NUMBER OF SEQUENCES: 206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036-5405  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/413,740A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04063  
; FILING DATE: 30-MAR-1995  
; APPLICATION NUMBER: 08/413,740  
; FILING DATE: 30-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bonham, David B.  
; REGISTRATION NUMBER: 34297  
; REFERENCE/DOCKET NUMBER: 2105/7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 429-1776  
; TELEFAX: (202) 429-0796  
; INFORMATION FOR SEQ ID NO: 162:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-413-740A-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATTCCTGCTGCCA 123  
Db 1 CTCCTACTCCTGCTGCCA 18

## RESULT 60

US-08-413-740A-164  
; Sequence 164, Application US/08413740A  
; Patent No. 6171859  
; GENERAL INFORMATION:  
; APPLICANT: HERRNSTADT, CORINNA  
; APPLICANT: PARKER, WILLIAM D.  
; APPLICANT: DAVIS, ROBERT  
; APPLICANT: MILLER, SCOTT W.  
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial  
; NUMBER OF SEQUENCES: 206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036-5405  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/413,740A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04063  
; FILING DATE: 30-MAR-1995  
; APPLICATION NUMBER: 08/413,740  
; FILING DATE: 30-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bonham, David B.  
; REGISTRATION NUMBER: 34297  
; REFERENCE/DOCKET NUMBER: 2105/7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 429-1776  
; TELEFAX: (202) 429-0796  
; INFORMATION FOR SEQ ID NO: 164:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-413-740A-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATTCCTGCTGCCA 123  
Db 1 CTCCTACTCCTGCTGCCA 18

## RESULT 61

US-09-422-978-7274/C  
; Sequence 7274, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marla  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 7274  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..18  
OTHER INFORMATION: upstream amplification primer 99-3391 for SEQ 3340,  
US-09-422-978-7274

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 25 CTCATGATGCTTGTAGTG 42  
18 CTCATCATGCTGTGTG 1

RESULT 62  
US-09-448-312-162  
Sequence 162, Application US/09448312  
Patent No. 6867197  
GENERAL INFORMATION:  
APPLICANT: HERRNSTADT, CORINNA  
PARKER, WILLIAM D.  
DAVIS, ROBERT  
MILLER, SCOTT W.  
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
Animal Models for Diseases Associated with Mitochondrial  
Defects  
NUMBER OF SEQUENCES: 206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,312  
FILING DATE: 23-MAR-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,740  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
APPLICATION NUMBER: 08/413,740  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-448-312-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATCTCTCTGCTCCCA 123  
1 CTCCTACTCTGCTCGCA 18

Db

RESULT 63  
US-09-448-312-164  
Sequence 164, Application US/09448312  
Patent No. 6867197  
GENERAL INFORMATION:  
APPLICANT: HERRNSTADT, CORINNA  
PARKER, WILLIAM D.  
DAVIS, ROBERT  
MILLER, SCOTT W.  
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
Animal Models for Diseases Associated with Mitochondrial  
Defects  
NUMBER OF SEQUENCES: 206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,312  
FILING DATE: 23-MAR-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,740  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
APPLICATION NUMBER: 08/413,740  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 164:  
US-09-448-312-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATTCTCTGCTCCCA 123  
Db 1 CTCCTACTCTGCTCCGA 18

RESULT 64  
US-09-769-787-365/c  
Sequence 365, Application US/09769787  
Patent No. 6936252  
GENERAL INFORMATION:  
APPLICANT: Microbial Techniques Limited  
APPLICANT: Gilbert, Christophe FG  
APPLICANT: Hansbro, Philip M  
TITLE OF INVENTION: Proteins  
FILE REFERENCE: PWC/P21129WO  
CURRENT APPLICATION NUMBER: US/09/769,787  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: GB 9816337.1  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/125164  
PRIOR FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 365  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-769-787-365

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CATGGGGCAGATCCCTC 27  
Db 18 CATGTGGCGGATCCCGC 1

RESULT 65  
PCT-US95-04063-162  
Sequence 162, Application PC/TUS9504063  
GENERAL INFORMATION:  
APPLICANT: HERRNSTADT, CORINNA  
APPLICANT: PARKER, WILLIAM D.  
APPLICANT: DAVIS, ROBERT  
APPLICANT: MILLER, SCOTT W.  
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial  
TITLE OF INVENTION: Defects  
NUMBER OF SEQUENCES: 206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-04063-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATTCTCTGCTCCCA 123  
Db 1 CTCCTACTCTGCTCCGA 18

RESULT 66  
PCT-US95-04063-164  
Sequence 164, Application PC/TUS9504063  
GENERAL INFORMATION:  
APPLICANT: HERRNSTADT, CORINNA  
APPLICANT: PARKER, WILLIAM D.  
APPLICANT: DAVIS, ROBERT  
APPLICANT: MILLER, SCOTT W.  
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial  
TITLE OF INVENTION: Defects  
NUMBER OF SEQUENCES: 206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-0796  
TELEFAX: (202) 429-1776  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-04063-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 106 CTCATCTCTGCTGCCA 123  
Db 1 CTCCTACTCTGCTGCCA 18

## RESULT 67

US-08-311-760A-343  
; Sequence 343, Application US/08311760A  
; Patent No. 559706  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: McSwigen, James  
; APPLICANT: Newton, Roger S.  
; APPLICANT: Ramnarack, Randy  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF  
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY  
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN  
; NUMBER OF SEQUENCES: 392  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,760A  
; FILING DATE: September 23, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 343:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-311-760A-343

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 62.5%; Pred. No. 46;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 41 TGCCATCCCTTGCTG 56  
Db 1 UGCACAGCCCTUGGUG 16

RESULT 68  
US-08-311-760A-385  
; Sequence 385, Application US/08311760A  
; Patent No. 559706

GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: McSwigen, James  
; APPLICANT: Newton, Roger S.  
; APPLICANT: Ramnarack, Randy  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF  
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY  
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN  
; NUMBER OF SEQUENCES: 392  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,760A  
; FILING DATE: September 23, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 385:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-311-760A-385

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 62.5%; Pred. No. 46;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 41 TGCCATCCCTTGCTG 56  
Db 1 UGCACAGCCCTUGGUG 16

RESULT 69  
US-08-486-421-24/C  
; Sequence 24, Application US/08486421  
; Patent No. 5672479  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
CLASSIFICATION: 435  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-421-24

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

147 CCCTTCCTCTGCGC 162  
16 CCCTTCCTCTGCGC 1

## RESULT 70

US-08-470-911-24/C  
Sequence 24, Application US/08470911  
Patent No. 5756684

GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,911  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-470-911-24

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

147 CCCTTCCTCTGCGC 162  
16 CCCTTCCTCTGCGC 1

## RESULT 71

US-08-173-489C-168  
Sequence 168, Application US/08173489C  
Patent No. 5861244

GENERAL INFORMATION:  
APPLICANT: MANG, C. -G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44MB storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 168:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 bases  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: third strand derived from Hepatitis B  
DESCRIPTION: isolate ayy sequence region in Seq ID No. 5861244167  
HYPOHETICAL: yes  
ANTI-SENSE: no  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 168 :FROM 1 TO 16  
US-08-173-489C-168

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

144 TCCCTTCCTCTGCTT 159  
1 TCCCTTCCTCTGCTT 16



```
RESULT 72
US-08-486-809-24/C
; Sequence 24, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-486-809-24

Query Match          5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      147 CCCTTCTCTCTGCGC 162
Db      16 CCCTTCTCTCTGCC 1

RESULT 73
US-08-774-310-343
; Sequence 343, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lyon & Lyon
```

```
STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,760
; FILING DATE: September 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-310-343

Query Match          5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      41 TGCATCCCTTGCGTG 56
Db      1 UGCAGCCCTTGCGTG 16

RESULT 74
US-08-774-310-385
; Sequence 385, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/774,310  
FILING DATE: December 23, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/311,760  
FILING DATE: September 23, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 385:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-310-385

Query Match 5.4%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 62.5%; Pred. No. 46;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 41 TGGCCTCCCTGGTG 56  
: |||||:|:|:|:  
Db 1 UGCGAGCCCUUGUG 16

## RESULT 75

US-08-290-978A-9  
Sequence 9, Application US/08290978A  
Patent No. 5624834

## GENERAL INFORMATION:

APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.

APPLICANT: MULDER, YVONNE

APPLICANT: KESTER, HERMANUS C.M.

APPLICANT: VISSER, JACOB

APPLICANT: VAN COYEN, ALBERT J.J.

APPLICANT: ROLIN, CLAUDE

TITLE OF INVENTION: CLONING AND EXPRESSION OF THE

TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,978A

FILING DATE: 17-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 4615-0044.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: 90-4030

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: p9ax NcoI antisense  
US-08-290-978A-9

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 39 AGTGCCATCCCTGG 54  
: |||||:|:|:|:  
Db 1 AGTGCCATCCCATGG 16

RESULT 76  
US-08-373-124A-176  
Sequence 176, Application US/08373124A  
Patent No. 5646042

## GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

Query Match 5.4%; Score 12.8; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 43;  
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 144 TCCCTCTCTCTCT 159  
Db 2 UCCUCCUCCUCCUCCU 17

## RESULT 77

US-08-373-124A-182  
Sequence 182, Application US/08373124A  
Patent No. 5646042  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
TITLE OF INVENTION: CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 182:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-373-124A-182

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 43;  
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 144 TCCCTCTCTCTCT 159  
Db 1 UCCUCCUCCUCCUCCU 16

## RESULT 78

US-08-373-124A-184  
Sequence 184, Application US/08373124A  
Patent No. 5646042  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
TITLE OF INVENTION: CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 184:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-373-124A-184

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 43;  
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 106 CTCATCTCTCTCTCC 121  
Db 1 CUCCUCCUCCUCCUCC 16

RESULT 79  
US-08-435-628-176  
Sequence 176, Application US/08435628  
Patent No. 5817796  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

US-08-435-628-176

```
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/435,628
? FILING DATE: 05-MAY-1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/373,124
? FILING DATE: January 13, 1995
? APPLICATION NUMBER: 08/245,466
? FILING DATE: May 18, 1994
? APPLICATION NUMBER: 08/192,943
? FILING DATE: February 7, 1994
? APPLICATION NUMBER: 07/987,132
? FILING DATE: December 7, 1992
? APPLICATION NUMBER: 07/936,422
? FILING DATE: August 26, 1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard
? REGISTRATION NUMBER: 32,327
? REFERENCE/DOCKET NUMBER: 209/035
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 176:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-435-628-176
?
Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 144 TCCCCCTTCCTCTCT 159
Db 2 UCCUCCUCCUCCUCCU 17

RESULT 80
US-08-435-628-182
? Sequence 182, Application US/08435628
? Patent No. 5817796
? GENERAL INFORMATION:
? APPLICANT: Stinchcomb, Dan T.
? APPLICANT: Draper, Kenneth
? APPLICANT: McSwigen, James
? APPLICANT: Jarvis, Thale
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
```

```
? STREET: Suite 4700
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/435,628
? FILING DATE: 05-MAY-1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/373,124
? FILING DATE: January 13, 1995
? APPLICATION NUMBER: 08/245,466
? FILING DATE: May 18, 1994
? APPLICATION NUMBER: 08/192,943
? FILING DATE: February 7, 1994
? APPLICATION NUMBER: 07/987,132
? FILING DATE: December 7, 1992
? APPLICATION NUMBER: 07/936,422
? FILING DATE: August 26, 1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard
? REGISTRATION NUMBER: 32,327
? REFERENCE/DOCKET NUMBER: 209/035
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 182:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-435-628-182
?
Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 144 TCCCCCTTCCTCTCT 159
Db 1 UCCUCCUCCUCCUCCU 16

RESULT 81
US-08-435-628-184
? Sequence 184, Application US/08435628
? Patent No. 5817796
? GENERAL INFORMATION:
? APPLICANT: Stinchcomb, Dan T.
? APPLICANT: Draper, Kenneth
? APPLICANT: McSwigen, James
? APPLICANT: Jarvis, Thale
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
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; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,978
; FILING DATE: 17-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4615-0044.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: pgax NcoI antisense
US-08-780-869-9

Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      39 AGTGCATCCCTTTGG 54
        ||| | | | | | | | | | | | | | | |
DB       1 AGTGCAATCTTCATGG 16

RESULT 83
US-09-827-998-466/c
; Sequence 466, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOFF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acemica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 466
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-466

Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      145 CCCGCTTCTCCTCTG 160
        ||| | | | | | | | | | | | | | | |
DB       17 CCCCGCTTCTCTCAG 2

RESULT 84
US-09-827-998-467/c
; Sequence 467, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
```

```
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MPMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-467
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      145 CCCCTTCTCTCTG 160
Db      16  CCCCTTCTCTCAG 1
```

```
RESULT 85
US-09-866-108A-200/c
; Sequence 200, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 200
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-200
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      109 ATTCTCTGCTCCAC 124
Db      17  ATCTCTGCTCCAC 2
```

```
RESULT 86
US-09-866-108A-201/c
; Sequence 201, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-201
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      109 ATTCTCTGCTCCAC 124
Db      16  ATCTCTGCTCCAC 1
```

```
RESULT 87
US-09-866-108A-2940/c
; Sequence 2940, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
US-09-866-108A-2940
```

```
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
FILE REFERENCE: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2940
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-2940

Query Match      5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      55 TGATGAGTGCAC 70
Db      17 TGATGAGTGCAC 2

RESULT 88
US-09-866-108A-2941/c
Sequence 2941, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10395
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2941
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-2941

Query Match      5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      55 TGATGAGTGCAC 70
Db      16 TGATGAGTGCAC 1

RESULT 89
US-09-866-108A-10395
Sequence 10395, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10395
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
```

US-09-866-108A-10395

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 106 CTCATCTCTGCTCC 121  
Db 2 CTCATCTCTGCTCC 17

RESULT 90

US-09-866-108A-10396  
Sequence 10396, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:

APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AECOMICA-7  
CURRENT FILING DATE: 2001-05-25  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aeomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 10396  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-10396

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 106 CTCATCTCTGCTCC 121  
Db 1 CTCATCTCTGCTCC 16

RESULT 91

US-09-404-912-310  
Sequence 310, Application US/09404912  
Patent No. 6703228  
GENERAL INFORMATION:  
APPLICANT: John Landers  
APPLICANT: David Houseman

APPLICANT: Barbara Jordan  
APPLICANT: Alain Charest  
TITLE OF INVENTION: Methods and Products Related to  
FILE REFERENCE: M0656/7045(HCL/MAT)  
CURRENT FILING DATE: 1999-09-24  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: US 60/101,757  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: PCT/US99/22283  
PRIOR FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 691  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 310  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-404-912-310

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 209 CATGCTTCTTGTCTG 224  
Db 1 CATGCTTCTTGTCTG 16

RESULT 92

US-09-404-912-558  
Sequence 558, Application US/09404912  
Patent No. 6703228  
GENERAL INFORMATION:  
APPLICANT: John Landers  
APPLICANT: David Houseman  
APPLICANT: Barbara Jordan  
APPLICANT: Alain Charest  
TITLE OF INVENTION: Methods and Products Related to  
FILE REFERENCE: M0656/7045(HCL/MAT)  
CURRENT FILING DATE: 1999-09-24  
CURRENT APPLICATION NUMBER: US/09/404,912  
CURRENT FILING DATE: 1999-09-24  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: US 60/101,757  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: PCT/US99/22283  
PRIOR FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 691  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 558  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-404-912-558

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 159 TGCCATGATTTTAA 174  
Db 2 TGCCATGATTTTAA 17

RESULT 93

US-10-156-306B-3650/C  
Sequence 3650, Application US/10156306B  
Patent No. 7022828  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
FILE REFERENCE: MBH01-664-A (400/050)



CURRENT APPLICATION NUMBER: US/10/156,306B  
CURRENT FILING DATE: 2002-05-28  
NUMBER OF SEQ ID NOS: 8014  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3650  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-156-306B-3650

Query Match 5.4%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 142 GCTCCCTTCCTCCT 157  
Db 16 GCTCCGCTTCCTCCT 1

RESULT 94  
US-08-684-672-27/c  
Sequence 27, Application US/08684672  
Patent No. 5700926  
GENERAL INFORMATION:  
APPLICANT: KERE, Juha  
APPLICANT: SCHLESSINGER, David  
APPLICANT: de la CHAPELLE, Albert  
APPLICANT: SRIVASTAVA, Anand Kumar  
TITLE OF INVENTION: MOLECULAR CLONING OF THE ANHIDROTIC  
TITLE OF INVENTION: ECTODERMAL DYSPLASIA GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 2213-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,672  
FILING DATE: 22-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052,997  
FILING DATE: 27-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Shaughnessy, Brian P.  
REGISTRATION NUMBER: 32,747  
REFERENCE/DOCKET NUMBER: 030956-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-684-672-27

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 93 AGCTGGCCCTCTCTC 108  
Db 18 AGCTGGCTCTCTCGC 3

RESULT 95  
US-08-811-028-26/c  
Sequence 26, Application US/08811028C  
Patent No. 5891671  
GENERAL INFORMATION:  
APPLICANT: SUZUKI, Yuji  
APPLICANT: MASUDA, Koji  
APPLICANT: MASUDA, Toyofumi  
TITLE OF INVENTION: METHOD FOR CLEAVING CHIMERIC ENZYME USING PROCESSING  
TITLE OF INVENTION: ENZYME  
FILE REFERENCE: 001560-294  
CURRENT APPLICATION NUMBER: US/08/811,028C  
CURRENT FILING DATE: 1987-03-04  
EARLIER APPLICATION NUMBER: JP 8-70906  
EARLIER FILING DATE: 1996-03-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer S12  
US-08-811-028-26

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 208 CCAGCTCTCTCTCT 223  
Db 17 CCAGCTCTCTCTCT 2

RESULT 96  
US-09-161-244-51  
Sequence 51, Application US/09161244  
Patent No. 6004814  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Cowseart, Lex M.  
TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION  
FILE REFERENCE: RTS-0007  
CURRENT APPLICATION NUMBER: US/09/161,244  
CURRENT FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 91  
SEQ ID NO 51  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-161-244-51

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 19 AGATCCCTCATGATG 34  
Db 1 AGATCCCTCACAATG 16

RESULT 97  
US-09-091-219-19  
Sequence 19, Application US/09091219  
Patent No. 6171592  
GENERAL INFORMATION:  
APPLICANT: STUDEBERT, Michael J.  
APPLICANT: CRAB, Brendan S.  
APPLICANT: FENG, Li

TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS  
FILE REFERENCE: 040268/0151  
CURRENT APPLICATION NUMBER: US/09/091,219  
CURRENT FILING DATE: 1998-10-05  
EARLIER APPLICATION NUMBER: PCT/AU96/00815  
EARLIER FILING DATE: 1996-12-18  
EARLIER APPLICATION NUMBER: AU PN7201  
EARLIER FILING DATE: 1995-12-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: equine rhinovirus 1  
US-09-091-219-19

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 131 ATGAGACCTGCTCC 146  
DB 3 AAGAGACCTGCTTC 18

RESULT 98  
US-09-071-433-67/c  
Sequence 67, Application US/09071433A  
Patent No. 6197584  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Cowsett, Lex M  
TITLE OF INVENTION: Antisense Modulation of CD40 Expression  
FILE REFERENCE: RTS-0002  
CURRENT APPLICATION NUMBER: US/09/071,433A  
CURRENT FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 67  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-071-433-67

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 44 CATCCCTTGCTGATG 59  
DB 18 CATCCTTGCTGCTG 3

RESULT 99  
US-09-920-760-61  
Sequence 61, Application US/09920760  
Patent No. 6492173  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION  
FILE REFERENCE: RTS-0275  
CURRENT APPLICATION NUMBER: US/09/920,760  
CURRENT FILING DATE: 2001-08-01  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 61  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-920-760-61

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 115 CTGCTCCACTCTTGC 130  
DB 3 CTGCTCCACTCTTC 18

RESULT 100  
US-09-660-541-19  
Sequence 19, Application US/09660541  
Patent No. 6531136  
GENERAL INFORMATION:  
APPLICANT: STUDEBERT, Michael J.  
APPLICANT: CRABB, Brendan S.  
APPLICANT: FENG, Li  
TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS  
FILE REFERENCE: 040268/0151  
CURRENT APPLICATION NUMBER: US/09/660,541  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/091,219  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN7201  
PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: equine rhinovirus 1  
US-09-660-541-19

Query Match 5.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 41;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 131 ATGAGACCTGCTCC 146  
DB 3 AAGAGACCTGCTTC 18

Search completed: October 2, 2006, 15:37:36  
Job time : 0.001 secs



```
XX AC AAV33949;
XX DT 15-FEB-1999 (first entry)
XX DE Gibbon interleukin-3 forward primer.
XX KM Fanconi anaemia complementation group C; FAC; apoptosis; haematopoiesis;
XX bone marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
XX Hls-ILFAC; PCR; primer; ss.
XX OS Synthetic.
XX OS Hylobates lar.
XX PN WO9851792-A1.
XX PD 19-NOV-1998.
XX PF 15-MAY-1998; 98WO-US009975.
XX PR 15-MAY-1997; 97US-0046546P.
XX PS (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX PI Youseoufian H;
XX DR WPI; 1999-009774/01.
XX PT New conjugate of Fanconi anaemia molecule and peptide selective for
XX haematopoietic precursor cells - inhibits apoptosis of these cells, for
XX treating Fanconi anaemia and patients undergoing high-dose chemotherapy
XX for cancer.
XX PS Example 1; Page 27; 72pp; English.
XX CC This is the nucleotide sequence of a forward primer for the PCR
XX amplification of gibbon interleukin-3 cDNA (see AAV33946) minus the
XX signal sequence. It includes a 5' BamHI site. The primer was used with a
XX reverse primer (see AAV33950) to amplify the gibbon IL3 mature coding
XX region. The PCR product was utilised in the construction of a prokaryotic
XX expression plasmid encoding a fusion between human Fanconi anaemia
XX complementation group C (FAC) protein (see AAW68546) and gibbon IL3 (see
XX AAW68547). This conjugate, or a nucleic acid encoding it, can be used to
XX deliver FAC to a haematopoietic progenitor cell, specifically to inhibit
XX apoptosis, particularly in patients exposed to high doses of chemotherapy
XX for treatment of non-myeloid cancers, also to treat Fanconi anaemia by
XX complementation of the genetic defect
XX CC
XX SQ Sequence 27 BP; 7 A; 11 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 9.2%; Score 21.8; DB 1; Length 27;
XX Best Local Similarity 92.0%; Pred. No. 6.9;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TGTCGGGTCATGGGGGCGAGATCCC 25
Db 26 TGTCGGGTCATGGAGCGAGATCCC 2
RESULT 2
ACLA1022
XX ID ACL41022 standard; RNA; 21 BP.
XX AC ACL41022;
XX OS 24-MAR-2005 (first entry)
XX DE C20orf103 siRNA antisense sequence, SEQ ID 2094.
XX KM Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX OS Synthetic.
```

```
XX PN WO2005001092-A2.
XX PD 06-JAN-2005.
XX PF 19-MAY-2004; 2004WO-US015645.
XX PR 20-MAY-2003; 2003US-0471729P.
XX PS (AMHP ) WYETH.
XX PI Be X, Wei L, Slonim DK, Howes SH;
XX DR WPI; 2005-075568/08.
XX PT Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX PS Claim 3; SEQ ID NO 2094; 113pp; English.
XX CC The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FL11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 21 BP; 2 A; 4 C; 3 G; 0 T; 12 U; 0 Other;
XX
XX Query Match 7.5%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 38.1%; Pred. No. 21;
XX Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
QY 150 TTCTCCTTCGCGCATGATTT 170
Db 1 UUCUUGUUCUGCAUGAUUUU 21
RESULT 3
ACLA0867/c
XX ID ACL40867 standard; DNA; 21 BP.
XX AC ACL40867;
XX OS 24-MAR-2005 (first entry)
XX DE C20orf103 target oligonucleotide, SEQ ID 1939.
XX KM Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX Homo sapiens.
XX PN WO2005001092-A2.
XX OS 06-JAN-2005.
XX PD 19-MAY-2004; 2004WO-US015645.
XX PF 20-MAY-2003; 2003US-0471729P.
XX PR (AMHP ) WYETH.
```

```
XX Be X, Wei L, Slonim DK, Howes SH;
PI WPI: 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX Claim 3, SEQ ID NO 1939, 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC target oligonucleotide from one such CRTP for which short interfering
CC RNA (siRNA) were produced. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
```

```
Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 149 CTTCTCTTCTGCCATGATT 169
DB 21 CTTCTTGTCTGCCATGATT 1
```

```
RESULT 4
ACLA0869
ID ACLA0869 standard; RNA; 21 BP.
XX
XX ACU40869;
AC
XX 24-MAR-2005 (first entry)
DT
XX C20orf103 siRNA antisense sequence, SEQ ID 1941.
DE
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
OS
XX WO2005001092-A2.
PN
XX 06-JAN-2005.
PD
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
PA
XX Be X, Wei L, Slonim DK, Howes SH;
PI WPI: 2005-075568/08.
DR
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT
```

```
PT treating cancer.
XX
XX Claim 3, SEQ ID NO 1941, 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 2 A; 5 C; 3 G; 0 T; 11 U; 0 Other;
SQ
```

```
Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 42.9%; Pred. No. 21;
Matches 9; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
OY 149 CTTCTCTTCTGCCATGATT 169
DB 1 CUUCUGUGUGCCAUCAUUV 21
```

```
RESULT 5
AEC02687
ID AEC02687 standard; DNA; 21 BP.
XX
XX AEC02687;
AC
XX 03-NOV-2005 (first entry)
DT
XX Human IGE short interfering nucleic acid SEQ ID NO 230.
DE
XX
XX antiallergic; antiinflammatory; antiasthmatic; dermatological;
XX immunosuppressive; expression; RNA interference; allergy;
XX atopic dermatitis; urticaria; dermatological disease;
XX immediate type hypersensitivity; immunosuppressive; asthma;
XX antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;
XX ear, nose, throat disease; inflammation; respiratory disease;
XX immune disorder; IGE; short interfering nucleic acid; siNA;
XX gene silencing; ss.
XX
XX Homo sapiens.
OS
XX WO2005080410-A1.
PN
XX 01-SEP-2005.
PD
XX 21-FEB-2005; 2005WO-NZ000021.
XX
XX 20-FEB-2004; 2004US-0546434P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Watson JD, Murison GJ, Grigor MR, Havukkala JU, Munro G;
PI Abernethy N, Webster G;
XX
XX WPI: 2005-591970/60.
DR
XX
XX New composition comprises small interfering nucleic acid molecule (siNA)
PT capable of reducing expression of a target gene that is active in a IGE-
PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
PT dermatitis.
XX
```

PS Disclosure; SEQ ID NO 290; 178bp; English.  
XX  
CC The invention describes a composition comprising a small interfering  
CC nucleic acid molecule (siNA) capable of reducing expression of a target  
CC gene that is active in a IGE-mediated disorder, a genetic construct that  
CC expresses the siNA, and a binding agent that specifically binds to a  
CC target antigen expressed on the surface of the cell. Also described are:  
CC a method for the treatment of an IGE-mediated disorder in a patient;  
CC prevention of IGE-mediated disorder in a patient; reduction of  
CC eosinophilia in a patient; modulating an IGE-mediated immune response to  
CC a specific antigen in a patient; and preventing or reducing the severity  
CC of an immune response to a specific antigen in a patient. The composition  
CC is useful in the preparation of a medicament useful for the treatment of  
CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,  
CC urticaria, atopic dermatitis, food allergies, diseases that benefit from  
CC the reduction of eosinophilia in the tissues of the respiratory system,  
CC or disorders having hypersensitivity immune reaction. This sequence  
CC represents a siNA for supression of human IGE expression.  
XX  
SQ Sequence 21 BP; 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 7.5%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 60 AGTGAATTACAGTGAAGCTG 80  
Db 1 AATGAGTTACATGAGACTG 21  
RESULT 6  
AAH37262/c  
ID AAH37262 standard; DNA; 19 BP.  
AC AAH37262;  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific lower PCR primer SEQ ID 58.  
XX  
KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KM SNEP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KM Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
PS Claim 1; Page 50; 83bp; English.  
XX  
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNEP) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the

CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC diseases of which a component is or may be genetic such as autoimmune  
CC diseases, including rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 19 BP; 6 A; 2 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 7.4%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 147 CCCTTCCTTCGCGCATG 165  
Db 19 CCCTTCCTTCGCGCATG 1  
RESULT 7  
AEC36449  
ID AEC36449 standard; RNA; 19 BP.  
AC AEC36449;  
DT 03-NOV-2005 (first entry)  
XX  
DE VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #3.  
XX  
KM short interfering nucleic acid; siNA; short interfering RNA; siRNA;  
KM gene silencing; RNA interference; transplant rejection;  
KM pulmonary disease; respiratory-gen.; respiratory disease; injury;  
KM vulnerrary; neurodegenerative disease; neuroprotective;  
KM neurological disease; cancer; neoplasia; cytotoxic; infection;  
KM antimicrobial; ocular disease; ophthalmological; cardiovascular disease;  
KM cardiovascular-gen.; prion disease; cerebroprotective; degeneration;  
KM inflammation; antiinflammatory; renal disease; nephrotropic;  
KM endocrine disease; genitourinary disease; liver disease; hepatotropic;  
KM gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;  
KM VEGF.  
XX  
XX Unidentified.  
XX  
OS  
XX  
PN WO2005078097-A2.  
XX  
PD 25-AUG-2005.  
XX  
PF 09-FEB-2005; 2005WO-US004270.  
XX  
PR 10-FEB-2004; 2004US-0543480P.  
XX  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Jadhav V, Zinnen S;  
XX  
XX  
DR WPI; 2005-571603/58.  
XX  
PT New multifunctional short interfering nucleic acid (siNA), useful for  
PT modulating RNA function and/or gene expression in a cell or for treating  
PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,

PT or ocular diseases.  
 XX  
 PS Example 7; SEQ ID NO 114; 168pp; English.  
 CC The specification describes a multifunctional short interfering nucleic  
 XX acid (siNA). This multifunctional siNA molecule is of two formulae given  
 CC in the specification. The multifunctional siNA of the invention is useful  
 CC for modulating RNA function and/or gene expression in a cell. It can be  
 CC used for down regulating or inhibiting the expression of one or more  
 CC target nucleic acid molecules. It is also useful for treating diseases or  
 CC conditions that responds to modulation of gene expression or actively in  
 CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue  
 CC grafting, or treatment of pulmonary disease (restenosis) or preventing  
 CC neointimal hyperplasia and atherosclerosis in grafts. It can further be  
 CC used for treating CNS lesions or injury, including treating  
 CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's  
 CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral  
 CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular  
 CC diseases, prion disease, inflammatory diseases, renal diseases, liver  
 CC diseases, mitochondrial diseases, endocrine diseases, or reproduction  
 CC related diseases and conditions. AEC36400-AEC36404 represent target  
 CC sequences from VEGF, for a multifunctional siNA of the invention which  
 CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary  
 CC sequences to the target sequences.  
 CC  
 SQ Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;  
 Query Match 7.4%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 24;  
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 Oy 147 CCCTTCCTCTGCGCATG 165  
 Db 1 CCCUCCUCCUCCGCAUG 19  
 RESULT 8  
 AEC36402/C  
 ID AEC36402 standard; RNA, 19 BP.  
 AC AEC36402;  
 XX  
 XX 03-NOV-2005 (first entry)  
 DE VEGF/VEGFR2 multifunctional siNA VEGF target sequence #3.  
 XX  
 XX Short interfering nucleic acid; siNA; short interfering RNA; siRNA;  
 KW gene silencing; RNA interference; transplant rejection;  
 KW pulmonary disease; respiratory-gen.; respiratory disease; injury;  
 KW vulnary; neurodegenerative disease; neuroprotective;  
 KW neurological disease; cancer; neoplasm; cytostatic; infection;  
 KW antimicrobial; ocular disease; ophthalmological; cardiovascular disease;  
 KW cardiovacular-gen.; prion disease; cerebroprotective; degeneration;  
 KW inflammation; antiinflammatory; renal disease; nephrotoxic;  
 KW endocrine disease; genitourinary disease; liver disease; hepatocytic;  
 KW gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;  
 KW VEGF.  
 KM  
 XX  
 XX Unidentified.  
 OS  
 XX  
 PN WO2005078097-A2.  
 XX  
 PD 25-AUG-2005.  
 XX  
 XX 09-FEB-2005; 2005WO-US004270.  
 PF  
 XX 10-FEB-2004; 2004US-0543480P.  
 PR 24-MAY-2004; 2004WO-US016390.  
 PR  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX Jadhav V, Zinnen S;  
 PI  
 XX

DR WPI; 2005-571603/58.  
 XX  
 XX New multifunctional short interfering nucleic acid (siNA), useful for  
 PT modulating RNA function and/or gene expression in a cell or for treating  
 PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,  
 PT or ocular diseases.  
 PS Example 7; SEQ ID NO 56; 168pp; English.  
 XX  
 CC The specification describes a multifunctional short interfering nucleic  
 CC acid (siNA). This multifunctional siNA molecule is of two formulae given  
 CC in the specification. The multifunctional siNA of the invention is useful  
 CC for modulating RNA function and/or gene expression in a cell. It can be  
 CC used for down regulating or inhibiting the expression of one or more  
 CC target nucleic acid molecules. It is also useful for treating diseases or  
 CC conditions that responds to modulation of gene expression or actively in  
 CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue  
 CC grafting, or treatment of pulmonary disease (restenosis) or preventing  
 CC neointimal hyperplasia and atherosclerosis in grafts. It can further be  
 CC used for treating CNS lesions or injury, including treating  
 CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's  
 CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral  
 CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular  
 CC diseases, prion disease, inflammatory diseases, renal diseases, liver  
 CC diseases, mitochondrial diseases, endocrine diseases, or reproduction  
 CC related diseases and conditions. AEC36400-AEC36404 represent target  
 CC sequences from VEGF, for a multifunctional siNA of the invention which  
 CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary  
 CC sequences to the target sequences.  
 CC  
 SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;  
 Query Match 7.4%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 147 CCCTTCCTCTGCGCATG 165  
 Db 19 CCCTTCCTCTCTGCGCATG 1  
 RESULT 9  
 AED05616/C  
 ID AED05616 standard; RNA, 23 BP.  
 AC AED05616;  
 XX  
 XX 01-DEC-2005 (first entry)  
 DE Short interfering sense sequence targeting human VEGF 121, seqid 81.  
 XX  
 XX vascular endothelial growth factor; RNA interference; gene silencing;  
 KW macular degeneration; ophthalmological; ocular disease;  
 KW diabetic retinopathy; antiangiogenic; cardiovascular disease; cancer;  
 KW cytosstatic; neoplasm; asthma; antiasthmatic; immune disorder;  
 KW inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;  
 KW ss; short interfering RNA; siRNA.  
 KM  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO2005089224-A2.  
 XX  
 PD 29-SEP-2005.  
 XX  
 XX 11-MAR-2005; 2005WO-US008182.  
 PF  
 XX 12-MAR-2004; 2004US-0552620P.  
 PR 05-APR-2004; 2004US-0559824P.  
 PR 25-JAN-2005; 2005US-0647191P.  
 PR  
 XX (ALNY-) ALNYLAM PHARM INC.  
 PA  
 XX De Fougerolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;  
 PI  
 XX

PI Hadwiger P;  
XX WPI; 2005-658984/67.  
XX  
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense  
PT sequence and an antisense sequence, useful for treating a human diagnosed  
PT as having or at risk for having adult macular degeneration.  
XX  
PS Claim 1; SEQ ID NO 81; 200pp; English.  
XX  
XX The present invention relates to the use of siRNA targeting vascular  
CC endothelial growth factor (VEGF). Specifically claimed is an isolated  
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and  
CC an antisense sequence, where the sense and the antisense sequences form  
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF  
CC RNA in a cell, using the iRNA agent, making an iRNA agent by the  
CC synthesis of the iRNA agent, where the sense and antisense strands  
CC comprise at least one modification that stabilizes the iRNA agent against  
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA  
CC agent; inhibiting VEGF expression; and treating a human diagnosed with  
CC adult macular degeneration (AMD), by administering a therapeutically  
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense  
CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ  
CC ID NO: 2-401, not defined in the specification. The iRNA agent further  
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one  
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent  
CC further comprises a phosphorothioate at the first internucleotide linkage  
CC at the 5' or 3' end of the antisense and sense sequences. The agent  
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for  
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma  
CC and angiogenic disorders. The present sequence is short interfering sense  
CC sequence targeting human VEGF 121.  
XX  
SQ Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;  
Query Match 7.4%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 147 CCCTTCCTTCCTTCGCATG 165  
DB 23 CCCTTCCTTCCTTCGCATG 5  
RESULT 10  
AED05619/c  
ID AED05619 standard; RNA; 23 BP.  
XX  
AC AED05619;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE Short interfering sense sequence targeting human VEGF 121, seqid 84.  
XX  
XX vascular endothelial growth factor; RNA interference; gene silencing;  
KM macular degeneration; ophthalmological; ocular disease;  
KM diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;  
KM cytosarctic; neoplasm; asthma; antiasthmatic; immune disorder;  
KM inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;  
KM ss; short interfering RNA; siRNA.  
XX  
OS Homo sapiens.  
XX  
PN WO2005089224-A2.  
XX  
PD 29-SEP-2005.  
XX  
PF 11-MAR-2005; 2005WO-US008182.  
XX  
PR 12-MAR-2004; 2004US-0552620P.  
PR 05-APR-2004; 2004US-0559824P.  
PR 25-JAN-2005; 2005US-0647191P.  
XX

PA (ALANY-) ALANYLAM PHARM INC.  
XX  
XX De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;  
PI Hadwiger P;  
XX WPI; 2005-658984/67.  
XX  
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense  
PT sequence and an antisense sequence, useful for treating a human diagnosed  
PT as having or at risk for having adult macular degeneration.  
XX  
PS Claim 1; SEQ ID NO 84; 200pp; English.  
XX  
XX The present invention relates to the use of siRNA targeting vascular  
CC endothelial growth factor (VEGF). Specifically claimed is an isolated  
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and  
CC an antisense sequence, where the sense and the antisense sequences form  
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF  
CC RNA in a cell, using the iRNA agent, making an iRNA agent by the  
CC synthesis of the iRNA agent, where the sense and antisense strands  
CC comprise at least one modification that stabilizes the iRNA agent against  
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA  
CC agent; inhibiting VEGF expression; and treating a human diagnosed with  
CC adult macular degeneration (AMD), by administering a therapeutically  
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense  
CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ  
CC ID NO: 2-401, not defined in the specification. The iRNA agent further  
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one  
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent  
CC further comprises a phosphorothioate at the first internucleotide linkage  
CC at the 5' or 3' end of the antisense and sense sequences. The agent  
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for  
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma  
CC and angiogenic disorders. The present sequence is short interfering sense  
CC sequence targeting human VEGF 121.  
XX  
SQ Sequence 23 BP; 7 A; 4 C; 11 G; 0 T; 1 U; 0 Other;  
Query Match 7.4%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 147 CCCTTCCTTCCTTCGCATG 165  
DB 20 CCCTTCCTTCCTTCGCATG 2  
RESULT 11  
AED05618/c  
ID AED05618 standard; RNA; 23 BP.  
XX  
AC AED05618;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE Short interfering sense sequence targeting human VEGF 121, seqid 83.  
XX  
XX vascular endothelial growth factor; RNA interference; gene silencing;  
KM macular degeneration; ophthalmological; ocular disease;  
KM diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;  
KM cytosarctic; neoplasm; asthma; antiasthmatic; immune disorder;  
KM inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;  
KM ss; short interfering RNA; siRNA.  
XX  
OS Homo sapiens.  
XX  
PN WO2005089224-A2.  
XX  
PD 29-SEP-2005.  
XX  
PF 11-MAR-2005; 2005WO-US008182.  
PR 12-MAR-2004; 2004US-0552620P.  
PR



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PR 05-APR-2004; 2004US-0559824P.
PR 25-JAN-2005; 2005US-0647191P.
XX
XX (ALNY-) ALNYLAM PHARM INC.
PA
PI De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI Hadwiger P;
XX WPI; 2005-658984/67.
XX
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
XX sequence and an antisense sequence, useful for treating a human diagnosed
XX as having or at risk for having adult macular degeneration.
XX
XX Claim 1; SEQ ID NO 83; 200pp; English.
XX
XX The present invention relates to the use of siRNA targeting vascular
XX endothelial growth factor (VEGF). Specifically claimed is an isolated
XX interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
XX an antisense sequence, where the sense and the antisense sequences form
XX an RNA duplex. Also claimed are methods of reducing the amount of VEGF
XX RNA in a cell, using the iRNA agent; making an iRNA agent by the
XX synthesis of the iRNA agent, where the sense and antisense strands
XX comprise at least one modification that stabilizes the iRNA agent against
XX nucleolytic degradation; a pharmaceutical composition comprising the iRNA
XX agent; inhibiting VEGF expression; and treating a human diagnosed with
XX adult macular degeneration (AMD), by administering a therapeutically
XX effective amount of the iRNA agent. The isolated iRNA agent has the sense
XX sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
XX ID NO: 2-401, not defined in the specification. The iRNA agent further
XX comprises a non-nucleotide moiety. The iRNA agent further comprises one
XX or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
XX further comprises a phosphorochiolate at the first internucleotide linkage
XX at the 5' or 3' end of the antisense and sense sequences. The agent
XX further comprises a 2'-modified nucleotide. The iRNA agent is useful for
XX treating adult macular degeneration, diabetic retinopathy, cancer, asthma
XX and angiogenic disorders. The present sequence is short interfering sense
XX sequence targeting human VEGF 121.
XX
XX Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
SQ
Query Match 7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 147 CCCTTCCTCTTCGCATG 165
21 CCCTCCTCTCTTCGCATG 3
Db
RESULT 12
AED05620/c
ID AED05620 standard; RNA; 23 BP.
XX
XX AED05620;
AC
XX 01-DEC-2005 (first entry)
DT
XX
XX Short interfering sense sequence targeting human VEGF 121, seqid 85.
XX
XX vascular endothelial growth factor; RNA interference; gene silencing;
XX macular degeneration; ophthalmological; ocular disease;
XX diabetic retinopathy; antiangiogenic; cardiovascular disease; cancer;
XX cytoskeletal; neoplasm; asthma; antiasthmatic; immune disorder;
XX inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
XX ss; short interfering RNA; siRNA.
XX
XX Homo sapiens.
XX
XX WO2005089224-A2.
XX
XX 29-SEP-2005.
XX

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PF 11-MAR-2005; 2005WO-US008182.
XX
XX 12-MAR-2004; 2004US-0552620P.
PR 05-APR-2004; 2004US-0559824P.
PR 25-JAN-2005; 2005US-0647191P.
XX
XX (ALNY-) ALNYLAM PHARM INC.
PA
PI De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI Hadwiger P;
XX WPI; 2005-658984/67.
XX
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
XX sequence and an antisense sequence, useful for treating a human diagnosed
XX as having or at risk for having adult macular degeneration.
XX
XX Claim 1; SEQ ID NO 85; 200pp; English.
XX
XX The present invention relates to the use of siRNA targeting vascular
XX endothelial growth factor (VEGF). Specifically claimed is an isolated
XX interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
XX an antisense sequence, where the sense and the antisense sequences form
XX an RNA duplex. Also claimed are methods of reducing the amount of VEGF
XX RNA in a cell, using the iRNA agent; making an iRNA agent by the
XX synthesis of the iRNA agent, where the sense and antisense strands
XX comprise at least one modification that stabilizes the iRNA agent against
XX nucleolytic degradation; a pharmaceutical composition comprising the iRNA
XX agent; inhibiting VEGF expression; and treating a human diagnosed with
XX adult macular degeneration (AMD), by administering a therapeutically
XX effective amount of the iRNA agent. The isolated iRNA agent has the sense
XX sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
XX ID NO: 2-401, not defined in the specification. The iRNA agent further
XX comprises a non-nucleotide moiety. The iRNA agent further comprises one
XX or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
XX further comprises a phosphorochiolate at the first internucleotide linkage
XX at the 5' or 3' end of the antisense and sense sequences. The agent
XX further comprises a 2'-modified nucleotide. The iRNA agent is useful for
XX treating adult macular degeneration, diabetic retinopathy, cancer, asthma
XX and angiogenic disorders. The present sequence is short interfering sense
XX sequence targeting human VEGF 121.
XX
XX Sequence 23 BP; 8 A; 3 C; 11 G; 0 T; 1 U; 0 Other;
SQ
Query Match 7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 147 CCCTTCCTCTTCGCATG 165
19 CCCTCCTCTCTTCGCATG 1
Db
RESULT 13
AED05617/c
ID AED05617 standard; RNA; 23 BP.
XX
XX AED05617;
AC
XX 01-DEC-2005 (first entry)
DT
XX
XX Short interfering sense sequence targeting human VEGF 121, seqid 82.
XX
XX vascular endothelial growth factor; RNA interference; gene silencing;
XX macular degeneration; ophthalmological; ocular disease;
XX diabetic retinopathy; antiangiogenic; cardiovascular disease; cancer;
XX cytoskeletal; neoplasm; asthma; antiasthmatic; immune disorder;
XX inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
XX ss; short interfering RNA; siRNA.
XX
XX Homo sapiens.
XX
XX WO2005089224-A2.
XX
XX
XX

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XX 29-SEP-2005.  
 PD  
 XX  
 PF 11-MAR-2005; 2005MO-US008182.  
 XX  
 XX 12-MAR-2004; 2004US-0552620P.  
 PR 05-APR-2004; 2004US-0559824P.  
 PR 25-JAN-2005; 2005US-0647191P.  
 XX  
 PA (ALNY-) ALNYLAM PHARM INC.  
 XX  
 PI De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;  
 PI Hadwiger P;  
 XX  
 DR WPI; 2005-658984/67.  
 XX  
 PT New isolated interfering ribonucleic acid (iRNA) agent comprising a sense  
 PT sequence and an antisense sequence, useful for treating a human diagnosed  
 PT as having or at risk for having adult macular degeneration.  
 XX  
 PS Claim 1; SEQ ID NO 82; 200pp; English.  
 XX  
 CC The present invention relates to the use of siRNA targeting vascular  
 CC endothelial growth factor (VEGF). Specifically claimed is an isolated  
 CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and  
 CC an antisense sequence, where the sense and the antisense sequences form  
 CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF  
 CC RNA in a cell, using the iRNA agent; making an iRNA agent by the  
 CC synthesis of the iRNA agent, where the sense and antisense strands  
 CC comprise at least one modification that stabilizes the iRNA agent against  
 CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA  
 CC agent; inhibiting VEGF expression; and treating a human diagnosed with  
 CC adult macular degeneration (AMD), by administering a therapeutically  
 CC effective amount of the iRNA agent. The isolated iRNA agent has the sense  
 CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ  
 CC ID NO: 2-401, not defined in the specification. The iRNA agent further  
 CC comprises a non-nucleotide moiety. The iRNA agent further comprises one  
 CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent  
 CC further comprises a phosphorothioate at the first internucleotide linkage  
 CC at the 5' or 3' end of the antisense and sense sequences. The agent  
 CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for  
 CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma  
 CC and angiogenic disorders. The present sequence is short interfering sense  
 CC sequence targeting human VEGF 121.  
 CC  
 XX  
 SQ Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;  
 Query Match 7.4%; Score 17.4; DB 1; Length 23;  
 Best Local Similarity 94.7%; Pred. No. 22;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 147 CCCTTCCTTCGCGCATG 165  
 DB 22 CCCTCTCTCTTCGCGCATG 4  
 RESULT 14  
 ABZ22095  
 ID ABZ22095 standard; DNA, 24 BP.  
 XX  
 AC ABZ22095;  
 XX  
 DT 11-MAR-2003 (first entry)  
 XX  
 DE Polyanionic polymer related oligonucleotide #49.  
 XX  
 KM Polyanionic polymer; bioactivity; water solubility; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W0200277036-A2.  
 XX  
 PD 03-OCT-2002.

XX 21-MAR-2002; 2002MO-US008614.  
 XX  
 XX 21-MAR-2001; 2001US-0277705P.  
 PR  
 XX  
 PA (LEUNG) LEUNG D W.  
 XX  
 PI Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;  
 PI Maggoner DW;  
 XX  
 DR WPI; 2003-058367/05.  
 XX  
 XX  
 PT Producing monodispersed preparation of polyanionic polymer for therapy,  
 PT by expressing vector comprising ligation product of oligonucleotides  
 PT encoding glutamate/aspartate residues in host cell and isolating the  
 PT product.  
 XX  
 PS Disclosure; Fig 5; 74pp; English.  
 XX  
 CC The present invention describes a method (M) for producing a  
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10  
 CC kD. (M) involves inserting into an expression vector (EV) a ligation  
 CC product formed by ligating together oligonucleotides that encode  
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating  
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is  
 CC approximately of the same molecular weight. Also described: (1) a  
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and  
 CC another polypeptide at either one end or at both ends of it; (2) a  
 CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and  
 CC leukine, where the polyanionic polymer is polyglutamic acid or  
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which  
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at  
 CC least one other nucleotide sequence, where the polyanionic polymer is  
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell  
 CC (IV) comprising (III) or a vector that comprises a nucleotide sequence  
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a  
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular  
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)  
 CC is useful for treating a disease or ailment in an individual by  
 CC administering (I) to the individual. (I) is also useful for delivering an  
 CC effective amount of a pharmaceutically active agent, a therapeutic  
 CC protein or a drug to a patient in need of it, or for diagnostic and  
 CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to  
 CC ABP56400 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 XX  
 SQ Sequence 24 BP; 0 A; 13 C; 0 G; 11 T; 0 U; 0 Other;  
 Query Match 7.3%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 23;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 140 CTGCTCCCTTCCTTCCTTCG 161  
 DB 1 CTCTCTCTCTCTTCCTTCCTTC 22  
 RESULT 15  
 ADO51553  
 ID ADO51553 standard; DNA, 20 BP.  
 XX  
 AC ADO51553;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human serine/threonine kinase 16 antisense oligo. ISIS 220645.  
 XX  
 KM Serine/threonine kinase 16; PKL12;  
 KM transforming growth factor-beta-stimulated factor 1; TSP1;  
 KM myristylated and palmitylated serine/threonine kinase; MPK;  
 KM hyperproliferative disorder; gene therapy; human; antisense;  
 KM phosphothioate backbone; ss.  
 XX

OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
FT Key  
FT modified\_base  
FT 1..20  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone in which all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base  
FT 1..5  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) bases"  
FT modified\_base  
FT 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) bases"  
XX  
XX US2004097444-A1.  
XX  
XX 20-MAY-2004.  
XX  
XX 16-NOV-2002; 2002US-00298953.  
XX  
XX 16-NOV-2002; 2002US-00298953.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Dobie KM;  
XX  
XX WPI; 2004-389186/36.  
XX  
XX  
XX New compounds, particularly oligonucleotides targeted to a nucleic acid  
XX encoding serine/threonine kinase 16, useful for treating diseases  
XX associated with serine/threonine kinase 16, e.g. hyperproliferative  
XX disorders.  
XX  
XX Example 15; SEQ ID NO 44; 36pp; English.  
XX  
XX The invention relates to compounds, compositions and methods for  
XX modulating the expression of serine/threonine kinase 16 (also called  
XX PK12, transforming growth factor-beta-stimulated factor 1; TSP1 and  
XX myristylated and palmitylated serine/threonine kinase; MSPX). The  
XX composition comprise antisense oligonucleotides targeted to PK12 gene.  
XX The compound, composition and methods are useful for treating a disease  
XX or condition associated with serine/threonine kinase 16, such as a  
XX hyperproliferative disorder. They are also useful in research and  
XX diagnostics for modulating the expression of serine/threonine kinase 16.  
XX The invention is also useful in gene therapy. The present sequence is an  
XX antisense oligonucleotide targeted to human serine/threonine kinase 16  
XX DNA. This sequence is used to illustrate the method of the invention.  
XX  
XX Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 7.1%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 106 CTCATTCTCTGCTCCCACT 125  
DB 1 CACATTCTCTGCTCCCAAT 20  
RESULT 16  
ACL40112/c  
ID ACL40112 standard; RNA; 21 BP.  
XX  
XX ACL40112;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX ABCC4 siRNA sense sequence, SEQ ID 1184.  
XX

KW Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
KW short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.  
XX  
XX Claim 3; SEQ ID NO 1184; 113pp; English.  
XX  
XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP, and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 7.1%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 171 AAGATTCCAGGAGCTTCACA 190  
DB 20 AAGATTCCAGGAGCTTCACA 1  
RESULT 17  
ACL41020/c  
ID ACL41020 standard; DNA; 21 BP.  
XX  
XX ACL41020;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX C20orf103 target oligonucleotide, SEQ ID 2092.  
XX  
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX

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XX 20-MAY-2003; 2003US-0471729P.
XX (AMHP ) WYETH.
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 2092; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present invention is a
XX target oligonucleotide from one such CRTP for which short interfering
XX RNAi (siRNA) were produced. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 11 A; 4 C; 4 G; 2 T; 0 U; 0 Other:
SQ
Query Match 7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 150 TTCTCCTTCGCGCATGATT 169
Db 21 TTCTGTGTCGCGCATGATT 2
XX
XX RESULT 18
XX ACL40781/c
XX ID ACL40781 standard; RNA; 21 BP.
XX
XX ACL40781;
XX
XX 24-MAR-2005 (first entry)
XX
XX ABCC4 siRNA sense sequence, SEQ ID 1853.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX KM short interfering RNA; gene silencing.
XX
XX Synthetic.
XX OS
XX WO2005001092-A2.
XX PN
XX 06-JAN-2005.
XX PD
XX 19-MAY-2004; 2004WO-US015645.
XX PF
XX 20-MAY-2003; 2003US-0471729P.
XX PR
XX (AMHP ) WYETH.
XX PA
XX Be X, Wei L, Slonim DK, Howes SH;
XX PI
XX WPI; 2005-075568/08.
XX DR
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XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1853; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other:
SQ
Query Match 7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 171 AAGATTCAGGAGCTTCACA 190
Db 20 AAGATTCAGGCGCTTCACA 1
XX
XX RESULT 19
XX ACL40870/c
XX ID ACL40870 standard; DNA; 21 BP.
XX
XX ACL40870;
XX
XX 24-MAR-2005 (first entry)
XX
XX C20orf103 target oligonucleotide, SEQ ID 1942.
XX DE
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX KM
XX Homo sapiens.
XX OS
XX WO2005001092-A2.
XX PN
XX 06-JAN-2005.
XX PD
XX 19-MAY-2004; 2004WO-US015645.
XX PF
XX 20-MAY-2003; 2003US-0471729P.
XX PR
XX (AMHP ) WYETH.
XX PA
XX Be X, Wei L, Slonim DK, Howes SH;
XX PI
XX WPI; 2005-075568/08.
XX DR
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1942; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
```

protein activity of a cancer-related transmembrane protein (CRTP) or gene  
an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
(b) a carrier. The pharmaceutical composition may also comprise a  
polynucleotide capable of inhibiting or decreasing the expression of the  
CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
FLJ1856, GPR34, HAVCR1, SLC30A4, TRG, and TRPM4. The  
pharmaceutical composition is useful for treating cancer, e.g. colon  
cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
cancer, stomach cancer, and esophageal cancer. The present sequence is a  
target oligonucleotide from one such CRTP for which short interfering  
RNAs (siRNA) were produced. Note: The sequence data for this patent did  
not form part of the printed specification, but was obtained in  
electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

Query Match 7.1%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

149 CTTCTCCTTCGCGCATGATT 168  
168 CTTCTCCTTCGCGCATGATT 1

RESULT 20  
ACL40872  
ID ACL40872 standard; RNA; 21 BP.  
XX  
AC ACL40872;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX C20orf103 siRNA antisense sequence, SEQ ID 1944.  
XX  
XX Cytoplastic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
XX short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX WO2005001092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 1944; 113pp; English.

The present invention relates to a novel pharmaceutical composition  
comprising: (a) an agent capable of modulating an expression level or  
protein activity of a cancer-related transmembrane protein (CRTP) or gene  
(b) an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
(b) a carrier. The pharmaceutical composition may also comprise a  
polynucleotide capable of inhibiting or decreasing the expression of the  
CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
FLJ1856, GPR34, HAVCR1, SLC30A4, TRG, and TRPM4. The  
pharmaceutical composition is useful for treating cancer, e.g. colon

cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

Query Match 7.1%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 45.0%; Pred. No. 27;  
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

149 CTTCTCCTTCGCGCATGATT 168  
168 CTTCTCCTTCGCGCATGATT 1

RESULT 21  
ABL58878  
ID ABL58878 standard; DNA; 24 BP.  
XX  
AC ABL58878;  
XX  
XX 22-JUL-2002 (first entry)  
XX  
XX Oligonucleotide 1-T.  
XX  
XX Marker oligonucleotide; microsatellite; single nucleotide polymorphism;  
XX SNP; food production; veterinary; medicine; ss.  
XX  
XX Synthetic.  
XX  
XX WO200238804-A1.  
XX  
XX 16-MAY-2002.  
XX  
XX 07-NOV-2001; 2001WO-EP012880.  
XX  
XX 08-NOV-2000; 2000DE-01055368.  
XX  
XX (AGRO-) AGROBIOGEN GMBH BIOTECHNOLOGIE.  
XX  
XX  
XX Brem G;  
XX  
XX WPI; 2002-435855/46.  
XX  
XX  
XX Marking DNA samples for identifying samples during subsequent analysis by  
XX adding microsatellite or single nucleotide polymorphism oligonucleotide.  
XX  
XX Disclosure; Page 6; 25pp; German.  
XX  
XX The invention relates to marking DNA-containing samples by treatment with  
XX a marker oligonucleotide that is either an artificial microsatellite  
XX oligonucleotide or an artificial single nucleotide polymorphism (SNP)  
XX oligonucleotide for analysis. The oligonucleotides are useful as internal  
XX markers for identifying samples used for e.g. characterising or typing an  
XX animal for monitoring food production and in human or veterinary  
XX medicine. The present sequence is that of a artificial oligonucleotide  
XX used to exemplify the invention  
XX  
XX  
XX Sequence 24 BP; 0 A; 12 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 7.1%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

140 CTTCTCCTTCGCGCATGATT 159  
159 CTTCTCCTTCGCGCATGATT 24

RESULT 22

```

AEC36403/c
ID AEC36403 standard; RNA; 19 BP.
XX
AC AEC36403;
XX
XX 03-NOV-2005 (first entry)
XX
DE VEGF/VEGFR2 multifunctional siNA VEGF target sequence #4.
XX
XX short interfering nucleic acid; siNA; short interfering RNA; siRNA;
XX gene silencing; RNA interference; transplant rejection;
XX pulmonary disease; respiratory-gen.; respiratory disease; injury;
XX vulnereary; neurodegenerative disease; neuroprotective;
XX neurological disease; cancer; neoplasm; cytostatic; infection;
XX antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
XX cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
XX inflammation; antiinflammatory; renal disease; nephrotropic;
XX endocrine disease; genitourinary disease; liver disease; hepatotropic;
XX gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
XX VEGF.
XX
XX Unidentified.
XX
XX WO2005078097-A2.
XX
XX 25-AUG-2005.
XX
XX 09-FEB-2005; 2005MO-US004270.
XX
XX 10-FEB-2004; 2004US-0543480P.
XX
XX 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Jadhav V, Zinnen S;
XX
XX WPI; 2005-571603/58.
XX
XX
XX New multifunctional short interfering nucleic acid (siNA), useful for
XX modulating RNA function and/or gene expression in a cell or for treating
XX or preventing pulmonary diseases, neurodegenerative conditions, cancers,
XX or ocular diseases.
XX
XX
XX Example 7; SEQ ID NO 57; 168bp; English.
XX
XX The specification describes a multifunctional short interfering nucleic
XX acid (siNA). This multifunctional siNA molecule is of two formulae given
XX in the specification. The multifunctional siNA of the invention is useful
XX for modulating RNA function and/or gene expression in a cell. It can be
XX used for down regulating or inhibiting the expression of one or more
XX target nucleic acid molecules. It is also useful for treating diseases or
XX conditions that responds to modulation of gene expression or activity in
XX a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
XX grafting, or treatment of pulmonary disease (restenosis) or preventing
XX neointimal hyperplasia and atherosclerosis in grafts. It can further be
XX used for treating CNS lesions or injury, including treating
XX neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
XX disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
XX sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
XX diseases, prion disease, inflammatory diseases, renal diseases, liver
XX diseases, mitochondrial diseases, endocrine diseases, or reproduction
XX related diseases and conditions. AEC36400-AEC36404 represent target
XX sequences from VEGF, for a multifunctional siNA of the invention which
XX targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
XX sequences to the target sequences.
XX
XX
XX Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 6.9%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 31;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 147 CCCTTCCTCTTGCCAT 164

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Db
18 CCCTTCCTCTTGCCAT 1
|||||
RESULT 23
AEC36450
ID AEC36450 standard; RNA; 19 BP.
XX
AC AEC36450;
XX
XX 03-NOV-2005 (first entry)
XX
XX VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #4.
XX
XX short interfering nucleic acid; siNA; short interfering RNA; siRNA;
XX gene silencing; RNA interference; transplant rejection;
XX pulmonary disease; respiratory-gen.; respiratory disease; injury;
XX vulnereary; neurodegenerative disease; neuroprotective;
XX neurological disease; cancer; neoplasm; cytostatic; infection;
XX antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
XX cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
XX inflammation; antiinflammatory; renal disease; nephrotropic;
XX endocrine disease; genitourinary disease; liver disease; hepatotropic;
XX gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
XX VEGF.
XX
XX Unidentified.
XX
XX WO2005078097-A2.
XX
XX 25-AUG-2005.
XX
XX 09-FEB-2005; 2005MO-US004270.
XX
XX 10-FEB-2004; 2004US-0543480P.
XX
XX 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Jadhav V, Zinnen S;
XX
XX WPI; 2005-571603/58.
XX
XX
XX New multifunctional short interfering nucleic acid (siNA), useful for
XX modulating RNA function and/or gene expression in a cell or for treating
XX or preventing pulmonary diseases, neurodegenerative conditions, cancers,
XX or ocular diseases.
XX
XX
XX Example 7; SEQ ID NO 115; 168bp; English.
XX
XX The specification describes a multifunctional short interfering nucleic
XX acid (siNA). This multifunctional siNA molecule is of two formulae given
XX in the specification. The multifunctional siNA of the invention is useful
XX for modulating RNA function and/or gene expression in a cell. It can be
XX used for down regulating or inhibiting the expression of one or more
XX target nucleic acid molecules. It is also useful for treating diseases or
XX conditions that responds to modulation of gene expression or activity in
XX a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
XX grafting, or treatment of pulmonary disease (restenosis) or preventing
XX neointimal hyperplasia and atherosclerosis in grafts. It can further be
XX used for treating CNS lesions or injury, including treating
XX neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
XX disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
XX sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
XX diseases, prion disease, inflammatory diseases, renal diseases, liver
XX diseases, mitochondrial diseases, endocrine diseases, or reproduction
XX related diseases and conditions. AEC36400-AEC36404 represent target
XX sequences from VEGF, for a multifunctional siNA of the invention which
XX targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
XX sequences to the target sequences.
XX
XX
XX Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;
XX

```



XX	Interleukin 3; colony-stimulating factor; IL3; transgenic animal;
XX	IL3 isogene; central nervous system disorder; multiple sclerosis;
XX	Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;
XX	inflammatory disorder; sequencing; primer; ss.
OS	Homo sapiens.
XX	
PN	WO200244410-A1.
XX	
PD	06-JUN-2002.
XX	
PF	28-NOV-2000; 2000WO-US032381.
XX	
PR	28-NOV-2000; 2000WO-US032381.
XX	
PA	(GENA-) GENAISSANCE PHARM INC.
XX	
PI	Chew A, Denton RR, Nandabalan K, Stephens JC;
XX	
DR	WPI; 2002-519590/55.
XX	
PT	Novel isolated polynucleotide comprising a sequence which is a
XX	polymorphic variant for a reference sequence for interleukin 3 gene
PT	useful for studying the expression and biological function of the
PI	protein.
XX	
PS	Example 1; Page 25; 62pp; English.
XX	
CC	The invention describes an isolated polynucleotide (I) comprising a
CC	sequence which is a polymorphic variant for a reference sequence for
CC	interleukin 3 (colony-stimulating factor) (IL3) gene or its fragment. (I)
CC	is useful for studying the expression and biological function of IL3, as
CC	well as in developing drugs targeting the IL3 protein. A transgenic
CC	animal is useful for studying expression of IL3 isogenes in vivo, for in
CC	vivo screening and testing of drugs targeted against IL3 protein, and for
CC	testing the efficacy of therapeutic agents and compounds for diseases of
CC	the central nervous system e.g. multiple sclerosis, Alzheimer's disease,
CC	Parkinson's disease and CNS injury, and immune or inflammatory disorders.
CC	The method described in the invention is useful in developing diagnostic
CC	tests and therapeutic treatments for diseases of the central nervous
CC	system and immune or inflammatory disorders. This sequence represents a
CC	sequencing primer used to sequence regions of the IL-3 gene in order to
CC	study polymorphisms in the gene
XX	
XX	
SQ	Sequence 21 BP; 2 A; 4 C; 9 G; 6 T; 0 U; 0 Other;
	Query Match 6.9%; Score 16.4; DB 1; Length 21;
	Best Local Similarity 94.4%; Pred. No. 29;
	Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 TGCTCGGTCATGGGAGC 18
DB	4 TGCTCGGTCATGGGAGC 21
RESULT 27	
ID	ABK96692/c
AB	ABK96692 standard; DNA; 21 BP.
XX	
AC	ABK96692;
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Interleukin-3 (IL-3) forward sequencing primer #4.
XX	
KW	Interleukin 3; colony-stimulating factor; IL3; transgenic animal;
KW	IL3 isogene; central nervous system disorder; multiple sclerosis;
KW	Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;
XX	inflammatory disorder; sequencing; primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200244410-A1.

XX	PD	06-JUN-2002.
XX	PF	28-NOV-2000; 2000WO-US032381.
XX	XX	28-NOV-2000; 2000WO-US032381.
XX	PR	(GENA-) GENNAISSANCE PHARM INC.
XX	PA	Chew A, Denton RR, Nandabalan K, Stephens JC;
XX	PI	WPI; 2002-519590/55.
XX	DR	
XX	PT	Novel isolated polynucleotide comprising a sequence which is a
XX	PT	polymorphic variant for a reference sequence for interleukin 3 gene
XX	PT	useful for studying the expression and biological function of the
XX	PT	protein.
XX	PS	Example 1; Page 26; 62pp; English.
XX	CC	The invention describes an isolated polynucleotide (I) comprising a
XX	CC	sequence which is a polymorphic variant for a reference sequence for
XX	CC	interleukin 3 (colony-stimulating factor) (IL3) gene or its fragment. (I)
XX	CC	is useful for studying the expression and biological function of IL3, as
XX	CC	well as in developing drugs targeting the IL3 protein. A transgenic
XX	CC	animal is useful for studying expression of IL3 isogenes in vivo, for in
XX	CC	vivo screening and testing of drugs targeted against IL3 protein, and for
XX	CC	testing the efficacy of therapeutic agents and compounds for diseases of
XX	CC	the central nervous system e.g. multiple sclerosis, Alzheimer's disease,
XX	CC	Parkinson's disease and CNS injury, and immune or inflammatory disorders.
XX	CC	The method described in the invention is useful in developing diagnostic
XX	CC	tests and therapeutic treatments for diseases of the central nervous
XX	CC	system and immune or inflammatory disorders. This sequence represents a
XX	CC	sequencing primer used to sequence regions of the IL-3 gene in order to
XX	CC	study polymorphisms in the gene
XX	SQ	Sequence 21 BP; 6 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
XX	QY	Query Match 6.9%; Score 16.4; DB 1; Length 21;
XX	QY	Best Local Similarity 94.4%; Pred. No. 29;
XX	QY	Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX	DB	1 TGTCTGGGTCATGGGGCC 18
XX	DB	18 TGTCTGGGTCATGGGAGC 1
XX	RESULT 28	
XX	AED05621/C	
XX	ID AED05621	standard; RNA; 23 BP.
XX	AC AED05621;	
XX	DT 01-DEC-2005	(first entry)
XX	DE	Short interfering sense sequence targeting human VEGF 121, seqid 86.
XX	KM	vascular endothelial growth factor; RNA interference; gene silencing;
XX	KM	macular degeneration; ophthalmological; ocular disease;
XX	KM	diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;
XX	KM	cytostatic; neoplasia; asthma; antiasthmatic; immune disorder;
XX	KM	inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
XX	KM	ss; short interfering RNA; siRNA.
XX	OS	Homo sapiens.
XX	PN	WO2005089224-A2.
XX	PD	29-SEP-2005.
XX	PF	11-MAR-2005; 2005WO-US008182.
XX	PR	12-MAR-2004; 2004US-0552620P.



PR 05-APR-2004; 2004US-0559824P.  
PR 25-JAN-2005; 2005US-0647191P.  
XX  
XX (ALNY-) ALNYLAM PHARM INC.  
XX  
XX De Fongereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;  
PI Hadwiger P;  
XX  
XX WPI, 2005-658984/67.  
XX  
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense  
PT sequence and an antisense sequence, useful for treating a human diagnosed  
PT as having or at risk for having adult macular degeneration.  
XX  
XX Claim 1; SEQ ID NO 86; 200pp; English.  
XX  
XX The present invention relates to the use of siRNA targeting vascular  
CC endothelial growth factor (VEGF). Specifically claimed is an isolated  
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and  
CC an antisense sequence, where the sense and the antisense sequences form  
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF  
CC RNA in a cell, using the iRNA agent; making an iRNA agent by the  
CC synthesis of the iRNA agent, where the sense and antisense strands  
CC comprise at least one modification that stabilizes the iRNA agent against  
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA  
CC agent; inhibiting VEGF expression; and treating a human diagnosed with  
CC adult macular degeneration (AMD), by administering a therapeutically  
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense  
CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ  
CC ID NO: 2-401, not defined in the specification. The iRNA agent further  
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one  
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent  
CC further comprises a phosphorothioate at the first internucleotide linkage  
CC at the 5' or 3' end of the antisense and sense sequences. The agent  
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for  
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma  
CC and angiogenic disorders. The present sequence is short interfering sense  
CC sequence targeting human VEGF 121.  
XX  
XX Sequence 23 BP; 9 A; 2 C; 11 G; 0 T; 1 U; 0 Other;  
SQ  
Query Match 6.9%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 147 CCTCTCTCTCTGCGCAT 164  
18 CCTCTCTCTCTGCGCAT 1  
DB  
RESULT 29  
AED05615/C  
ID AED05615 standard; RNA; 23 BP.  
XX  
XX AED05615;  
AC  
XX  
XX 01-DEC-2005 (first entry)  
DT  
XX  
XX Short interfering sense sequence targeting human VEGF 121, seqid 80.  
DE  
XX  
XX vascular endothelial growth factor; RNA interference; gene silencing;  
XX macular degeneration; ophthalmological; ocular disease;  
XX diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;  
XX cytostatic; neoplasm; asthma; antiasthmatic; immune disorder;  
XX inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;  
XX ss; short interfering RNA; siRNA.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2005089224-A2.  
FN  
XX  
XX 29-SEP-2005.  
PD  
XX

PF 11-MAR-2005; 2005WO-US008182.  
XX  
XX  
XX 12-MAR-2004; 2004US-0552620P.  
PR  
XX 05-APR-2004; 2004US-0559824P.  
PR  
XX 25-JAN-2005; 2005US-0647191P.  
XX  
XX (ALNY-) ALNYLAM PHARM INC.  
XX  
XX De Fongereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;  
PI Hadwiger P;  
XX  
XX WPI, 2005-658984/67.  
XX  
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense  
PT sequence and an antisense sequence, useful for treating a human diagnosed  
PT as having or at risk for having adult macular degeneration.  
XX  
XX Claim 1; SEQ ID NO 80; 200pp; English.  
XX  
XX The present invention relates to the use of siRNA targeting vascular  
CC endothelial growth factor (VEGF). Specifically claimed is an isolated  
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and  
CC an antisense sequence, where the sense and the antisense sequences form  
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF  
CC RNA in a cell, using the iRNA agent; making an iRNA agent by the  
CC synthesis of the iRNA agent, where the sense and antisense strands  
CC comprise at least one modification that stabilizes the iRNA agent against  
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA  
CC agent; inhibiting VEGF expression; and treating a human diagnosed with  
CC adult macular degeneration (AMD), by administering a therapeutically  
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense  
CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ  
CC ID NO: 2-401, not defined in the specification. The iRNA agent further  
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one  
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent  
CC further comprises a phosphorothioate at the first internucleotide linkage  
CC at the 5' or 3' end of the antisense and sense sequences. The agent  
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for  
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma  
CC and angiogenic disorders. The present sequence is short interfering sense  
CC sequence targeting human VEGF 121.  
XX  
XX Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;  
SQ  
Query Match 6.9%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 148 CCTCTCTCTGCGCATG 165  
23 CCTCTCTCTGCGCATG 6  
DB  
RESULT 30  
ABX97349  
ID ABX97349 standard; DNA; 23 BP.  
XX  
XX ABX97349;  
AC  
XX  
XX 20-MAY-2003 (first entry)  
DT  
XX  
XX Human NOV-associated probe from primer-probe set Ag3550.  
DE  
XX  
XX NOVA; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;  
XX hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;  
XX human; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200272757-A2.  
FN  
XX  
XX 19-SEP-2002.  
PD  
XX



```

PR 20-MAR-2001; 2001US-0277327P-
PR 20-MAR-2001; 2001US-0277338P-
PR 21-MAR-2001; 2001US-0277791P-
PR 22-MAR-2001; 2001US-0277833P-
PR 23-MAR-2001; 2001US-0278152P-
PR 26-MAR-2001; 2001US-0278894P-
PR 27-MAR-2001; 2001US-0278999P-
PR 27-MAR-2001; 2001US-0279036P-
PR 28-MAR-2001; 2001US-0279344P-
PR 30-MAR-2001; 2001US-0279995P-
PR 30-MAR-2001; 2001US-0280233P-
PR 02-APR-2001; 2001US-0280802P-
PR 02-APR-2001; 2001US-0280822P-
PR 02-APR-2001; 2001US-0280900P-
PR 04-APR-2001; 2001US-0281444P-
PR 13-APR-2001; 2001US-0283675P-
PR 30-APR-2001; 2001US-0287424P-
PR 02-MAY-2001; 2001US-0288066P-
PR 03-MAY-2001; 2001US-0288342P-
PR 15-MAY-2001; 2001US-0288528P-
PR 16-MAY-2001; 2001US-0291099P-
PR 16-MAY-2001; 2001US-0291240P-
PR 30-MAY-2001; 2001US-0294485P-
PR 31-MAY-2001; 2001US-0294889P-
PR 18-JUN-2001; 2001US-0298027P-
PR 19-JUN-2001; 2001US-0299303P-
PR 19-JUN-2001; 2001US-0299310P-
PR 10-JUL-2001; 2001US-0304354P-
PR 31-JUL-2001; 2001US-0309198P-
PR 16-AUG-2001; 2001US-0312903P-
PR 10-SEP-2001; 2001US-0318462P-
PR 12-SEP-2001; 2001US-0318770P-
PR 27-SEP-2001; 2001US-0325430P-
PR 18-OCT-2001; 2001US-0330380P-
PR 31-OCT-2001; 2001US-0335301P-
PR 14-NOV-2001; 2001US-0332172P-
PR 14-NOV-2001; 2001US-0332771P-
PR 14-NOV-2001; 2001US-0332722P-
PR 14-NOV-2001; 2001US-0333184P-
PR 21-NOV-2001; 2001US-0333722P-
PR 03-DEC-2001; 2001US-0337425P-
PR 03-DEC-2001; 2001US-0338092P-
PR 04-DEC-2001; 2001US-0337185P-
PR 03-JAN-2002; 2002US-0345705P-
XX
PA (PADIGARU M.
PA (SPYTEK K A.
PA (SHENOY S G.
PA (TAUPIER R J.
PA (PENNA C E A.
PA (LILL L L.
PA (ZERHUSEN B D.
PA (GUSEV V Y.
PA (JTW W.
PA (GORMAN L.
PA (MILLER C E.
PA (KEKUDA R.
PA (PATTURAJAN M.
PA (GANGOLI E A.
PA (VERNET C A M.
PA (GUOX X S.
PA (TCHERNEV V T.
PA (FERNANDES E R.
PA (CASMAN S J.
PA (MALYANKAR U M.
PA (GERLACH V.
PA (LIUY Y.
PA (ANDERSON D W.
PA (SPADERNA S K.

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PA (CATTERTON E.
PA (LEITE M W.
PA (ZHONG H.
PA (ALSOBROOK J P.
PA (LEPLEY D M.
PA (RIEGER D K.
PA (BURGESS C E.
XX
PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;
PI Zernusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangoli EA, Vernet CM, Guo XS, Tchernev VT;
PI Fernandes ER, Casman SJ, Malynkar UM, Gerlach V, Liu Y;
PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;
PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
DR WPI, 2004-225693/21.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
PT infection or obesity, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Example C; SEQ ID NO 521; 786pp; English.
XX
CC The invention relates to an isolated polypeptide (designated NOVX, or
CC NOVX-NOV127) comprising a sequence selected from 178 fully defined amino
CC acid sequences (and their mature forms, variants and fragments). Also
CC included are an isolated nucleic acid molecule encoding NOVX, a vector
CC comprising the nucleic acid, a cell comprising the vector, methods for
CC determining the presence or amount of the polypeptide or the nucleic acid
CC molecule in a sample, methods for determining the presence of or
CC predisposition to a disease associated with altered levels of expression
CC of the above polypeptide or nucleic acid molecule in a first mammalian
CC subject, a method for identifying an agent that binds to the above
CC polypeptide, a method for identifying a potential therapeutic agent for
CC use in the treatment of a pathology that is related to aberrant
CC expression or physiological interactions of the polypeptide, a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide and a method for modulating
CC the activity of the polypeptide cited above. The composition and methods
CC are useful for diagnosing, preventing or treating diseases such as
CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
CC Parkinson's disease, immune disorders, haematopoietic disorders,
CC dyslipidaemias, and other chronic diseases. These may also be used in
CC chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The polypeptides are also useful as vaccines. The
CC present sequence is an RTQ-PCR (real time quantitative PCR) probe used to
CC assay tissue specific expression of a NOVX mRNA.
XX
SQ Sequence 23 BP; 1 A; 13 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 6.9%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 100 CCCCTCTCATTCCTCTCCTC 120
Db 2 CCGCCTCTCTCTCTCCGCTC 22

```

## RESULT 32

ABN89272 standard; DNA; 20 BP.

ABN89272;

29-AUG-2002 (first entry)

Human Talin antisense phosphorothioate oligonucleotide SEQ ID NO:85.  
 Human; Talin; antimicrobial; antiinflammatory; cytostatic; inhibitor;  
 antisense gene therapy; infection; inflammation; Talin inhibitor; tumour;

XV		antisense oligonucleotide; phosphorochioate; ss.
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT	/tag= b	
FT	/note= OTHER	
FT	/mod_base= "phosphorochioate backbone"	
FT	1..5	
FT	/tag= a	
FT	/mod_base= OTHER	
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides"	
FT	16..20	
FT	/tag= C	
FT	/mod_base= OTHER	
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides"	
XX		
PN	US6372492-B1.	
PD	16-APR-2002.	
XX		
PB	30-OCT-2000; 2000US-00702251.	
PR	30-OCT-2000; 2000US-00702251.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
PI	Bennett CF, Cowsett LM;	
DR	WPI; 2002-470102/50.	
XX		
PT	New antisense compound useful for inhibiting expression of Talin and for preventing or delaying infection, inflammation or tumor formation.	
PS	Claim 14; Col 42; 46pp; English.	
XX		
CC	The present invention describes an antisense compound (I), 16 to 30 bases in length targeted to specific base regions of a nucleic acid encoding human Talin. Also described: (a) an antisense compound up to 30 bases in length which inhibits the expression of human Talin; (b) a composition (ii) comprising (i) or (a); and (c) inhibiting the expression of human Talin in human cells or tissues comprising contacting the cells or tissues in vitro with (i) or (a). (I) has anti-tumoral, anti-inflammatory and cytoskeletal activities, and can be used in antisense gene therapy and as a Talin expression inhibitor. (I) can be used: to inhibit the expression of human Talin in human cells or tissues; to prevent or delay infection, inflammation or tumour formation; and in diagnostics, therapeutics, prophylaxis, and in research reagents and kits. The present sequence represents a human Talin antisense chimeric phosphorothioate oligonucleotide, having 2'-methoxyethyl (2'-MOE) wings of 5 nucleotides at the 5' and 3' ends and a 2'-nucleotide deoxy gap in the middle, which is used in an example from the present invention	
SQ	Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;	
OY	Query Match 6.8%; Score 16; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 33; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	105 TGTGATTCCTCGTGC 120           3 TGTCAITCCTCGTGC 18	
RESULT_33		
ID	ADG90535	
AC	ADG90535 standard; DNA; 20 BP.	
DT	11-MAR-2004 (first entry)	

DE	Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:85.
XX	
XX	Human; talin; cellular adhesion; muscle strength; cardiac function;
KW	cardiomyocyte; platelet; prostate; androgen downregulation;
KM	prostate cancer; talin-related disorder;
KW	cellular adhesion-related disorder; expression inhibition;
KM	antisense therapy; phosphorothioate; antisense oligonucleotide; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	1..20
FT	/tag= a
FT	/mod base
FT	/note= "This oligonucleotide has a phosphorothioate backbone and 2'-methoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytosine nucleotides are 5-methylcytosines"
FT	
FT	
XX	
PN	WO200268446-A1.
XX	
PD	06-SEP-2002.
XX	
Pf	30-OCT-2001; 2001WO-US048435.
XX	
PR	22-FEB-2001; 2001US-00791942.
XX	
PA	(ISIS-) ISIS PHARM INC.
PA	(BOEH ) BOEHRINGER INGELHEIM PHARM INC.
PI	Bennett CF, Rothlein R, Kishimoto TK, Cowse LM;
DR	WPI; 2002-691651/74.
XX	
PT	New antisense oligonucleotides targeted to nucleic acid molecules encoding human Talin, useful for inhibiting the expression of human Talin and for treating a human having a disease or condition associated with Talin.
PT	
PS	Example 15; SEQ ID NO 85; 114pp; English.
XX	
CC	Sequences ADS90460-ADS90539 represent phosphorothioate targeted to the human talin gene, which inhibit its expression. The antisense were designed to target different regions of human talin RNA, and were analysed for their effect on talin expression by quantitative real-time PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins such as actin, myosin and vinculin to integrins, thereby linking the extracellular matrix to other cells. It is thought to be involved in the regulation of cellular adhesion and cell morphology. Talin is highly expressed in platelets, and may play a role in platelet adhesion as its subcellular distribution differs between resting non-adhesive platelets and activated adhesive platelets. It could also play a major role in determining muscle strength and cardiac function as it has been found to participate in the transmission of contractile force to the extracellular matrix in cardiomyocytes, and exhibits mechanical loading-dependent expression at myotendinous junctions. The expression of talin is downregulated by androgens in prostate tissues, a phenomenon known to contribute to the development of prostate cancer. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of talin-related disorders, such as those related to cellular adhesion. The present sequence represents a human c-Ha-ras phosphorothioate antisense oligonucleotide used as a positive control in determining optimal oligonucleotide concentration for a particular cell line.
CC	
SQ	Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;
XX	
Query Match	6.8%; Score 16; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 33;
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	105 TGTGATTCCTGCTC 120       3 TGTGATTCCTGCTC 18

## RESULT 34

AB084461/c  
ID AB084461 standard; DNA; 20 BP.

XX AC AB084461;

XX DT 20-FEB-2003 (first entry)

XX DE DPP10 PCR primer #92.

XX KW DPP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma;  
XX KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;  
XX KW antiinflammatory; vaccine; gene therapy; inflammatory disease;  
XX KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;  
XX KW chromosome 2q14; PCR primer; ss.

XX OS Homo sapiens.  
XX OS Synthetic.

XX PN WO200286113-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-GB001887.

XX PR 24-APR-2001; 2001GB-00010044.

XX PR 24-APR-2001; 2001GB-00010046.

XX PR 12-OCT-2001; 2001GB-00024575.

XX PR 12-OCT-2001; 2001GB-00024594.

XX PA (ISIS-) ISIS INNOVATIONS LTD.

XX P1 Cockson WOCM, Moffat MF, Allen M, Lench N;

XX DR WPI; 2003-093132/08.

XX PT New nucleic acid sequence comprising DPP10 mRNA, useful for the

XX PT manufacture of a medicament for regulating DPP10 protein expression or

XX PT for preventing or treating inflammatory disease e.g., inflammatory bowel

XX PT disease.

XX PS Claim 43; Page 314; 321pp; English.

XX CC The present invention describes a new isolated nucleic acid sequence (1)  
XX CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also  
XX CC known as prolyloligopeptidase). (1) has antiinflammatory, antiasthmatic,  
XX CC antipsoriatic, antiarthritic and antirheumatic activities, and can be  
XX CC used for the manufacture of a medicament for regulating DPP10 expression  
XX CC or for preventing or treating inflammatory disease e.g., inflammatory  
XX CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (1) can  
XX CC also be used in an assay for detecting or measuring DPP10 in a sample. A  
XX CC host cell comprising (1) can be used for producing recombinant DPP10 gene  
XX CC products, or in drug screening systems to identify agents for diagnosis  
XX CC or treatment of individuals having or susceptible to inflammatory  
XX CC disease. Human DPP10 is located on chromosome 2, more specifically  
XX CC chromosome 2q14. AB0844612 to AB084612 and ABP55569 to ABP55629 represent  
XX CC sequences used in the exemplification of the present invention

XX SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 6.8%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 AGAGCAATGCTAC 206

Db 18 AGAGCAATGCTAC 3

RESULT 35

## ADP85740

ID ADP85740 standard; DNA; 20 BP.

XX AC ADP85740;

XX DT 26-AUG-2004 (first entry)

XX DE Human Talin antisense oligonucleotide, ISIS #109184.

XX KW Antisense; Talin; muscular disorder; hematologic disorder;  
XX KW cardiac disorder; hyperproliferative disorder; cancer; human;  
XX KW phosphorothioate; ss.

XX OS Homo sapiens.  
XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified\_base 1..20

XX FT /tag= b

XX FT /mod\_base= OTHER

XX FT /note= "Phosphorothioate backbone where all cytidine

XX FT residues are 5-methylcytidines"

XX FT modified\_base 1..5

XX FT /tag= a

XX FT /mod\_base= OTHER

XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX FT /tag= c

XX FT /mod\_base= OTHER

XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX PN US2004110705-A1.

XX PD 10-JUN-2004.

XX PF 11-SEP-2003; 2003US-00415463.

XX PR 30-OCT-2000; 2000US-00702251.

XX PR 30-OCT-2001; 2001WO-US047585.

XX PA (BENN/) BENNETT C F.

XX PA (COMS/) COMSERT L M.

XX PI Bennett CF, Cowsett LM;

XX DR WPI; 2004-440384/41.

XX PT New compounds, particularly antisense oligonucleotides targeted to a

XX PT nucleic acid encoding talin, useful for treating muscular, cardiac,

XX PT hematologic, or hyperproliferative disorders.

XX PS Claim 3; SEQ ID NO 85; 48pp; English.

XX SQ Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 6.8%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCTCATTCCTGCTC 120

Db 3 TCTCATTCCTGCTC 18

RESULT 36

ACT41021/c

```

ID  ACL41021 standard; RNA; 21 BP.
XX
XX  ACL41021;
AC
XX  24-MAR-2005 (first entry)
DT
XX  C20orf103 siRNA sense sequence, SEQ ID 2093.
DE
XX  Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX  short interfering RNA; gene silencing.
XX
XX  Synthetic.
OS
XX  WO2005001092-A2.
XX
XX  06-JAN-2005.
PD
XX
XX  19-MAY-2004; 2004WO-US015645.
PF
XX  20-MAY-2003; 2003US-0471729P.
PR
XX  (AMHP ) WYETH.
PA
XX  Be X, Wei L, Slonim DK, Howes SH;
PI
XX  WPI; 2005-075568/08.
DR
XX
XX  Pharmaceutical composition comprising an agent capable of modulating an
PT  expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT  activated by the polypeptide or antibody, and a carrier, useful for
PT  treating cancer.
XX
XX  Claim 3; SEQ ID NO 2093; 113bp; English.
PS
XX
XX  The present invention relates to a novel pharmaceutical composition
CC  comprising: (a) an agent capable of modulating an expression level or
CC  protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC  (b) an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC  (b) a carrier. The pharmaceutical composition may also comprise a
CC  polynucleotide capable of inhibiting or decreasing the expression of the
CC  CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC  invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC  FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC  pharmaceutical composition is useful for treating cancer, e.g. colon
CC  cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC  cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC  CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 21 BP; 10 A; 3 C; 4 G; 0 T; 4 U; 0 Other;
SQ
Query Match 6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 150 TTCTCTTCCTGCCATGATT 168
DB 19 TTCTTGTTCGCATGATT 1

```

```

XX  Homo sapiens.
OS
XX  WO2005001092-A2.
XX
XX  06-JAN-2005.
PD
XX
XX  19-MAY-2004; 2004WO-US015645.
PF
XX  20-MAY-2003; 2003US-0471729P.
PR
XX  (AMHP ) WYETH.
PA
XX  Be X, Wei L, Slonim DK, Howes SH;
PI
XX  WPI; 2005-075568/08.
DR
XX
XX  Pharmaceutical composition comprising an agent capable of modulating an
PT  expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT  activated by the polypeptide or antibody, and a carrier, useful for
PT  treating cancer.
XX
XX  Claim 3; SEQ ID NO 1852; 113bp; English.
PS
XX
XX  The present invention relates to a novel pharmaceutical composition
CC  comprising: (a) an agent capable of modulating an expression level or
CC  protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC  (b) an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC  (b) a carrier. The pharmaceutical composition may also comprise a
CC  polynucleotide capable of inhibiting or decreasing the expression of the
CC  CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC  invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC  FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC  pharmaceutical composition is useful for treating cancer, e.g. colon
CC  cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC  cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC  target oligonucleotide from one such CRTP for which short interfering
CC  RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC  not form part of the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 172 AGATTCCAGCGACTTCACA 190
DB 21 AGATTCCAGCGCTTCACA 3

```

```

RESULT 37
ACLA0780/C
ID  ACLA0780 standard; DNA; 21 BP.
XX
XX  ACLA0780;
AC
XX  24-MAR-2005 (first entry)
DT
XX  ABCC4 target oligonucleotide, SEQ ID 1852.
DE
XX  Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX

```

```

RESULT 38
ACLA0113
ID  ACLA0113 standard; RNA; 21 BP.
XX
XX  ACLA0113;
AC
XX  24-MAR-2005 (first entry)
DT
XX  ABCC4 siRNA antisense sequence, SEQ ID 1185.
DE
XX  Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX  short interfering RNA; gene silencing.
XX
XX  Synthetic.
OS
XX  WO2005001092-A2.
XX
XX  06-JAN-2005.
PD
XX
XX  19-MAY-2004; 2004WO-US015645.
PF

```

XX 20-MAY-2003; 2003US-0471729P.  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX WPI; 2005-075568/08.  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABCc4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.  
XX  
XX Claim 3; SEQ ID NO 1185; 113pp; English.  
XX  
XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABCc4, C20orf103, CACNA1D, CD46, CST, ENPP3,  
XX FLJ11866, GPR84, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 21 BP; 5 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

```

Query Match          6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 68.4%; Pred.No.34;
Matches    13; Conservative   4; Mismatches    2; Indels    0; Gaps    0

Oy      172 AGATTCCAGGGGACTTCACA 190
        |||::||| |::|||
Db       1 AGAUTCACAGCGCCTUCACA 19

RESULT 39
ACL40111/c
ID     ACL40111 standard; DNA; 21 BP.
XX
XX     ACL40111;
AC
XX     DT      24-MAR-2005 (first entry)
DT
XX     ABCC4 target oligonucleotide, SEQ ID 1183.
DE
XX     Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX     Homo sapiens.
OS
XX     WO2005001092-A2.
XN
XX     06-JAN-2005.
PD
XX     19-MAY-2004; 2004MO-US015645.
PE
XX     20-MAY-2003; 2003US-0471729P.
PR
XX     (AMHP ) WYETH.
PA
XX
XX     Be X, Wei L, Slonim DK, Howes SH;
PI
XX     WPI; 2005-075568/08.
DR
XX
XX     Pharmaceutical composition comprising an agent capable of modulating an
PT

```

PT	expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT	activated by the polypeptide or antibody, and a carrier, useful for
PT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 1183; 113pp; English.
XX	
CC	The present invention relates to a novel pharmaceutical composition
CC	comprising: (a) an agent capable of modulating an expression level or
CC	protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC	(b), an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC	FLU11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRTP for which short interfering
CC	RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SO	Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
Query Match	6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity	89.5%;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	

Qy	172	AGATTCGAGGACTTCACA	190
Db	21	AGATTCGAGGCGCTTCACA	3
RESULT 40			
ACL40868/c			
ID	ACL40868	standard; RNA, 21 BP.	
XX			
AC	ACL40868;		
XX			
DT	24-MAR-2005	(first entry)	
XX			
DE	C20orf103	siRNA sense sequence, SEQ ID 1940.	
XX			
KW	Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;		
XX	short interfering RNA; gene silencing.		
OS	Synthetic.		
XX			
EN	W02005001092-A2.		
XX			
PD	06-JAN-2005.		
XX			
PF	19-MAY-2004; 2004WO-US015645.		
XX			
FR	20-MAY-2003; 2003US-0471729P.		
XX			
PA	(AMHP ) WYETH.		
XX			
PI	Be X, Wei L, Slonim DK, Howes SH;		
XX			
DR	WPI; 2005-075568/08.		
XX			
PT	pharmaceutical composition comprising an agent capable of modulating an		
XX	expression level or protein activity of a gene, e.g. ABCc4, or a T cell		
PT	activated by the polypeptide or antibody, and a carrier, useful for		
XX	treating cancer.		
XX			
CS	Claim 3; SEQ ID NO 1940; 113pp; English.		
CC	The present invention relates to a novel pharmaceutical composition		
CC	comprising: (a) an agent capable of modulating an expression level or		

CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11556, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 21 BP; 9 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 6.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCCCATGAT 167  
Db 19 CTTCTGTTCTGCATGAT 1

## RESULT 41

ACLA0782  
ID ACLA0782 standard; RNA; 21 BP.

AC ACLA0782;

XX 24-MAR-2005 (first entry)

DE ABCC4 siRNA antisense sequence, SEQ ID 1854.

XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;

KW short interfering RNA; gene silencing.

XX Synthetic.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

PA (AMHP ) WYETH.

PI Be X, Wei L, Stonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.

XX Claim 3; SEQ ID NO 1854; 113bp; English.

XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11556, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 21 BP; 5 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 6.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 68.4%; Pred. No. 34;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 172 AGATTCCAGGACTTCACA 190  
Db 1 AGATTCCAGGCGCTUCACA 19

RESULT 42  
ACA8981  
ID ACA8981 standard; DNA; 22 BP.

AC ACA8981;

XX 08-JUL-2003 (first entry)

DE Selection and amplification of genetic markers PCR related primer #92.

XX Genetic marker selection; multiplex PCR amplification;

KW prenatal diagnostic testing; foetal sex determination;

KW genetic identification; DNA profiling; DNA fingerprinting;

XX forensic analysis; PCR; primer; ss.

XX Homo sapiens.

XX WO2003031646-A1.

XX 17-APR-2003.

XX 14-OCT-2002; 2002WO-AU001388.

XX 12-OCT-2001; 2001AU-00008234.

XX 12-OCT-2001; 2001AU-00008235.

PA (UYQU ) UNIV QUEENSLAND.

PI Findlay I, Matthews PL, Mulcahy BK;

XX WPI; 2003-381725/36.

XX Selecting genetic markers as targets for nucleic acid sequence  
XX amplification, useful for improving genetic testing, e.g. fetal sex  
XX determination, comprises selecting each of the genetic markers according  
XX to a heterozygosity index.

XX Claim 36; Page 40; 64pp; English.

XX The invention describes a method of selecting genetic markers as targets  
XX for nucleic acid sequence amplification comprising selecting each of the  
XX genetic markers according to a heterozygosity index of 0.5 or greater.  
XX Selecting and amplification of genetic markers are useful as targets for  
XX nucleic acid sequence amplification, for genetic testing or facilitating  
XX multiplex PCR amplification from limiting amounts of target nucleic acid.  
XX The methods are also useful for improving genetic diagnostic and  
XX screening methods, such as prenatal diagnostic testing, foetal sex  
XX determination or genetic identification, e.g. DNA profiling or DNA  
XX fingerprinting. The nucleic acid sequence amplification is also useful in  
XX forensic analysis of degraded, old, ancient and difficult samples that  
XX are difficult to amplify and identify. This sequence represents a PCR  
XX primer used in the selection and amplification of genetic markers  
XX

Sequence 22 BP; 2 A; 8 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 6.6%; Score 15.6; DB 1; Length 22;



Best Local Similarity 81.8%; Pred. No. 34;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 144 TCCCTCTCTCTCTGCGCATG 165  
 |||||  
 DB 1 TTCTCTTCACCTTCTGCGCATG 22

RESULT 43  
 ADU84382  
 ID ADU84382 standard; DNA; 17 BP.  
 AC ADU84382;  
 XX  
 XX 10-FEB-2005 (first entry)  
 DT  
 XX  
 DE Human MetAP-2 hammerhead ribozyme substrate sequence #391.

KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW proleuk-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ds.

XX Homo sapiens.  
 OS  
 XX  
 XX WO200116312-A2.  
 PV  
 XX 08-MAR-2001.  
 PD  
 XX 30-AUG-2000; 2000WO-US023998.  
 PF  
 XX 31-AUG-1999; 99US-0151711P.  
 PR 27-SEP-1999; 99US-0040664J.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-0047443Z.  
 PR 29-DEC-1999; 99US-0173612E.  
 PR 30-DEC-1999; 99US-00476387.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-0053102S.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-0057822J.  
 PR 09-AUG-2000; 2000US-0063638S.

XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpelsky A, Matulic-Adamic J, Svedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 XX WPI, 2001-244406/25.  
 DR

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 PT  
 XX  
 XX Example 3; Page 249; 717p; English.  
 PS  
 XX

CC The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),

CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for a ribozyme used in  
 CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
 CC more than once in the specification, but these have different sequences  
 CC associated with them.

XX Sequence 17 BP; 4 A; 1 C; 5 G; 7 T; 0 U; 0 Other;  
 XX

XX Query Match 6.5%; Score 15.4; DB 1; Length 17;  
 XX Best Local Similarity 94.1%; Pred. No. 41;  
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 75 GAGCTGGTTGTTGAAA 91  
 |||||  
 DB 1 GAGCTGGTTTGTGAAA 17

RESULT 44  
 ACN08391  
 ID ACN08391 standard; RNA; 17 BP.  
 XX  
 XX ACN08391;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8394.  
 DE  
 XX  
 XX MNV; West Nile Virus; antiinflammatory; cytoprotective; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.  
 OS  
 XX  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, McSwiggen JA;  
 PI  
 XX WPI, 2002-706994/76.  
 DR

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (MNV), useful for treating a condition related to MNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PT  
 XX  
 XX Claim 23; SEQ ID NO 8394; 495pp; English.  
 PS  
 XX

CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
 CC treating a condition related to MNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	
SQ	Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;
DQ	
Db	Query Match Best Local Similarity 52.5%; Score 15.4; DB 1; Length 17; Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0  143 CTCGCCCTTCCTCCTTCT 159    :::  : 1 CUCUCCUCCUCCUCCU 17
RESULT 45	
ID	ACN06460/C
XX	ACN06460 standard; RNA; 17 BP.
AC	ACN06460;
DT	22-APR-2004 (first entry)
XX	
DE	MNV Amberzyme substrate SEQ ID NO 6463.
XX	
KW	MNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viral; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; Amberzyme; Zinzyme; ss.
XX	
OS	West Nile Virus.
XX	
PN	WO200268637-A2.
PD	06-SEP-2002.
PF	19-OCT-2001; 2001WO-US048350.
PR	20-OCT-2000; 2000US-0242411P.
PA	(RIBO-) RIBOZYME PHARM INC. (BLATT) BLATT L. (MCSW/) MCSWIGGEN J A.
PI	Blatt L, Mcswiggen JA;
DR	WPI, 2002-706994/76.
PT	New nucleic acid molecule that modulates replication of West Nile Virus (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS	Claim 23; SEQ ID NO 6463; 495bp; English.
XX	
CC	The invention relates to nucleic acid molecules that modulate replication
CC	of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC	treating a condition related to MNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, Inozyme, G-Cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention

[illegible]



```

DT 23-MAR-2006 (first entry)
XX
XX Human hepatocarcinoma-associated VEGF PCR primer 1.
DE
XX Protein production; protein purification; tumor marker; hepatocarcinoma;
XX cytoskeletal; diagnosis; vascular endothelial cell growth factor; VEGF;
XX PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1629304-A.
XX
XX 22-JUN-2005.
XX
XX 02-DEC-2003; 2003CN-01116861.
XX
XX 02-DEC-2003; 2003CN-01116861.
XX
XX (HUJ/) HU J.
XX
XX Hu J, Yang J;
XX
XX WPI; 2005-726682/75.
XX
XX Chinese Han nationality vascular endothelial growth factor recombinant
XX gene, useful in hepatic carcinoma clinical diagnosis and treatment.
XX
XX Claim 2; Page 3; 10pp; Chinese.
XX
XX The invention relates to a method for the recombinant production and
XX purification of a human vascular endothelial growth factor (VEGF) protein
XX encoded by a polynucleotide originally obtained from human
XX hepatocarcinoma tissue. The method involves the inducible expression of
XX the VEGF protein in Escherichia coli, followed by protein extraction and
XX affinity chromatography to yield high purity VEGF protein. The invention
XX also relates to the isolation and cloning of the hepatocarcinoma-
XX associated VEGF polynucleotide, and to the use of the recombinantly
XX expressed VEGF protein or variants and derivatives thereof in the
XX diagnosis or treatment of hepatocarcinoma. Sequences ABP40118-ABP40119
XX represent human VEGF PCR primers which are specifically claimed for
XX isolating the hepatocarcinoma-associated VEGF polynucleotide.
XX
XX Sequence 22 BP; 7 A; 5 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 6.5%; Score 15.4; DB 1; Length 22;
XX Best Local Similarity 94.1%; Pred. No. 36;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 149 CTCTCTCTTCGCGCATG 165
XX |||||
XX 22 CTCCTCTCTTCGCGCATG 6
XX
XX RESULT 50
XX AA248049/C
XX ID AA248049 standard; DNA; 20 BP.
XX
XX AA248049;
XX
XX 08-MAR-2000 (first entry)
XX
XX Human foetal 5'-UTR IGF-II antisense oligonucleotide GT14009.
XX
XX Human; IGF-II; insulin-like growth factor II; cell growth modulation;
XX tumour; inhibition; antisense oligonucleotide; phosphorothioate;
XX metastasis; antitumour; antiproliferative; angiogenesis; apoptosis;
XX tumour cell migration; proliferative disease; atherosclerosis; psoriasis;
XX ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX

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FT modified_base 1..20
FT /*tag= a
FT /mod_base
FT /note="phosphorothioate linkages"
XX
XX WO9955854-A2.
XX
XX 04-NOV-1999.
XX
XX 23-APR-1999; 99WO-CA000323.
XX
XX 23-APR-1998; 98US-0082791P.
XX
XX (GENE-) GENESENSE TECHNOLOGIES INC.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2000-062027/05.
XX
XX Antisense oligonucleotides against mRNA of insulin-like growth factor II,
XX for treating tumors and other proliferative diseases.
XX
XX Claim 4; Page 18; 72pp; English.
XX
XX AA248041 to AA248070 represent specifically claimed antisense
XX oligonucleotides (I) complementary to the mRNA of human insulin-like
XX growth factor II (IGF-II). The present invention also describes a method
XX for inhibiting growth or metastasis of mammalian tumours by administering
XX (I). (I) have antitumour and antiproliferative activity, and inhibits
XX (i) the autocrine and paracrine functions of IGF-II which promote tumour-
XX induced angiogenesis and tumour cell migration; and (ii) autocrine growth
XX of tumour cells, possibly including induction of apoptosis. (I) may also
XX function as ribozymes. (I) are used for inhibiting growth and metastasis
XX of mammalian tumours, also: (i) for treatment of other proliferative
XX diseases, e.g. atherosclerosis and psoriasis; (ii) when labeled, as
XX probes for detecting IGF-II mRNA; and (iii) as molecular weight markers.
XX (I) that bind to the 5'-untranslated region of the foetal transcript (the
XX form present in tumour cells) should not affect the adult transcript.
XX They are effective against drug-resistant tumours
XX
XX Sequence 20 BP; 5 A; 4 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 6.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 40;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 98 GGGCCCTCTCATTTCTCTG 117
XX |||||
XX 20 GGGCCCTCTCTCTCTCCG 1
XX
XX RESULT 51
XX AA71802/C
XX ID AA71802 standard; DNA; 20 BP.
XX
XX AA71802;
XX
XX 08-JAN-2001 (first entry)
XX
XX FFA FANCIPI1 interactor PCR primer FANCIPI1-SPI.
XX
XX FFA: FANCIPI1; Fanconi anemia protein of complementation group A;
XX interactor; antitumor; ancytopenia; defective DNA repair; gene therapy;
XX cell-cycle aberration; tumorigenesis; tumor progression; PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200046244-A1.
XX
XX 10-AUG-2000.
XX
XX 24-JAN-2000; 2000WO-EP000506.
XX

```

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PR 05-FEB-1999; 99DE-01004650.
XX
XX (MULT-) MULTIGENE BIOTECH GMBH.
XX
XX Gross HJ, Reuter T, Hoehn H, Herterich S;
XX
XX WPI; 2000-524414/47.
XX
XX New nucleic acid encoding Fanconi anemia protein interactor, useful e.g.
XX for diagnosis, treatment and prevention of tumors and cytopenia.
XX
XX Discloure; Fig 4; 33pp; German.
XX
XX This invention describes a novel nucleic acid (I) encoding an interactor
XX of the Fanconi anemia protein of complementation group A (FAA), described
XX as FANCIPI. The products of the invention have antitumor and
XX anticypopenia activity. The protein encoded by (I) interacts with FAA,
XX and becomes part of the complex or signal transduction cascade that, when
XX defective, results in Fanconi anemia. (I) is used to express the
XX corresponding polypeptide (II) and this is used to raise specific
XX antibodies (Ab), or to identify compounds (A) that react with and/or
XX alter regions of (II). Compositions containing (I), vectors or cells that
XX contain (I), (II), Ab or (A) are used for diagnosis of disease associated
XX with defective DNA repair, cell-cycle aberrations, cytopenia,
XX tumorigenesis and/or tumor progression, or predisposition to the
XX disorders, and to treat or prevent the diagnosed disease, e.g. by gene
XX therapy. Modified forms of (I) are useful as antisense sequences and
XX ribozymes. This sequence represents a PCR primer used in the isolation of
XX the FAA interactor protein FANCIPI which is described in the method of
XX the invention
XX
SQ Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 103 CCTCTCATTCCTCTCTCC 122
Db 20 CCTCTCATTCCTCTCTCC 1
XX
RESULT 52
AAK95233/C
ID AAK95232 standard; DNA; 20 BP.
XX
XX AAK95232;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human cDNA clone-specific primer, SEQ ID NO: 4477.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX
XX 11-JAN-2000; 2000JP-00118774.
XX
XX 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
XX

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```

PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX Example 18; Page 134; 1380pp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a primer used to amplify a human cDNA
XX clone provided in the invention
XX
SQ Sequence 20 BP; 9 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 141 TGCTCCCTCTCTCTCTCTG 160
Db 20 TGCTCCCTCTCTCTCTCTG 1
XX
RESULT 53
ABL45325/C
ID ABL45325 standard; DNA; 20 BP.
XX
XX ABL45325;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 21q22.1 PCR primer SEQ ID NO:2369.
XX
XX Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 6; Page 52; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each well of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX

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CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention

XX  
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 16 GGCGAGTCCCTCATGTAATCG 35  
DB 20 GGCGAGTCCCTCATGTAATCG 1

RESULT 54  
ABV72231/C  
ID ABV72231 standard; DNA; 20 BP.

XX  
AC ABV72231;  
XX  
DT 05-DEC-2002 (first entry)

XX Antisense oligonucleotide targeting human IGF-II foetal mRNA.

KW Antisense oligonucleotide; insulin-like growth factor II; IGF-II;  
KW tumour growth; proliferative disorder; cancer; psoriasis;  
KW atherosclerosis; ss.

XX Homo sapiens.

XX US6417169-B1.

XX 09-JUL-2002.

XX 22-APR-1999; 99US-002955593.

XX 23-APR-1998; 98US-0082791P.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX Wright JA, Young AH, Lee YS;

XX WPI; 2002-634739/68.

XX Novel antisense compounds targeted to insulin-like growth factor mRNA,  
XX useful for inhibiting tumor growth and metastasis in mammals.

XX Claim 4; Col 10; 40pp; English.

XX ABV7223-37 represent antisense oligonucleotides which are targeted to  
XX human insulin-like growth factor II (IGF-II) foetal mRNA. The  
XX oligonucleotides are complementary to the 5' untranslated region  
XX consisting of exons 4, 5 or 6 of human fetal IGF-II mRNA. The antisense  
XX oligonucleotides of the invention are useful for inhibiting the growth of  
XX human tumour, where a chemotherapeutic agent is also administered. They  
XX are also useful for treating proliferative disorders including various  
XX forms of cancer, psoriasis, and atherosclerosis, as hybridisation probes  
XX to detect the presence of IGF-II mRNA in mammalian cells, and as  
XX molecular weight markers

XX Sequence 20 BP; 5 A; 4 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 98 GGCCCTCTCATCTTCTCTG 117  
||||||| ||| ||||| |

DB 20 GGCCCTCTCTTCTCCG 1

RESULT 55  
ABL94297  
ID ABL94297 standard; DNA; 20 BP.

XX ABL94297;

XX 29-JUL-2002 (first entry)

XX Human/mouse C/EBP beta antisense oligonucleotide, SEQ ID:63.

KW Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;  
KW human; LBP; TCFS; CRP2; NF16; IL6BP; NF-M; AGP/EBP; Apc/EBP;

KW transcription factor; tissue development; cellular function;

KW proliferation; differentiation; hormone responsiveness;

KW oxidative stress response; IL-6 signalling mediator; interleukin-6;  
KW carbohydrate metabolism; immunity; Th1 response; female fertility;

KW gluconeogenesis; ovarian; cancer; tumour formation; type II; diabetes;  
KW infection; inflammation; expression inhibition; phosphorothioate;

KW antisense oligonucleotide; ss.

XX Homo sapiens.

XX Mus musculus.

XX Key

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate linkages"

FT modified\_base 1..5

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE

FT cytosines are 5-methylcytosine"

FT modified\_base 16..20

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE

FT cytosines are 5-methylcytosine"

XX US6271030-B1.

XX 07-AUG-2001.

XX 14-JUN-2000; 2000US-00593711.

XX 14-JUN-2000; 2000US-00593711.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Butler MM, Wyatt J;

XX WPI; 2002-214451/27.

XX Novel antisense compound targeted to nucleic acids encoding human or

XX mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for

XX inhibiting expression of human or mouse C/EBP beta in cells/tissues.

XX Claim 1; Col 43-44; 69pp; English.

XX Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted

XX to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)

XX gene, which inhibit its expression. The antisense oligonucleotides were

XX designed to target different regions of the human and/or mouse C/EBP

XX alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels

XX by quantitative real-time PCR. The C/EBP family of proteins are a family

XX of transcription factors which regulate the expression of a wide range of

XX genes that control normal tissue development, cellular function, cellular

XX proliferation and functional differentiation. C/EBP beta (also known as

XX C/EBP2, LAP, TCFS, CRP2, NF16, IL6BP, NF-M, AGP/EBP and Apc/EBP)

XX primarily regulates hormone responsiveness and oxidative stress responses

CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is  
 CC thought to be involved in carbohydrate metabolism, immunity, the Th1  
 CC response, female fertility and gluconeogenic pathways. C/EBP beta is  
 CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the  
 CC highest expression found in the lung. It is also expressed at a higher  
 CC level in malignant ovarian tissue compared with normal ovarian tissue,  
 CC and its expression in pancreas is upregulated in response to chronically  
 CC elevated levels of glucose, indicating that it is involved in the  
 CC impairment of insulin secretion in type II diabetes. The oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with C/EBP beta expression, such as cancer  
 CC (particularly ovarian cancer), tumour formation, diabetes (particularly  
 CC type II diabetes), infection, or inflammation

XX Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 133 GAGACAGCTGCTCCCTTC 152  
 Db 1 GCGACAGCTGCTCCACCTTC 20

RESULT 56  
 AB194414  
 ID AB194414 standard; DNA; 20 BP.

XX AB194414;  
 AC  
 XX  
 DT 29-JUN-2002 (first entry)

XX Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:180.

XX  
 XX Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;  
 KM LAP; TCF5; CRP2; NFIL6; IL6BP; NF-M; AGP/EBP; Apc/EBP;  
 KM transcription factor; tissue development; cellular function;  
 KM proliferation; differentiation; hormone responsiveness;  
 KM oxidative stress response; IL-6 signalling mediator; interleukin-6;  
 KM carbohydrate metabolism; immunity; Th1 response; female fertility;  
 KM gluconeogenesis; ovarian; cancer; tumour formation; type II diabetes;  
 KM infection; inflammation; expression inhibition; phosphorothioate;  
 KM antisense oligonucleotide; ss.

XX  
 OS Mus musculus.

XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT modified\_base 1..5  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
 FT cytosines are 5-methylcytosine"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
 FT cytosines are 5-methylcytosine"

XX  
 XX US6271030-B1.  
 XX  
 XX 07-AUG-2001.  
 XX  
 XX 14-JUN-2000; 2000US-00593711.  
 XX  
 XX 14-JUN-2000; 2000US-00593711.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX

PI Montia BP, Butler MM, Wyatt J;  
 XX  
 DR WPI: 2002-214451/27.

XX  
 PT Novel antisense compound targeted to nucleic acids encoding human or  
 PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for  
 PT inhibiting expression of human or mouse C/EBP beta in cells/tissues.

XX  
 PS Example 17; Col 51-52; 69pp; English.

XX  
 XX Sequences AB194252-AB194476 represent antisense oligonucleotides targeted  
 CC to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)  
 CC gene, which inhibit its expression. The antisense oligonucleotides were  
 CC designed to target different regions of the human and/or mouse C/EBP  
 CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels  
 CC by quantitative real-time PCR. The C/EBP family of proteins are a family  
 CC of transcription factors which regulate the expression of a wide range of  
 CC genes that control normal tissue development, cellular function, cellular  
 CC proliferation and functional differentiation. C/EBP beta (also known as  
 CC C/EBP2, LAP, TCF5, CRP2, NFIL6, IL6BP, NF-M, AGP/EBP and Apc/EBP)  
 CC primarily regulates hormone responsiveness and oxidative stress responses  
 CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is  
 CC thought to be involved in carbohydrate metabolism, immunity, the Th1  
 CC response, female fertility and gluconeogenic pathways. C/EBP beta is  
 CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the  
 CC highest expression found in the lung. It is also expressed at a higher  
 CC level in malignant ovarian tissue compared with normal ovarian tissue,  
 CC and its expression in pancreas is upregulated in response to chronically  
 CC elevated levels of glucose, indicating that it is involved in the  
 CC impairment of insulin secretion in type II diabetes. The oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with C/EBP beta expression, such as cancer  
 CC (particularly ovarian cancer), tumour formation, diabetes (particularly  
 CC type II diabetes), infection, or inflammation

XX  
 SQ Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 136 ACACCTGCTCCCTTC 155  
 Db 1 ACACCTGCTCCACCTTC 20

RESULT 57  
 AB259163/C  
 ID AB259163 standard; DNA; 20 BP.

XX AB259163;  
 AC  
 XX  
 DT 28-APR-2003 (first entry)

XX  
 XX Nucleotide sequence of antisense oligo r-invent102.

XX  
 DE AChE; acetylcholinesterase; neuroprotective; relaxant; vasotropic;  
 KM anticonvulsant; neuroleptic; gene therapy; antisense; rat; ss.

XX  
 OS Synthetic.  
 OS Rattus sp.

XX  
 XX WO2003002739-A1.  
 XX  
 XX 09-JAN-2003.  
 XX  
 XX 23-MAY-2002; 2002WO-IL000411.  
 XX  
 XX 24-MAY-2001; 2001IL-00143379.  
 XX  
 XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX  
 XX Soreq H;  
 XX

XX WPI; 2003-210276/20.

DR New composition comprising an the antisense oligodeoxynucleotide hEN101,  
XX useful for treating or preventing a progressive neuromuscular disorder,  
PT e.g. myasthenia gravis, Eaton-Lambert disease, muscular dystrophy or  
PT sclerosis.

XX Example; Page 37; 84pp; English.

XX The invention relates to a pharmaceutical composition, which comprises an  
CC antisense oligonucleotide hEN101 that inhibits the human AChE  
CC (acetylcholinesterase) mRNA. The composition is for the treatment and/or  
CC prevention of a progressive neuromuscular disorder, for improving  
CC straining, and/or for use in chronic muscle fatigue. This composition  
CC facilitates the passage of compounds through the blood-brain barrier  
CC (BBB). It is useful for treating and/or preventing a progressive  
CC neuromuscular disorder, particularly a disorder associated with an excess  
CC of AChE mRNA or protein, an excess of acetylcholinesterase 'readthrough',  
CC variant or isoform (AChE-R) mRNA, or impairment of cholinergic  
CC transmission. The composition is also useful for treating and/or  
CC preventing a progressive neuromuscular disorder involving muscle  
CC distortion, muscle re-innervation or neuromuscular junction (NMJ)  
CC abnormalities, e.g. myasthenia gravis, Eaton-Lambert disease, muscular  
CC dystrophy, amyotrophic lateral sclerosis, post-traumatic stress disorder  
CC (PTSD), multiple sclerosis, dysionia, post-stroke sclerosis, post-injury  
CC muscle damage, excessive re-innervation, post-surgery paralysis of  
CC unknown origin, or post-exposure to AChE inhibitors. The composition is  
CC also useful for improving straining in physical exercise or in decreasing the  
CC muscle fatigue. This is also useful for treating conditions affecting the  
CC central nervous system, where the BBB would normally impede their  
CC delivery, e.g. ischaemia, brain tumours, hypoxia, epilepsy, anxiety or  
CC schizophrenia. The present sequence represents a rat AChE mRNA inhibiting  
CC antisense oligo

XX Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;

XX Query Match 6.4%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 CCTCTCATTTCTCTCTCC 121  
Db 20 CCTCTCTCTCTCTCTCTCC 1

RESULT 58  
ACCA4831/c  
ID ACC4831 standard; DNA; 20 BP.

XX ACC4831;

XX 11-AUG-2003 (first entry)

XX Campylobacter jejuni wlaK gene PCR primer LS16.

XX Infection; classification; glycosylation; wlaK gene; antibacterial; PCR;  
KM primer; ss.

XX Campylobacter jejuni.

XX WO2003020958-A2.

XX 13-MAR-2003.

XX 03-SEP-2002; 2002WO-EP009857.

XX 04-SEP-2001; 2001EP-00307499.

XX (EXPO-) EXPONENTIAL BIOTHERAPIES INC.

XX Carlton RM, Wren BW;

DR WPI; 2003-300898/29.

XX Producing progeny of bacteriophages having genes encoding proteaseous  
PT molecules allowing binding of the phage to Campylobacter spp, by  
PT contacting phage with Campylobacter mutant devoid of component present in  
PT wild-type.

XX Example 1; Page 26; 66pp; English.

XX The present sequence is PCR primer LS16 for the Campylobacter jejuni wlaK  
CC gene. LS16 was used in the construction of an insertional knockout mutant  
CC of the wlaK gene of C. jejuni NCTC 11168. Mutagenesis of the gene was  
CC shown to disrupt binding by SBA lectin, and a role in protein  
CC glycosylation was indicated. The invention relates to methods for the  
CC detection, diagnosis and treatment or prevention of Campylobacter  
CC infections, especially in poultry. A method is provided for producing or  
CC selecting for progeny of phage comprising a nucleic acid encoding a  
CC protein allowing targeting or binding of the phage to Campylobacter spp.  
CC This involves contacting a phage library with a Campylobacter spp. mutant  
CC devoid of a surface component present in the wild-type, e.g. a  
CC glycosylated component. The phage can be used in the classification of a  
CC C. jejuni variant, and in a pharmaceutical composition for treating a  
CC Campylobacter infection

XX Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

XX Query Match 6.4%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 117 GCTCCCACTTGTGATGAGA 136  
Db 20 GCTCCCACTTGTGATGAGA 1

RESULT 59  
ADG47261/c  
ID ADG47261 standard; DNA; 20 BP.

XX ADG47261;

XX 11-MAR-2004 (first entry)

XX Human IGF-II antisense oligonucleotide #GRI4009.

XX Insulin like growth factor II; IGF-II; tumour; metastasis; cytostatic;  
KM gene therapy; antisense; human; ss.

XX Homo sapiens.

XX US2002187954-A1.

XX 12-DEC-2002.

XX 17-APR-2002; 2002US-00125181.

XX 23-APR-1998; 98US-0082791P.

XX 22-APR-1999; 99US-00295593.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX Wright JA, Young AH, Lee YS;

XX WPI; 2004-040950/04.

XX Inhibiting the growth of a human tumor by administering a cytostatic  
PT antisense oligonucleotide of twenty to one hundred nucleotides.

XX Claim 7; SEQ ID NO 9; 41pp; English.

XX The present invention relates to oligonucleotides complementary to  
CC insulin like growth factor II (IGF-II) genes which modulate tumour cell  
CC growth in mammals. The invention is useful for inhibiting the growth or





Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 110 TTCTCTGCTCCGACTCTG 129  
 |||||  
 Db 1 TTCTCTGCTCCGACTTTGG 20

RESULT 62  
 ADP12005/c  
 ID ADP12005 standard; DNA; 20 BP.

AC ADEP12005;  
 DT 12-AUG-2004 (first entry)  
 XX

DE Set 2 right PCR primer for marker probe #111.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;  
 KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

XX Homo sapiens.

OS WO2004042346-A2.

PN 21-MAY-2004.

PD 24-APR-2003; 2003WO-US012346.

PF 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Mohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
 PI Rosenberg S;

XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,  
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant  
 PT rejection, in an individual, comprises detecting the expression level of  
 PT the genes.

PS Claim 58; SEQ ID NO 2014; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant  
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual  
 CC comprising detecting the expression level of one or more genes. The  
 CC methods, system and kits are useful in diagnosing or monitoring  
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
 CC islet, lung, bone marrow or stem cell transplant rejection,  
 CC xenotransplant rejection or mechanical organ replacement rejection, in an  
 CC individual. The method is also useful in assessing the immune status of  
 CC an individual. The methods are also useful in diagnosing and monitoring  
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
 CC viral, bacterial or fungal infection. The present sequence represents a  
 CC primer for a 50 mer oligonucleotide marker for diagnosis and monitoring  
 CC of allograft rejection and other disorders.

XX Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 134 AGACACTGCTCCCTTCT 153  
 |||||  
 Db 20 AGACCTCTCTCCCTTCT 1

RESULT 63  
 ADP82177/c

ID ADP82177 standard; DNA; 20 BP.

XX ADP82177;

DT 26-AUG-2004 (first entry)

DE Human DRI-associated protein 1 target oligonucleotide #9.

XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;  
 KM developmental disorder; therapy; human; ss.

XX Homo sapiens.

PN US2004110703-A1.

PD 10-JUN-2004.

PF 10-DEC-2002; 2002US-00317279.

PR 10-DEC-2002; 2002US-00317279.

XX (ISIS-) ISIS PHARM INC.

XX Chiang M, Dobie KW;

DR WPI; 2004-440383/41.

XX New compounds, particularly oligonucleotides targeted to a nucleic acid  
 PT encoding DRI-associated protein 1, useful for treating diseases  
 PT associated with DRI-associated protein 1, e.g. developmental disorders.  
 XX Example 15; SEQ ID NO 56; 33pp; English.

XX The present sequence is directed to antisense oligonucleotides targeted  
 CC to DRI-associated protein 1 (also known as DRAP1 and negative cofactor 2  
 CC alpha (NC2-alpha)) and which modulates to the expression of DRI-  
 CC associated protein 1. The invention is useful for treating a disease or  
 CC condition associated with DRI-associated protein 1 such as a  
 CC developmental disorder. The present sequence is human DRI-associated  
 CC protein 1 target oligonucleotide. This sequence is used in the  
 CC exemplification of the invention.

XX Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 108 CATTCTCTGCTCCGACTCT 127  
 |||||  
 Db 20 CATCTCTGCTCCGACTCT 1

RESULT 64  
 ADP82163  
 ID ADP82163 standard; DNA; 20 BP.

AC ADP82163;

DT 26-AUG-2004 (first entry)

DE Human DRI-associated protein 1 antisense oligonucleotide ISIS #171311.

XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;  
 KM developmental disorder; therapy; human; antisense;

XX phosphorothioate backbone; ss.

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT modified\_base 1..20  
 FT /\*tag= b

```
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone where all cytidines are
FT 5-methyl cytidines"
FT modified_base
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2, -methoxyethyl nucleotides"
FT modified_base
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2, -methoxyethyl nucleotides"
XX US200410703-A1.
XX 10-JUN-2004.
XX 10-DEC-2002; 2002US-00317279.
XX 10-DEC-2002; 2002US-00317279.
XX (ISIS-) ISIS PHARM INC.
XX Chiang M, Dobie KW;
XX MPI; 2004-440383/41.
XX New compound, particularly oligonucleotides targeted to a nucleic acid
XX encoding DRI-associated protein 1, useful for treating diseases
XX associated with DRI-associated protein 1, e.g. developmental disorders.
XX Example 15; SEQ ID NO 42; 33pp; English.
XX The present sequence is directed to antisense oligonucleotides targeted
XX to DRI-associated protein 1 (also known as DRP1 and negative cofactor 2
XX alpha (NC2-alpha)) and which modulates to the expression of DRI-
XX associated protein 1. The invention is useful for treating a disease or
XX condition associated with DRI-associated protein 1 such as a
XX developmental disorder. The present sequence is human DRI-associated
XX protein 1 antisense oligonucleotide. This sequence is used in the
XX exemplification of the invention.
XX Sequence 20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 6.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 40;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 108 CATTCTCTGCTCCACTCT 127
XX 1 CATCTCTCTGCTCCAGTCT 20
XX
XX RESULT 65
XX AEC34439/c
XX ID AEC34439 standard; DNA; 20 BP.
XX AC AEC34439;
XX 17-NOV-2005 (first entry)
XX Human EGFR regulatory region SNP detection primer SEQ ID NO.10.
XX 66; primer; PCR; Epidermal growth factor receptor; EGFR; cancer;
XX cytosclatic; neoplasm; polymorphism; diagnostic.
XX Homo sapiens.
XX WO2005085473-A2.
XX 15-SEP-2005.
XX 01-MAR-2005; 2005WO-US006559.
XX
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PR 01-MAR-2004; 2004US-0549069P.
XX (UYGH-) UNIV CHICAGO.
XX Ratain MJ, Liu W, Innocenti F;
XX MPI; 2005-630736/64.
XX
XX Evaluating potential efficacy of epidermal growth factor receptor (EGFR)-
XX targeting therapeutic agent for treating cancer or disease associated
XX with dysregulation of EGFR, by determining sequence of polymorphism in
XX EGFR genes in patient.
XX Example 1; SEQ ID NO 10; 66pp; English.
XX The invention relates to a method of evaluating (M1) the potential
XX efficacy of an epidermal growth factor receptor (EGFR)-targeting
XX therapeutic agent for treating cancer or a disease associated with the
XX regulation of EGFR in a patient, comprising determining the sequence of a
XX polymorphism in one or both EGFR genes in the patient. Also included are:
XX predicting (M2) the clinical prognosis for a cancer patient, comprising
XX determining the sequence of a polymorphism in one or both EGFR genes in
XX the patient; evaluating (M3) a patient's risk of toxicity to an EGFR-
XX targeting therapeutic agent, comprising determining the sequence of a
XX polymorphism in one or both EGFR genes in the patient; predicting the
XX expression level of EGFR in a cell, comprising determining the sequence
XX at position 216 in one or both alleles of the EGFR gene in the cell,
XX where thymine at position 216 in one or both alleles is indicative of a
XX higher expression level; and a kit for performing (M1), comprising a
XX nucleic acid, or restriction enzyme for determining the sequence of a
XX polymorphism in an EGFR gene locus. (M1) is useful for evaluating the
XX potential efficacy of EGFR-targeting therapeutic agent, where the EGFR-
XX targeting therapeutic agent is an EGFR-tyrosine kinase inhibitor or
XX monoclonal antibody. The present sequence represents a PCR primer used to
XX detect single nucleotide polymorphisms (SNPs) in the human EGFR
XX regulatory region.
XX Sequence 20 BP; 7 A; 1 C; 11 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 6.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 40;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 101 CCCCTCATCTCTCTCTC 120
XX 20 CTCTCGCATCTCTCTCTC 1
XX
XX RESULT 66
XX AAQ08505/c
XX ID AAQ08505 standard; DNA; 21 BP.
XX AC AAQ08505;
XX 25-MAR-2003 (revised)
XX 29-MAR-1992 (first entry)
XX Sequence of 5' probe, complementary to a sequence encoding part of the
XX human interleukin-3 (huIL-3) leader.
XX Lymphokine; bone marrow proliferation; cytopenia therapy; ss.
XX Homo sapiens.
XX WO9001039-A.
XX 08-FEB-1990.
XX 14-JUN-1989; 89WO-US002599.
XX 20-JUL-1988; 88US-00221699.
XX (IMMV) IMMUNEX CORP.
XX
```

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XX Anderson DM, Coeman DJ, Price VL;
PI
XX WPI; 1990-067162/09.
DR
XX Compens. contg. recombinant non-glycosylated human interleukin-3 - has
PT increased biological activity and binding affinity, for treating
PT cytopenias.
XX
XX Example; Page 10; 23pp; English.
XX
XX The inventors claim a pharmaceutical compsn. which contains an effective
CC amt. of a recombinant human interleukin-3 protein analogue, rhIL-3,
CC (Asp15, Asp70). The rhIL-3 analogue has AA SQ in AAR09326. The compsn.
CC may also comprise the N-terminal octapeptide in AAR09327, and a diluent
CC and 1 or more than 1 biological response modifier. The compsn. has a
CC biological specific activity of equal to or more than 4.0 x 10 to the 7
CC mcg/mg in a human bone marrow proliferation assay, and a binding affinity
CC for human monocyte IL-3 receptors of equal to or more than 4.0 x 10 to
CC the 10 (M to the minus 1). (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 107 TCATTCTCCGCTCCCACTC 126
DB 20 TCCTGCTCTGCTCCCACTC 1

RESULT 67
AAQ10344/C
ID AAQ10344 standard; DNA; 21 BP.
XX
XX AAQ10344;
XX
XX 25-MAR-2003 (revised)
DT 10-APR-1991 (first entry)
XX
XX Probe to the human interleukin-3 gene.
XX
XX huIL-3; urticaria; granulopoesis; erythropoesis; thrompoeosis;
KM neutropaenia; anaemia; thrombocytopenia; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9100350-A.
PN
XX
XX 10-JAN-1991.
PD
XX 30-JUN-1989; 89US-00374667.
PF
XX 30-JUN-1989; 89US-00374667.
PR
XX (IMMV ) IMMUNEX CORP.
PA
XX Urdal DL, Sassenfeld H;
PI
XX WPI; 1991-036745/05.
DR
XX Non-glycosylated human interleukin-3 analog proteins - expressed by
PT transformed yeast of Saccharomyces cerevisiae which do not give
PT detectable urticaria.
XX
XX Example A; Page 7; 18pp; English.
XX
XX Probes were used in the isolation of human IL-3, which was then expressed
CC in a modified form, with a mutation in the N-glycosylation sites. The
CC modified IL-3 does not result in urticaria or infiltration of mast cells
CC and lymphocytes into the dermis. It stimulates granulopoesis,
CC erythropoesis and thrompoeosis in vivo and may used to treat

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CC neutropaenia, anaemia and thrombocytopenia. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 107 TCATTCTCCGCTCCCACTC 126
DB 20 TCCTGCTCTGCTCCCACTC 1

RESULT 68
AAQ42803/C
ID AAQ42803 standard; cDNA; 21 BP.
XX
XX AAQ42803;
XX
XX 25-MAR-2003 (revised)
DT 15-SEP-1993 (first entry)
XX
XX Human IL-3 probe.
DE
XX Mast cell growth factor; interleukin; haematopoietic progenitor cell;
KM bone marrow cell; proliferation; differentiation; functional activation;
KW peripheral blood leukocyte; circulating granulocyte; ss.
XX
XX Synthetic.
XX
XX WO9310229-A1.
PN
XX
XX 27-MAY-1993.
PD
XX 19-NOV-1992; 92WO-US009848.
PF
XX 22-NOV-1991; 91US-00797553.
PR
XX (IMMV ) IMMUNEX CORP.
PA
XX Williams DE;
PI
XX WPI; 1993-182546/22.
DR
XX MGE-Interleukin-3 fusion proteins having enhanced activity - used for
PT regulating immune and inflammatory responses.
PT
XX
XX Example 1; Page 17; 41pp; English.
XX
XX Two oligonucleotides were synthesised, with sequences complementary to
CC selected 5' and 3' sequences of the huIL-3 gene. The 5' probe, has the
CC complementary to a sequence encoding part of the huIL-3 leader, has the
CC sequence given in AAQ42803. The 3' probe, corresp. to a region encoding
CC amino acids 123-130 of the mature protein, has the sequence given in
CC AAQ42804. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 107 TCATTCTCCGCTCCCACTC 126
DB 20 TCCTGCTCTGCTCCCACTC 1

RESULT 69
AAZ61533/C
ID AAZ61533 standard; DNA; 21 BP.
XX
XX AAZ61533;
AC

```

XX	19-JUN-2000	(first entry)
DT		
DE	primer 6U for a human 5'-OT EST (oxytocin expressed sequence tag).	
KW	Oxytocin expressed sequence tag; 5'-OT EST; obesity; fertility; male;	
KW	transgenic animal; human late onset obesity; late onset visceral obesity;	
KW	male infertility; wasting; anorexia; cachexia; malabsorptive state;	
KW	catabolic state; inflammatory condition; Crohn's disease; AIDS wasting;	
KW	burn; cancer; bone disease; PCR primer; probe; ss.	
OS	Homo sapiens.	
PN	W0200009686-A1.	
PD	24-FEB-2000.	
XX		
PF	12-AUG-1999; 99MO-GB002658.	
PR	12-AUG-1998; 98GB-00017566.	
PR	06-MAY-1999; 99GB-00010522.	
XX		
PA	(MED1-) MEDICAL RES COUNCIL.	
XX		
PI	Robinson ICAF, Scove JF, Flavell D, Wells SE, Le Tissier P;	
DR	WPI, 2000-224331/19.	
PT	New anti-obesity polypeptide useful for treating obesity or infertility	
PT	in mammals.	
XX		
PS	Disclosure; Page 26; 162pp; English.	
XX		
CC	PCR primers and probes AAG1533-34 are used to amplify and identify human	
CC	5'-OT-EST (oxytocin expressed sequence tag) cDNA sequences. The 5'-OT EST	
CC	gene is involved in the control of obesity and fertility in males. 5'-OT	
CC	EST nucleic acids are useful for producing transgenic animals. The	
CC	transgenic animals created serve as a model for human late onset obesity	
CC	and other related disorders and are also used for identifying the genetic	
CC	cause of obesity. Compounds which modulate 5'-OT EST expression or	
CC	activity are useful in the treatment or modulation of late onset visceral	
CC	obesity or male infertility particularly in the disorders related to	
CC	these conditions such as wasting, or anorexia, or cachexia associated	
CC	with prolonged illness, or malabsorptive states or catabolic states	
CC	associated with other diseases such as inflammatory conditions, Crohn's	
CC	disease or AIDS wasting, or burns, or cancer, or bone disease	
CC		
XX	Sequence 21 BP; 6 A; 3 C; 12 G; 0 T; 0 U; 0 Other;	
SO		
	Query Match 6.4%; Score 15.2; DB 1; Length 21;	
	Best Local Similarity 85.0%; Pred. No. 39;	
	Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0	
OY	139 CCTGCTCCCTTCCTTC 158	
DB	20 CCTGCTCCCGCTCTCTGC 1	
RESULT 70		
ADP29145		
ID	ADP29145 standard; DNA; 21 BP.	
XX		
AC	ADP29145;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Human secreted protein encoding sequence SEQ ID #1143.	
XX		
KW	Cycostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; Inflammatory; Immune; ds; human secreted protein.	
XX		
OS	Homo sapiens.	
XX		

PN	MO2004035732-A2.
XX	
PD	29-APR-2004.
XX	
PF	28-AUG-2003; 2003MO-US026780.
XX	
PR	29-AUG-2002; 2002JUS-0406576P
PR	29-AUG-2002; 2002JUS-0406579P
PR	29-AUG-2002; 2002JUS-0406585P
PR	29-AUG-2002; 2002JUS-0406588P
PR	29-AUG-2002; 2002JUS-0406608P
PR	29-AUG-2002; 2002JUS-0406611P
PR	29-AUG-2002; 2002JUS-0406612P
PR	29-AUG-2002; 2002JUS-0406616P
PR	29-AUG-2002; 2002JUS-0406640P
PR	29-AUG-2002; 2002JUS-0406646P
PR	29-AUG-2002; 2002JUS-0406653P
PR	29-AUG-2002; 2002JUS-0406655P
PR	29-AUG-2002; 2002JUS-0406666P
PR	17-SEP-2002; 2002JUS-0410937P
PR	17-SEP-2002; 2002JUS-0410946P
PR	17-SEP-2002; 2002JUS-0410947P
PR	17-SEP-2002; 2002JUS-0410958P
PR	17-SEP-2002; 2002JUS-0410959P
PR	17-SEP-2002; 2002JUS-0410960P
PR	17-SEP-2002; 2002JUS-0410961P
PR	17-SEP-2002; 2002JUS-0410962P
PR	17-SEP-2002; 2002JUS-0411019P
PR	17-SEP-2002; 2002JUS-0411022P
PR	17-SEP-2002; 2002JUS-0411023P
PR	17-SEP-2002; 2002JUS-0411024P
PR	17-SEP-2002; 2002JUS-0411032P
PR	17-SEP-2002; 2002JUS-0411035P
PR	17-SEP-2002; 2002JUS-0411037P
PR	17-SEP-2002; 2002JUS-0411041P
PR	17-SEP-2002; 2002JUS-0411045P
PR	17-SEP-2002; 2002JUS-0411046P
PR	17-SEP-2002; 2002JUS-0411048P
PR	17-SEP-2002; 2002JUS-0411052P
PR	17-SEP-2002; 2002JUS-0411055P
PR	17-SEP-2002; 2002JUS-0411073P
PR	17-SEP-2002; 2002JUS-0411082P
PR	17-SEP-2002; 2002JUS-0411101P
PR	17-SEP-2002; 2002JUS-0411111P
PR	18-APR-2003; 2003JUS-0463700P
PR	18-APR-2003; 2003JUS-0463708P
PR	18-APR-2003; 2003JUS-0463716P
PR	18-APR-2003; 2003JUS-0463732P
PR	02-MAY-2003; 2003JUS-0466719P
PR	02-MAY-2003; 2003JUS-0466720P
PR	02-MAY-2003; 2003JUS-0467203P
PR	02-MAY-2003; 2003JUS-0467230P
PR	19-MAY-2003; 2003JUS-0471306P
PR	19-MAY-2003; 2003JUS-0471336P
PR	22-MAY-2003; 2003JUS-0472420P
PR	02-JUN-2003; 2003JUS-0472430P
PR	09-JUN-2003; 2003JUS-0476609P
PR	09-JUN-2003; 2003JUS-0476614P
PR	09-JUN-2003; 2003JUS-0485218P
PR	08-JUL-2003; 2003JUS-0485223P
PR	08-JUL-2003; 2003JUS-0485224P
PR	08-JUL-2003; 2003JUS-0485252P
PR	14-JUL-2003; 2003JUS-0486446P
PR	14-JUL-2003; 2003JUS-0486480P
PR	15-JUL-2003; 2003JUS-0486691P
PR	08-AUG-2003; 2003JUS-0486690P
PR	08-AUG-2003; 2003JUS-0493341P
PR	08-AUG-2003; 2003JUS-0493373P
PR	08-AUG-2003; 2003JUS-0493377P

PR 08-AUG-2003; 2003US-0493577P.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang WM, Kochakota S, Haisan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
DR WPI; 2004-348438/32.  
XX  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX  
XX Claim 1; SEQ ID NO 1143; 428bp; English.  
XX  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein encoding sequence. The  
CC present sequence is available on WIPOMED and is not in the specification.  
XX  
XX  
SQ Sequence 21 BP; 1 A; 13 C; 0 G; 7 T; 0 U; 0 Other;  
Query Match 6.4%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 139 CCTGCTCCCTCTCTCTTC 158  
Db 1 CCTCTCTCTCTCTCTTC 20  
RESULT 71  
ADU26666  
ID ADU26666 standard; DNA; 21 BP.  
XX  
XX ADU26666;  
XX  
XX 27-JAN-2005 (first entry)  
XX  
XX Knock-down target sequence #64.  
XX  
XX de; RNA production; protein production; drug development;  
XX  
XX knock-down target.  
XX  
XX Unidentified.  
XX  
XX OS  
XX PN WO2004094636-A1.  
XX  
XX 04-NOV-2004.  
XX  
XX 24-APR-2003; 2003WO-EP004362.  
XX  
XX 24-APR-2003; 2003WO-EP004362.  
XX  
XX PR 24-APR-2003; 2003WO-EP004362.  
XX  
XX (GALA-) GALAPAGOS GENOMICS NV.  
XX  
XX PA (VSCN/) VAN DER SCHUREN J.  
XX  
XX PI Arts GJF, Lambrecht WJ, Djokic K, Clasen RJ, Meisic E;  
PI Griffioen S, Bergs CUI;  
XX  
XX WPI; 2004-775940/76.  
XX  
XX  
XX New knockdown sequences, useful in lowering the amount of RNA and/or  
PT protein production in cells used in drug development process.  
XX  
XX  
XX Claim 11; SEQ ID NO 67; 402bp; English.  
XX  
XX The invention relates to a polynucleotide comprising an RNA sequence. The

CC polynucleotides, vector, libraries, and method are useful in lowering the  
CC amount of RNA and/or protein production in cells used in drug development  
CC process. The present sequence represents a knock-down target sequence.  
XX  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 U; 0 Other;  
Query Match 6.4%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 24 CCTCATGATGCTTTAGTGC 43  
Db 2 CATCATGAGCGTTAGTGC 21  
RESULT 72  
ACL41023/C  
ID ACL41023 standard; DNA; 21 BP.  
XX  
XX ACL41023;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX  
XX C20orf103 target oligonucleotide, SEQ ID 2095.  
XX  
XX  
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.  
XX  
XX  
XX Homo sapiens.  
XX  
XX WO200501092-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
XX  
XX  
XX Claim 3; SEQ ID NO 2095; 113bp; English.  
XX  
XX  
XX The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLCA3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC target oligonucleotide from one such CRTP for which short interfering  
CC RNAs (siRNA) were produced. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPOMED at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 21 BP; 9 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 6.4%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 146 CCCCTTCCTCTGCGATG 165  
 |||||  
 DB 20 CCACCTTCCTCTGCGATG 1

## RESULT 73

ID AD219613  
 AD219613 standard; RNA; 21 BP.

AC AD219613;

DT 16-JUN-2005 (first entry)

DE Human siRNA targeted against the human PIK3CB gene Seq 497.

XX screening; synthetic lethal interaction; RNA interference;  
 KW gene silencing; siRNA; short interfering RNA; tumor suppressor; cancer;  
 KW cytostatic; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc\_feature 20..21

FT /\*tag= A  
 /note= "dtr dinucleotide to enhance siRNA binding"

PN WO2005031002-A2.

PD 07-APR-2005.

PE 22-SEP-2004; 2004WO-US031629.

XX 22-SEP-2003; 2003US-0505229P.

PR 27-FEB-2004; 2004US-0546568P.

PR 17-MAR-2004; 2004US-0554284P.

PA (ROSE-) ROSETTA INPHARMATICS LLC.

XX (MERI) MERCK & CO INC.

P1 Linsley PS, Mao M, Kim AS, Friend SH, Bartz SR, Cleary MA;

DR WPI; 2005-273396/28.

XX Identifying a gene product modulating the effect of an agent comprises

PT transfecting the cells with small interfering RNAs.

XX Example 3; SEQ ID NO 497; 284bp; English.

PS This invention relates to a novel screening method for identifying a gene  
 CC whose product modulates the effect of an agent on a cell of a cell type.  
 CC Specifically, it refers to identifying lethal/ synthetic lethal  
 CC interactions between a gene (or its product) and an agent such as a drug,  
 CC using RNA interference. The present invention describes screening of an  
 CC siRNA library for genes that interact with inhibitors of the KSP gene  
 CC (kinesin-like motor protein gene). In particular it illustrates STX6 and  
 CC TP53 as two genes that each independently exhibit synthetic lethal  
 CC interactions with KSP such that they can be used therapeutically to  
 CC inhibit tumor cell growth and hence for the treatment of cancer. The  
 CC invention further describes RNAi-mediated silencing of the CHEK1 and TP53  
 CC genes that leads to synthetic lethality in human tumor cells. It also  
 CC provides semi-automated siRNA screens for the identification of cellular  
 CC response genes that enhance or reduce cell killing by DNA damaging  
 CC agents. Accordingly, compositions derived thereof be used therapeutically  
 CC such that they exhibit cytostatic activity. This oligonucleotide sequence  
 CC is an siRNA oligo that was used to identify a human gene that enhances  
 CC cell killing by DNA damaging agents (doxorubicin screen), given in an  
 CC exemplification of the invention.

XX Sequence 21 BP; 4 A; 3 C; 7 G; 2 T; 5 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;

Best Local Similarity 65.0%; Pred. No. 39;

Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 OY 64 AGTTACCTGAGAGCTGTT 83  
 |||||  
 DB 2 AGUTCAUGCAGCGCGT 21

## RESULT 74

ID AEC02602  
 AEC02602 standard; DNA; 21 BP.

AC AEC02602;

DT 03-NOV-2005 (first entry)

DE Human IGE short interfering nucleic acid SEQ ID NO 205.

XX anti-allergic; anti-inflammatory; antiasthmatic; dermatological;  
 KW immunosuppressive; expression; RNA interference; allergy;  
 KW atopic dermatitis; urticaria; dermatological; dermatological disease;  
 KW immediate type hypersensitivity; immunosuppressive; asthma;  
 KW antiasthmatic; allergic rhinitis; anti-allergic; anti-inflammatory;  
 KW ear, nose, throat disease; inflammation; respiratory disease;  
 KW immune disorder; IGE; short interfering nucleic acid; siNA;  
 KW gene silencing; ss.

XX Homo sapiens.

PN WO2005080410-A1.

PD 01-SEP-2005.

PE 21-FEB-2005; 2005WO-NZ000021.

PR 20-FEB-2004; 2004US-0546434P.

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Murison GJ, Grigor MR, Havukkala IU, Munro G;

P1 Abernethy N, Webster G;

DR WPI; 2005-591970/60.

XX New composition comprises small interfering nucleic acid molecule (siNA)  
 PT capable of reducing expression of a target gene that is active in a IGE-  
 PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic  
 PT dermatitis.

PS Disclosure; SEQ ID NO 205; 178bp; English.

XX The invention describes a composition comprising a small interfering  
 CC nucleic acid molecule (siNA) capable of reducing expression of a target  
 CC gene that is active in a IGE-mediated disorder; a genetic construct that  
 CC expresses the siNA, and a binding agent that specifically binds to a  
 CC target antigen expressed on the surface of the cell. Also described are:  
 CC a method for the treatment of an IGE-mediated disorder in a patient;  
 CC prevention of IGE-mediated disorder in a patient; reduction of  
 CC eosinophilia in a patient; modulating an IGE-mediated immune response to  
 CC a specific antigen in a patient; and preventing or reducing the severity  
 CC of an immune response to a specific antigen in a patient. The composition  
 CC is useful in the preparation of a medicament useful for the treatment of  
 CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,  
 CC urticaria, atopic dermatitis, food allergies, diseases that benefit from  
 CC the reduction of eosinophilia in the tissues of the respiratory system,  
 CC or disorders having hypersensitivity immune reaction. This sequence  
 CC represents a siNA for suppression of human IGE expression.

XX Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 39; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 31 AATGGTTAGTGCATCCCC 50  
 CC |||||  
 CC AEC30534  
 Db 2 AATGGCTTGCGCTTCCC 21

RESULT 75  
 ID AEC30534 standard; DNA; 21 BP.  
 XX  
 AC AEC30534;  
 XX  
 DT 17-NOV-2005 (first entry)  
 XX  
 DE Human locus-specific oligonucleotide #1822.  
 XX  
 KW Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;  
 KW major histocompatibility complex; MHC; HLA; human leukocyte antigen;  
 KW immune disorder; inflammation; inflammatory bowel disease;  
 KW ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes;  
 KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;  
 KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;  
 KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;  
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;  
 KW idiopathic thrombocytopenia purpura; Sjogren's syndrome;  
 KW multiple sclerosis; Reiter's syndrome; psoriasis; anti-inflammatory;  
 KW gastroenteric-antigen; antileuk; immunomodulator; immunosuppressive;  
 KW antiarthritic; antirheumatic; antidiabetic; muscular-gen.;  
 KW neuroprotective; dermatological; antihypert; hepatotropic; antianemic;  
 KW hemostatic; ophthalmological; uropathic; antipsoriatic; ss;  
 KW SNP detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005082110-A2.  
 XX  
 PD 09-SEP-2005.  
 XX  
 PF 28-FEB-2005; 2005WO-US006628.  
 XX  
 PR 26-FEB-2004; 2004US-0547823P.  
 XX  
 PA (ILLU-) ILLUMINA INC.  
 XX  
 PI Oliphant A, Murray S;  
 XX  
 DR WPI; 2005-638856/65.  
 XX  
 XX Identifying single nucleotide polymorphism (SNP) haplotype that  
 PT correlates with the HLA type, useful for diagnosing an immunological or  
 PT inflammatory condition, comprises providing SNPs in the major  
 PT histocompatibility complex region.  
 XX  
 XX Example 1; SEQ ID NO 6554; 175bp; English.  
 XX  
 CC The invention relates to a method of identifying the nucleotide for each  
 CC of a set of single nucleotide polymorphisms (SNPs) in the major  
 CC histocompatibility complex (MHC) region in a population of individuals,  
 CC comprising providing the HLA type for the individuals and identifying an  
 CC SNP haplotype in the population that correlates with the HLA type, where  
 CC the SNP haplotype comprises the SNPs in the MHC region. The invention  
 CC also relates to a method of predicting the HLA type of an individual, a  
 CC method of determining the presence or absence of an allelic variant of an  
 CC MHC gene in an individual, a method of identifying an SNP haplotype that  
 CC correlates with susceptibility to a disease or condition, and a method of  
 CC determining the susceptibility of an individual to a disease or  
 CC condition. The disease or condition is an immune disorder or inflammatory  
 CC condition selected from inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,  
 CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,  
 CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic  
 CC lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,  
 CC pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia  
 CC purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and

CC psoriasis. This sequence represents a human locus-specific  
 CC oligonucleotide used in the scope of the invention.  
 XX  
 SQ Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Qy 174 ATTCCAGGAGCTTCACAAG 193  
 CC |||||  
 CC 1 ATTCCAGAGCTTCACAAG 20  
 Db

RESULT 76  
 ID AAT72472/c  
 XX AAT72472 standard; DNA; 20 BP.  
 XX  
 AC AAT72472;  
 XX  
 DT 29-SEP-1997 (first entry)  
 XX  
 DE Human CII-3 gene exon A primer HuGPS1.Forw1.  
 XX  
 KW Mammalian artificial chromosome; MAC; selectable marker; CII-3;  
 KW mitochondrial electron transport chain complex II; transgenic animal;  
 KW polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9716533-A1.  
 XX  
 PD 09-MAY-1997.  
 XX  
 PF 29-OCT-1996; 96WO-US017476.  
 XX  
 PR 31-OCT-1995; 95US-00550717.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Scheffler IE;  
 XX  
 DR WPI; 1997-272103/24.  
 XX  
 XX New mammalian artificial chromosomes - comprising a mammalian centromere  
 PT and a unique cloning site, used for stable expression of large fragments  
 PT of DNA.  
 XX  
 XX Example 2; Page 45; 71bp; English.  
 XX  
 CC Primers HuGPS1.Forw1 (AAT72472) and pUOS2.T7 (AAT72473) are respectively  
 CC complementary to exon A (see also AAT72462) and fragment Y (see also  
 CC AAT72465) of the human CII-3 gene that encodes a subunit (AAW21674) of  
 CC complex II of the human mitochondrial electron transport chain. They were  
 CC used to amplify genomic DNA from HeLa cells, hamster B9 cells, hamster  
 CC XEM5.1.1(+) cells containing a complete human chromosome 1, XEM5.1.1(-)  
 CC cells, and hamster XEM8.2.3 cells congt. mammalian artificial chromosome  
 CC MAC8.2.3. A PCR product of expected size (1.05 bp) was obtd. from HeLa,  
 CC XEM5.1.1(+) and XEM8.2.3 cell DNA, indicating that cloned human genomic  
 CC CII-3 sequences are present on chromosome 1, including the portion of  
 CC chromosome 1 comprising MAC8.2.3  
 XX

Qy 178 CAGGACTTCACAAG 192  
 CC |||||  
 CC 16 CAGGACTTCACAAG 2  
 Db

Query Match 6.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

RESULT 77
ADK96774/c
ID ADK96774 standard; DNA; 20 BP.
XX
XX
AC ADK96774;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #2494.
XX
XX human; single nucleotide polymorphism; SNP; ss; primer.
XX
XX Synthetic.
XX
XX JP2003259875-A.
XX
XX 16-SEP-2003.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX MPI; 2004-093977/10.
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
XX fragment from another set of sequences, or for detecting single
XX nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 5803; 2627bp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
XX Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 6.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 CCTCTCATTCTCCTG 117
Db 19 CCTCTCATTCTCCTG 5

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PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
XX Van Ommereen GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;
PI MPI; 2004-691060/67.
XX
XX
DR MPI; 2004-691060/67.
XX
XX
PT Generating an oligonucleotide for treating diseases, comprises
PT determining from a structure of RNA from an exon, a region that assumes a
PT structure hybridized to another part of the RNA and a region that is not
PT hybridized in the structure.
XX
XX Example 1; Page 89; 117bp; English.
XX
XX The invention relates to generating an oligonucleotide and involves
XX determining from a secondary structure of RNA from an exon, a region that
XX assumes a structure that is hybridized to another part of the RNA (closed
XX structure) and a region that is not hybridized in the structure (open
XX structure), and subsequently generating an oligonucleotide, where at
XX least a part of the oligonucleotide is complementary to the closed
XX structure and at least another part of the oligonucleotide is
XX complementary to the open structure. In generating an oligonucleotide,
XX the open and closed structures are adjacent to each other. The
XX oligonucleotide is complementary to a consecutive part of 14-50
XX nucleotides of the RNA. It also comprises RNA, where the RNA contains a
XX modification, preferably a 2'-O-methyl modified ribose (RNA) or
XX deoxyribose (DNA) modification. The pre-mRNA comprising the exon exhibits
XX undesired splicing in a subject. The absence of the exon from mRNA
XX produced from the pre-mRNA generates a coding region for a protein. The
XX gene from which the RNA comprising the exon is transcribed encodes an
XX aberrant Duchenne muscular dystrophy gene (DMD), a collagen VI alpha 1
XX gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dyfexlin gene
XX (DYF1), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular
XX dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). Preferably, the
XX gene is the DMD gene. The oligonucleotide, its equivalent, or the
XX compound is useful for at least in part altering recognition of the exon
XX or exons in a pre-mRNA; for the preparation of a medicament for the
XX treatment of an inherited disease; for inducing exon skipping in a pre-
XX mRNA; for altering exon-recognition in a pre-mRNA; for altering the
XX efficiency with which a splice donor or splice acceptor sequence is used
XX by a splicing machinery; for inducing exon-skipping of two, three, or
XX more exons in a pre-mRNA; or for inducing skipping of the at least two
XX exons and a sequence located between the at least two exons (intervening
XX sequence) on the pre-mRNA, where intervening sequence further comprises
XX exon or exons. Sequences ADS73865-ADS73903 represent antisense
XX oligonucleotides (AONs) used to study targeted skipping of 15 different
XX DMD exons.
SQ
Sequence 19 BP; 3 A; 3 C; 5 G; 0 T; 8 U; 0 Other;
QY Query Match 6.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 171 AAGATTCAGGACTTCA 188
Db 19 AAGATTCAGGACTTCA 2

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RESULT 78
ADS73903/c
ID ADS73903 standard; RNA; 19 BP.
XX
XX
AC ADS73903;
XX
XX
DT 16-DEC-2004 (first entry)
XX
DE DMD gene specific antisense oligonucleotide h59A0N2.
XX
XX DMD; Duchenne muscular dystrophy; collagen VI alpha 1; COL6A1;
XX myotubular myopathy 1; MTM1; dyfexlin; DYF1; laminin-alpha 2; LAMA2;
XX emery-dreyfuss muscular dystrophy; EMD; calpain 3; CAPN3; antisense; ss.
XX
XX Synthetic.
XX
XX WO2004083446-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-NL000196.
XX
XX 21-MAR-2003; 2003WO-NL000214.
XX

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RESULT 79
AEB93316/c
ID AEB93316 standard; DNA; 19 BP.
XX
XX
AC AEB93316;
XX
XX
DT 03-NOV-2005 (first entry)
XX
DE Human siRNA transcribed in the inventive optimized system, SEQ ID 79.
XX
XX Short interfering RNA; ds; gene silencing; RNA interference;
XX pharmaceutical; siRNA.
XX
XX Homo sapiens.
XX

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PN WO2005078089-A1.
XX
PD 25-AUG-2005.
XX
PF 03-FEB-2005; 2005WO-EP001079.
XX
PR 11-FEB-2004; 2004EP-00003079.
PR 03-AUG-2004; 2004EP-00018376.
XX
PA (UYBE-) UNIV BERLIN CHARITE.
XX
PI Trusa M, Hagemeyer C;
XX
DR WPI; 2005-582876/59.
XX
PT Small interfering RNA molecule useful for generating transgenic non-human
PT animal, comprises 5 prime-protruding end that corresponds to consensus
PT sequence of nucleotides of natural promoter of DNA-dependent RNA-
PT polymerase.
XX
PS Example 1, SEQ ID NO 79; 56pp; English.
XX
CC The invention relates to a small interfering (siRNA) molecule (I),
CC comprising a 5'-protruding end that corresponds to the consensus sequence
CC of the nucleotides 0 to +5 of the natural promoter of a DNA-dependent RNA
CC -polymerase (e.g. T7, T3 or SP6 polymerase). Also included are a DNA
CC molecule encoding the siRNA, an expression vector comprising the DNA, a
CC host cell transfected/infected with the vector, a transgene comprising
CC the DNA and/or vector, a transgenic non-human animal (one or more of its
CC cells comprising the transgene, where the transgene is expressed in one
CC or more cells of the transgenic animal resulting in the animal exhibiting
CC ribonucleic acid interference (RNAi) of the target gene by the expressed
CC siRNA), a cell derived from the transgenic animal and producing an siRNA
CC by in vitro-method (involving providing the expression vector, admixing
CC the vector with a recombinant DNA-dependent RNA-polymerase,
CC ribonucleotides, suitable buffers and RNase inhibitor, incubating the
CC mixture at a suitable temperature for 30 minutes-24 hours for
CC transcription, optionally inactivating the DNA template, and purifying
CC expressed siRNA). The siRNA is useful for generating a non-human
CC transgenic animal. The vector is useful for in vitro production of the
CC siRNA. The siRNA is useful for the transient application in cell culture
CC and animal models. The siRNA enables high-throughput projects in genomic
CC research, in target gene validation, in pharmaceutical industry,
CC biological interference with vector-based siRNA systems. The siRNA is
CC biocompatible, cost effective, easy to use and suitable for
CC automation. The present sequence is a human siRNA produced by the
CC method of the invention. NOTE: The present sequence is described as an
CC siRNA but is clearly a DNA molecule.
XX
SQ Sequence 19 BP; 8 A; 1 C; 9 G; 1 T; 0 U; 0 Other;
Oy
Query Match 6.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
109 ATTCTCTGCTCCACTC 126
19 ATTCTCTGCTCTTCTC 2
Db
RESULT 80
AAS45831
ID AAS45831 standard; DNA; 20 BP.
XX
AC AAS45831;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse PARP-2 antisense inhibitor ISIS #110297.
XX
KW Mouse; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
KW cytoskeletal; neurotrophic; neuroprotective; antiinflammatory; antidiabetic;
KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;

```

```

KW oxidative stress; neurological disorder; parkinsonism; apoptosis;
KW meningitis-associated intracranial complication; ischaemia; probe;
KW inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note="Phosphorothioate backbone"
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="All cytidine residues are 5-methyl cytidine"
FT modified_base 1..5
FT /*tag= c
FT /mod_base= OTHER
FT /note="2'-methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= d
FT /mod_base= OTHER
FT /note="2' methoxyethyl nucleotides"
XX
XX WO200164955-A1.
XX
XX 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US006572.
XX
XX 02-MAR-2000; 2000US-00517467.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Popoff I, Cowseert LM;
XX
XX WPI; 2001-602570/68.
XX
PT Antisense compound useful for treating hyperproliferative, neurological,
PT inflammatory and autoimmune disorders and diabetes inhibits human PARP.
XX
XX Example 17; Page 89; 16pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to human
CC PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
CC (ADP-ribose) polymerase) plays an important role in chromatin
CC decondensation, DNA replication, DNA repair, gene expression, malignant
CC transformation, cellular differentiation and apoptosis. The antisense
CC oligonucleotide inhibitors are useful for inhibiting the expression of
CC PARP in human cells or tissues. They are also useful for treating a human
CC with a disease associated with PARP especially hyperproliferative
CC disorders (e.g. cancer), cellular injury resulting from oxidative stress,
CC neurological (e.g. parkinsonism, meningitis-associated intracranial
CC complications and ischaemia), inflammatory and autoimmune disorders (e.g
CC arthritis) and diabetes. The present sequence is an antisense
CC oligonucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
Oy
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
41 TGGCATCCCTTGATGAT 58
1 TCCCATCCCTTGATGCT 18
Db
RESULT 81
ADE43868/c
ID ADE43868 standard; DNA; 20 BP.
XX
AC ADE43868;

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```

XX 29-JAN-2004 (first entry)
DT
XX
DE Human eotaxin gene SSCP PCR primer #1.
XX
XX Human; ss; primer; eotaxin; SNP; single nucleotide polymorphism;
XX antiaesthetic; antiinflammatory; antiallergic; gene therapy; asthma;
XX rhinitis; inflammatory condition; eosinophil accumulation;
XX respiratory tract; single-strand conformation polymorphism; SSCP;
XX amplification refractory mutation system; ARMS; PCR.
OS Homo sapiens.
XX
XX US6548245-B1.
XX
XX 15-APR-2003.
XX
XX 12-MAY-1998; 98US-00076259.
XX
XX 16-MAY-1997; 97US-0046720P.
XX
XX (BGM) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Lilly CM, Luster AD, Drazen JM;
XX
XX WPI; 2003-605370/57.
XX
XX Diagnosing, predicting or treating asthma or other inflammatory
XX conditions of respiratory tract and other tissues, comprises identifying
XX a nucleic acid sequence that exhibits a polymorphism in an eotaxin gene.
XX
XX Claim 12; SEQ ID NO 2; 12pp; English.
XX
XX The invention relates to diagnosing or predicting asthma or an
XX inflammatory condition of respiratory tissues that is associated with
XX tissue accumulation of eosinophils, comprising identifying a nucleic acid
XX sequence that exhibits a polymorphism in an eotaxin gene, where the
XX polymorphism comprises a substitution of adenine for guanine 67 base
XX pairs following the ATG initiation codon of the gene, and where counting
XX is initiated at the A in that codon. The method uses a single-strand
XX conformation polymorphism (SSCP) technique or by amplification refractory
XX mutation system (ARMS) technique. The method is useful in diagnosing,
XX predicting and treating asthma, rhinitis and other inflammatory
XX conditions associated with eosinophil accumulation in respiratory tract
XX and other tissues. The present sequence is an SSCP primer used in the
XX method of the invention to detect the polymorphism.
XX
XX Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 6.3%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 44;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 70 CGTGAGAGCTGTTGTTT 87
XX ||||| |||||
XX 20 CGTGAGAGCTGTTGTTT 3
XX
XX
XX RESULT 82
XX ADF77306/C
XX ID ADF77306 standard; DNA; 20 BP.
XX
XX
XX ADF77306;
XX
XX 26-FEB-2004 (first entry)
XX
XX PCR primer #1 for human eotaxin gene.
XX
XX Asthma; polymorphism detection; eotaxin;
XX single-strand conformation polymorphism; SSCP;
XX amplification refractory mutation system; ARMS; inflammatory condition;
XX eosinophil accumulation; respiratory tissue; rhinitis; atopy;
XX antiaesthetic; antiallergic; antiinflammatory; dermatological; human;

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```

XX PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003165980-A1.
XX
XX 04-SEP-2003.
XX
XX 14-APR-2003; 2003US-00413255.
XX
XX 16-MAY-1997; 97US-0046720P.
XX
XX 12-MAY-1998; 98US-00076259.
XX
XX (BGM) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Lilly CM, Luster AD, Drazen JM;
XX
XX WPI; 2003-898062/82.
XX
XX Diagnosing, predicting and/or treating asthma or other inflammatory
XX conditions associated with eosinophil accumulation in respiratory and
XX other tissues, such as rhinitis and atopy, using an eotaxin coding
XX sequence polymorphism.
XX
XX Claim 8; SEQ ID NO 2; 12pp; English.
XX
XX The present invention relates to a method for diagnosing and/or
XX predicting asthma. The method comprises identifying a nucleic acid
XX sequence exhibiting a polymorphism in an eotaxin gene, where the
XX polymorphism comprises a substitution of adenine for guanine 67 bp
XX following the ATG initiation codon of the gene, where counting is
XX initiated at the A in that codon. The method involves amplifying the
XX nucleic acid by PCR, and testing the nucleic acid by a single-strand
XX conformation polymorphism (SSCP) or by an amplification refractory
XX mutation system (ARMS) technique. The method of the invention is useful
XX for diagnosing, predicting and/or treating asthma or an inflammatory
XX condition associated with eosinophil accumulation in respiratory and
XX other tissues, including rhinitis and atopy. The present sequence
XX represents a PCR primer used in the method of the present invention.
XX
XX Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 6.3%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 44;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 70 CGTGAGAGCTGTTGTTT 87
XX ||||| |||||
XX 20 CGTGAGAGCTGTTGTTT 3
XX
XX
XX RESULT 83
XX ADG43900/C
XX ID ADG43900 standard; DNA; 20 BP.
XX
XX
XX ADG43900;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human DYRK4 antisense oligonucleotide ISIS 206819.
XX
XX ss; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4;
XX DYRK4; Down syndrome; mental retardation; cancer; infection;
XX inflammation; tumour; antisense.
XX
XX Synthetic.
XX
XX US2003211606-A1.
XX
XX 13-NOV-2003.
XX
XX 10-MAY-2002; 2002US-00144140.
XX

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PR 10-MAY-2002; 2002US-00144140.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KW, Freier SM,
XX WPI; 2003-901593/82.
XX
PT New compound that hybridizes with nucleic acid molecules encoding dual-
PT specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4) and
PT inhibits expression of DYRK4, useful for treating e.g. cancer or Down
PT syndrome.
XX
XX Example 15; SEQ ID NO 28; 46bp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
CC (DYRK4). The compound is useful for inhibiting the expression of DYRK4 in
CC cells or tissues. It can also be used for treating a disease or condition
CC associated with DYRK4, preferably Down syndrome, mental retardation or
CC cancer. The antisense compounds can also be used as research agents, in
CC diagnostics, or as prophylaxis to prevent or delay infection, in
CC inflammation or tumour formation. The present sequence represents a human
CC dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4, DYRK4,
CC antisense oligonucleotide.
XX
SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 172 AGATTCGAGGACTTCAC 189
DB 18 AGATTCGAGGACTTCAC 1
RESULT 84
ADJ96199
ID ADJ96199 standard; DNA; 20 BP.
XX
XX ADJ96199;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human TNFR-6alpha amplifying RT-PCR primer #1.
XX
XX Tumour necrosis factor receptor; TNFR; inflammation;
XX inflammatory bowel disease; encephalitis; atherosclerosis; psoriasis;
XX autoimmune disorder; systemic lupus erythematosus; arthritis;
XX multiple sclerosis; Crohn's disease; autoimmune encephalitis;
XX graft vs. host disease; GVHD; allergy; asthma; gene therapy; human;
XX RT-PCR; reverse-transcriptase; primer; ss.
XX
XX Homo sapiens.
XX
XX US2004013664-A1.
XX
XX 22-JAN-2004.
XX
XX 18-APR-2003; 2003US-00418242.
XX
XX 14-JAN-1997; 97US-0035496P.
XX 13-JAN-1998; 98US-00006352.
XX 12-MAR-1999; 99US-0121774P.
XX 12-MAR-1999; 99US-0124092P.
XX 27-APR-1999; 99US-0131279P.
XX 30-APR-1999; 99US-0131964P.
XX 02-AUG-1999; 99US-0146371P.
XX 01-DEC-1999; 99US-0168235P.
XX 03-MAR-2000; 2000US-00518931.
XX 25-AUG-2000; 2000US-0227596P.
XX 21-NOV-2000; 2000US-0252131P.
XX
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PR 06-JUL-2001; 2001US-0303224P.
PR 24-AUG-2001; 2001US-00935727.
PR 19-APR-2002; 2002US-0373604P.
XX
XX (GENTZ/) GENTZ R L.
XX (YUGG/) YU G.
XX (NIJJ/) NI J.
XX (EBNER/) EBNER R.
XX (FENG/) FENG P.
XX (RUBE/) RUBEN S M.
XX
XX Gentz RL, Yu G, Ni J, Ebner R, Feng P, Ruben SM,
XX WPI; 2004-121528/12.
XX
XX
XX Treating or preventing an inflammatory or autoimmune disorder, graft vs
XX host disease (GVHD), allergy or asthma comprises administering to an
XX animal Tumour Necrosis Factor Receptor protein.
XX
XX Example 28; SEQ ID NO 50; 165bp; English.
XX
CC The present invention relates to novel tumour necrosis factor receptors
CC (TNFR) proteins and their encoding nucleic acids. The invention is useful
CC for treating and preventing inflammatory disorders such as inflammatory
CC bowel disease, encephalitis, atherosclerosis and psoriasis, autoimmune
CC disorders such as systemic lupus erythematosus, arthritis, multiple
CC sclerosis, Crohn's disease and autoimmune encephalitis, graft vs. host
CC disease (GVHD), allergy and asthma. The invention is also useful in gene
CC therapy. The present sequence is human TNFR-6alpha amplifying RT-PCR
CC primer. The primer is used in the exemplification of the invention.
XX
SQ Sequence 20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 92 GAGCCTGGCCCCCTCA 109
DB 3 GATCTGGCCCCCTCTTA 20
RESULT 85
AEC22797/c
ID AEC22797 standard; DNA; 20 BP.
XX
XX AEC22797;
XX
XX 20-OCT-2005 (first entry)
XX
XX Human myocardial infarction (MI) gene marker PCR primer SEQ ID NO 7.
XX
XX cardiant; C-reactive-protein-reducer; leukotriene-synthesis-antagonist;
XX ss; PCR; myocardial infarction; cardiovascular disease; FLP;
XX 5-lipoxygenase activating protein; primer; genetic marker.
XX
XX Homo sapiens.
XX
XX WO2005075022-A2.
XX
XX 18-AUG-2005.
XX
XX 31-JAN-2005; 2005WO-US003312.
XX
XX 30-JAN-2004; 2004US-00769542.
XX 30-JAN-2004; 2004US-00769744.
XX 22-APR-2004; 2004US-00829674.
XX 22-APR-2004; 2004US-00830477.
XX 10-JAN-2005; 2005US-0642909P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Helgadottir A, Hakonarson H, Gulcher JR, Gurney ME;
XX
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XX	WT; 2005-648933/66.
DR	
XX	A method of prophylaxis therapy for myocardial infarction (MI) comprises
PT	administering to the subject a composition comprising an MI therapeutic
PT	agent that inhibits leukotriene synthesis in vivo.
XX	
PS	Example 9; SEQ ID NO 7; 395bp; English.
XX	
CC	The invention relates to a method of prophylaxis therapy for myocardial
CC	infarction (MI) comprising administering to the subject a composition
CC	comprising an MI therapeutic agent that inhibits leukotriene synthesis in
CC	vivo. The methods and composition are useful for the prophylactic
CC	treatment of myocardial infarction. The leukotriene synthesis inhibitor
CC	and statin are useful for the manufacture of a medicament for reducing
CC	CRP levels in the human subject. The present sequence represents the DNA
CC	encoding the 5-lipoxygenase activating protein located in the human
CC	myocardial infarction (MI) gene located on chromosome 13q12-13.
XX	
SQ	Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 44;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Oy	18 CAGATCCTCATGATCG 35                                 Db 18 CAGCTCCTCATGACTGG 1
RESULT 86	
AEF72123/C	
ID	AEF72123 standard; DNA; 20 BP.
XX	
AC	AEF72123;
XX	
DT	06-APR-2006 (first entry)
XX	
DE	Human FLAP gene microsatellite marker-specific PCR primer - SEQ ID 7.
KW	prophylaxis; SNP detection; myocardial infarction; candiant;
KM	5-lipoxygenase activating protein; FLAP; PCR; primer; ss.
OS	Homo sapiens.
XX	
PN	US2006019269-A1.
XX	
PD	26-JAN-2006.
XX	
PF	30-MAR-2005; 2005US-00096191.
XX	
PR	17-OCT-2002; 2002US-0419433P.
PR	21-FEB-2003; 2003US-0448331P.
PR	17-SEP-2003; 2003US-0503587P.
PR	16-OCT-2003; 2003WO-US032556.
PR	30-JAN-2004; 2004US-00769744.
PR	22-APR-2004; 2004US-00830477.
PR	17-SEP-2004; 2004WO-US030582.
PR	10-JAN-2005; 2005US-0642909P.
PR	31-JAN-2005; 2005WO-US003312.
XX	
PA	(DECO-) DECODE GENETICS INC.
XX	
PI	Helgaodottir A, Hakonarson H, Gulcher JR, Gurney ME;
XX	
DR	WPI; 2006-124282/13.
XX	
PT	Prophylaxis therapy for myocardial infarction comprises selecting a human
PT	by screening for genetic variation in e.g. 5-lipoxygenase activating
PT	protein gene, administering a composition comprising a agent and
PT	monitoring inflammatory marker.
XX	
PS	Example 9; SEQ ID NO 7; 134bp; English.

XX	The invention comprises a method of prophylaxis therapy for myocardial									
CC	infarction. The method involves selecting a human subject susceptible to									
CC	myocardial infarction by screening for a genetic variation in either the									
CC	5-lipoxygenase activating protein (FLAP) gene or the leukotriene A4									
CC	hydroxylase (LTA4H) gene. The method further involves administration of a									
CC	therapeutic agent and monitoring at least one inflammatory marker in the									
CC	subject before and during the prophylaxis treatment. The method of the									
CC	invention is useful for prophylaxis therapy for myocardial infarction.									
CC	The present DNA sequence represents a PCR primer that was used to amplify									
CC	a microsatellite marker from within the human FLAP gene.									
XX										
XX	Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;									
QY	Query Match 6.3%; Score 14.8; DB 1; Length 20;									
Db	Best Local Similarity 88.9%; Pred. No. 44;									
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0									
	18 CAGATCCCTCATGATGCG 35									
	18 CAGCTCCCTCATGATGCG 1									
RESULT 87										
AAQ82294/c										
ID	AAQ82294 standard; DNA; 21 BP.									
XX	AAQ82294;									
AC										
XX	25-MAR-2003 (revised)									
DT	07-SEP-1995 (first entry)									
XX										
DE	Chromosome 11 (locus D11S1131) STS primer CSRL-4a3-tZ.									
XX										
KW	sequence sampled mapping; genomic analysis; complex genome mapping;									
KM	cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.									
XX										
OS	Synthetic.									
PN	W09429486-A1.									
PD	22-DEC-1994.									
XX										
PF	15-JUN-1994; 94WO-US006810.									
PR	15-JUN-1993; 93US-00078471.									
PR	07-SEP-1993; 93US-00117952.									
PA	(SALK ) SALK INST BIOLOGICAL STUDIES.									
XX										
P1	Evans GA, Smith MW;									
DR	WPI; 1995-036508/05.									
XX										
PT	Sequencing complex genomes, present as fragments in a cosmid library - by									
PT	sequencing end-specific nucleotides of each clone then correlating with									
PT	spatial relationship of cosmid, esp. for mammalian chromosomes.									
CC										
PS	Example 4; Page 75; 128pp; English.									
XX										
CC	Sequences were determined from the ends of chromosome 11-specific cosmids									
CC	by automated sequencing without intermediate subcloning. A sample of 371									
CC	DNA sequence fragments were determined and of these, 277 were suitable									
CC	for STS primer prediction by computer analysis (using the "Primer"									
CC	program available from E. Landier, MIT). The STSs and cosmids were mapped									
CC	by in situ hybridisation, somatic cell hybrid analysis or both. Using									
CC	this method, 370 STSs specific for human chromosome 11 were generated and									
CC	most of them were regionally mapped. This procedure illustrates a novel									
CC	method for sequencing complex genomes, designated "sequence sampled									
CC	mapping". The sequence sampled mapping method is useful for the									
CC	completion of high density sequence-based maps, and ultimately, for the									
CC	complete sequencing of genomic DNA directly from cosmid clones. See									
CC	AAQ82001-Q82706 for STS primers. (Updated on 25-MAR-2003 to correct PN									

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CC field.)
XX
SQ Sequence 21 BP; 8 A; 5 C; 1 G; 7 T; 0 U; 0 Other;

Query Match
Best Local Similarity 6.3%; Score 14.8; DB 1; Length 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 74 AGAGCTGGTGTGAAA 91
Db 18 AAAGCTGTTTGGAAA 1

RESULT 88
ADG77905
ID ADG77905 standard; DNA; 21 BP.
AC ADG77905;
XX
XX 11-MAR-2004 (first entry)
XX
DE Canine disease marker-related PCR primer 749.
XX
XX genetic disease; genetic trait; dog; carrier of recessive disease;
XX copper toxicosis; CT; canine genome map; breed-specific profile;
XX DNA fingerprint; dog identification; PCR; primer; ss.
XX
XX Canis familiaris.
XX
XX MO9731011-A1.
XX
XX 28-AUG-1997.
XX
XX 18-FEB-1997; 97WO-US002396.
XX
XX 22-FEB-1996; 96US-0012060P.
XX
XX (UNMI ) UNIV MICHIGAN.
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
XX
XX WPI; 1997-435082/40.
XX
XX New oligonucleotide primers for diagnosis of genetic diseases and traits
XX PT in dogs - amplify specific regions of the genome containing
XX PT microsatellite repeats, especially for diagnosing copper toxicosis and
XX PT carriers.
XX
XX Claim 1; Page 18; 40pp; English.
XX
XX This invention relates to novel oligonucleotide PCR primers which may be
XX CC used to identify markers associated with genetic diseases and traits in
XX CC dogs, in particular to diagnose genetic diseases that are not
XX CC phenotypically visible and to identify carriers of recessive diseases. A
XX CC specific application is diagnosis of copper toxicosis (CT). The invention
XX CC can also be used to create a genetic map of the canine genome; to
XX CC generate breed-specific profiles; to establish paternity and to identify
XX CC dogs from DNA fingerprints. The method provides rapid analysis of the
XX CC target sequences from only a small sample of DNA. Diagnosis can be done
XX CC at any time in the dog's life. The present sequence is that of a PCR
XX CC primer of the invention.
XX
XX Sequence 21 BP; 0 A; 9 C; 3 G; 9 T; 0 U; 0 Other;

Query Match
Best Local Similarity 6.3%; Score 14.8; DB 1; Length 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 145 CCCCTTCTCTCTGCC 162
Db 1 CTTGCTTCTCTCTGCC 18

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RESULT 89
AAS43670
ID AAS43670 standard; DNA; 21 BP.
XX
XX AAS43670;
AC
XX 18-DEC-2001 (first entry)
DT
XX
XX Corneodesmosin PCR primer #140.
DE
XX
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX KM antiporiatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200162788-A2.
XX
XX 30-AUG-2001.
PD
XX
XX 23-FEB-2001; 2001WO-GB000795.
PF
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
XX (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX
XX WPI; 2001-570627/64.
XX
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX PT polymorphisms useful in treating, diagnosing or determining
XX PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX PT diseases.
XX
XX Disclosure; Page 38; 60pp; English.
XX
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX CC encoding the corneodesmosin gene, where the gene comprises a base
XX CC substitution, deletion or insertion at one or more positions. (I) and
XX CC (II) are useful for screening for agents for use in prognosis, diagnosis
XX CC and treatment of individuals having or being susceptible to
XX CC corneodesmosin-mediated disease, by monitoring the reaction between the
XX CC molecules and the agents. The nucleotide and amino acid polymorphisms are
XX CC useful for diagnosing or determining susceptibility to corneodesmosin-
XX CC mediated disease, which facilitates subsequent treatment of the disease
XX CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX CC are useful in diagnostic, prognostic or therapeutic methods and as
XX CC research tools for e.g. in drug screening. (II) is useful as probes or
XX CC primers for detecting an allele of the polymorphism or in the regulation
XX CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX CC screening DNA clone libraries for cells secreting the antigen. (II) is
XX CC useful as a model to investigate the role of corneodesmosin in normal
XX CC skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX CC invention.
XX
XX Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match
Best Local Similarity 6.3%; Score 14.8; DB 1; Length 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 18 CAGATCCCTCATGATG 35
Db 4 CAGATGCTTCATGATG 21

RESULT 90
AAS43680
ID AAS43680 standard; DNA; 21 BP.
XX
XX AAS43680;
AC

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XX 18-DEC-2001 (first entry)
XX Corneodesmosin PCR primer #150.
DE Homo sapiens.
XX WO200162788-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-GB000795.
XX 23-FEB-2000; 2000GB-00004312.
XX (OXAG-) OXAGEN LTD.
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX Disclosure; Page 38; 60pp; English.
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptibility to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 6.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 42;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 18 CAGATCCTCATGAATGG 35
DB 4 CAGATGCTTCATGAATGG 21
RESULT 91
AAS43678 ID AAS43678 standard; DNA; 21 BP.
XX AAS43678;
XX 18-DEC-2001 (first entry)
XX Corneodesmosin PCR primer #148.
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX
```

```
KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX Homo sapiens.
XX WO200162788-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-GB000795.
XX 23-FEB-2000; 2000GB-00004312.
XX (OXAG-) OXAGEN LTD.
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX Disclosure; Page 38; 60pp; English.
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptibility to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 6.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 42;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 18 CAGATCCTCATGAATGG 35
DB 4 CAGATGCTTCATGAATGG 21
RESULT 92
AAS43672 ID AAS43672 standard; DNA; 21 BP.
XX AAS43672;
XX 18-DEC-2001 (first entry)
XX Corneodesmosin PCR primer #142.
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX Homo sapiens.
XX WO200162788-A2.
XX
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PD 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
XX (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX
XX Disclosure; Page 38; 60pp; English.
XX
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptible to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 CAGATCCCTCATGATGG 35
DB 4 CAGATGCTTCATGATGG 21
RESULT 93
AAS43676
ID AAS43676 standard; DNA; 21 BP.
XX
XX AAS43676;
XX
XX 18-DEC-2001 (first entry)
XX
XX Corneodesmosin PCR primer #146.
XX
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX antiapoptotic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200162788-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
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PA (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX
XX Disclosure; Page 38; 60pp; English.
XX
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptible to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 CAGATCCCTCATGATGG 35
DB 4 CAGATGCTTCATGATGG 21
RESULT 94
AAS43674
ID AAS43674 standard; DNA; 21 BP.
XX
XX AAS43674;
XX
XX 18-DEC-2001 (first entry)
XX
XX Corneodesmosin PCR primer #144.
XX
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX antiapoptotic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200162788-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
XX (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX
```



PT Corneodesmosin protein and polynucleotide encoding it, having one or more  
PT polymorphisms useful in treating, diagnosing or determining  
PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory  
PT diseases.  
XX  
PS Disclosure; Page 38; 60pp; English.  
XX  
CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)  
CC encoding the corneodesmosin gene, where the gene comprises a base and  
CC substitution, deletion or insertion at one or more positions. (I) and  
CC (II) are useful for screening for agents for use in prognosis, diagnosis  
CC and treatment of individuals having or being susceptible to  
CC corneodesmosin-mediated disease, by monitoring the reaction between the  
CC molecules and the agents. The nucleotide and amino acid polymorphisms are  
CC useful for diagnosing or determining susceptibility to corneodesmosin-  
CC mediated disease, which facilitates subsequent treatment of the disease  
CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)  
CC are useful in diagnostic, prognostic or therapeutic methods and as  
CC research tools for e.g. in drug screening. (II) is useful as probes or  
CC primers for detecting an allele of the polymorphism or in the regulation  
CC of corneodesmosin gene. Antibodies which binds to (I) are useful for  
CC screening DNA clone libraries for cells secreting the antigen. (II) is  
CC useful as a model to investigate the role of corneodesmosin in normal  
CC skin function. AAS43492-AAS43749 represent corneodesmosin coding  
CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the  
CC invention  
XX  
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 6.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 18 CAGATCCCTCATGATGG 35  
|||||  
4 CAGATGCTTCATGATGG 21  
Db  
RESULT 95  
ADU26863/c  
ID ADU26863 standard; DNA; 21 BP.  
XX  
AC ADU26863;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Knock-down target sequence #261.  
XX  
KW de; RNA production; protein production; drug development;  
XX knock-down target.  
XX  
OS Unidentified.  
XX  
PS WO2004094636-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 24-APR-2003; 2003WO-EP004362.  
XX  
PR 24-APR-2003; 2003WO-EP004362.  
XX  
PA (GALA-) GALAPAGOS GENOMICS NV.  
XX (VSCB/) VAN DER SCHUEREN J.  
XX  
PI Arts GUF, Lambrecht MJY, Djokic K, Clasen RJ, Mesic E;  
XX Griffioen S, Bergs CJL;  
XX  
DR WPI: 2004-775940/76.  
XX  
PT New knockdown sequences, useful in lowering the amount of RNA and/or  
PT protein production in cells used in drug development process.  
XX  
PS Claim 11; SEQ ID NO 264; 402pp; English.

XX  
CC The invention relates to a polynucleotide comprising an RNA sequence. The  
CC polynucleotides, vector, libraries, and method are useful in lowering the  
CC amount of RNA and/or protein production in cells used in drug development  
CC process. The present sequence represents a knock-down target sequence.  
XX  
SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 6.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 150 TTCTCCTTCTGCCATGAT 167  
|||||  
18 TTCTACTTCTGCCATGCT 1  
Db  
RESULT 96  
ACLA0871/c  
ID ACLA0871 standard; RNA; 21 BP.  
XX  
AC ACLA0871;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE C20orf103 siRNA sense sequence, SEQ ID 1943.  
XX  
KW Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;  
KW short interfering RNA; gene silencing.  
XX  
OS Synthetic.  
XX  
PN WO2005001092-A2.  
XX  
PD 06-JAN-2005.  
XX  
PF 19-MAY-2004; 2004WO-US015645.  
XX  
PR 20-MAY-2003; 2003US-0471729P.  
XX  
PA (AMHP ) WYETH.  
XX  
PI Be X, Wei L, Slonim DK, Howes SH;  
XX  
DR WPI: 2005-075568/08.  
XX  
PT Pharmaceutical composition comprising an agent capable of modulating an  
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
XX  
PS Claim 3; SEQ ID NO 1943; 113pp; English.  
XX  
CC The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 21 BP; 8 A; 5 C; 5 G; 0 T; 5 U; 0 Other;  
Query Match 6.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCGCATCA 166  
Db 18 CTTCTGTTTCGCATCA 1

RESULT 97  
ADM85397/C  
ID ADM85397 standard; DNA; 21 BP.  
XX  
AC ADM85397;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE MAP3K9 marker amplification forward primer #1336.  
XX  
XX mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;  
KM antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;  
KM antiasthmatic; antipruritic; neuroprotective; gastrointestinal-gen.;  
KM respiratory disease; chronic obstructive pulmonary disease;  
KM chronic bronchitis; inflammation; ss; primer; PCR.  
XX  
XX Unidentified.  
OS  
XX WO2005007144-A2.  
PN  
XX 27-JAN-2005.  
PD  
XX 14-JUL-2004; 2004WO-US022446.  
PF  
XX 14-JUL-2003; 2003US-0487072P.  
PR  
XX 05-APR-2004; 2004US-0559611P.  
PR  
XX (DECO-) DECODE GENETICS EHF.  
PA  
XX Hakanarson H, Gurney ME, Halapi E;  
PI  
XX WPI: 2005-122681/13.  
DR  
XX  
XX Use of mixed lineage kinase family kinase inhibitor in the manufacture of  
PT a medicament for treatment of asthma associated at-risk haplotype for  
PT asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein  
PT expression or activity.  
XX  
XX  
XX Disclosure: Fig 12; 640pp; English.

The invention relates to the novel use of a mixed lineage kinase (MLK) family kinase inhibitor for treating asthma. Where the asthma is associated with a risk factor selected from an at-risk haplotype for asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9 mRNA isoform, and/or increased MLK1 protein expression. The invention further comprises: a method for the diagnosis or identification of susceptibility to asthma; a method for the use of a first nucleic acid molecule for diagnosing asthma or susceptibility to asthma in a sample; a method for assaying the presence of a first nucleic acid molecule in a sample; a method for assessing the response to treatment with an MLK family kinase nucleic acid inhibitor in a target population or in an individual with an at-risk haplotype for asthma, at-risk haplotype in the MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1 protein expression, increased MLK1 biochemical activity or increased MLK1 protein isoform expression; a method for assessing the response to treatment with an MLK1 inhibitor in a target population including an individual with an at-risk haplotype for asthma, as above; a kit for assaying a sample for the presence or absence of at least one haplotype comprising 2 or more alleles associated with asthma comprising: at least one nucleic acid capable of detecting the presence or absence of at least one specific allele; a reagent kit for assaying the presence of at least one haplotype comprising 2 or more alleles comprising: at least one labeled nucleic acid capable of detecting at least one specific allele of

the haplotype, and reagents for detection of the label; and a reagent kit for assaying a sample for the presence of at least one haplotype comprising 2 or more alleles comprising: at least one nucleic acid comprising at least one nucleotide sequence that is at least partially complementary to a part of nucleotide sequence of MAP3K9, capable of acting as a primer for a primer extension reaction and capable of detecting 2 or more specific alleles of the haplotype. The MLK family kinase inhibitor has the following activities: antiasthmatic, respiratory-gen., antiinflammatory, antirheumatic, antipruritic, antipruritic, neuroprotective, and gastrointestinal-gen. The MLK family kinase inhibitor is useful for the treatment of asthma associated with a risk factor selected from at-risk haplotype for asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1 protein expression, increased MLK1 biochemical activity and/or increased MLK1 protein isoform expression; and in diagnosis or identification of susceptibility to asthma. The inhibitor is also useful for the treatment of other respiratory diseases associated with MAP3K9 or other members of the JNK pathway such as chronic obstructive pulmonary disease, chronic bronchitis and other inflammatory diseases such as rheumatoid arthritis, psoriasis, multiple sclerosis and inflammatory bowel disease. This polynucleotide sequence represents a forward primer which is used in amplifying a marker of the MAP3K9 kinase, where MAP3K9 is a part of Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of the invention.

Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 6.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 CCTTGGTATGAGGAGT 66  
Db 21 CCTTGGTATGAGGAGT 4

RESULT 98  
AEC02566  
ID AEC02566 standard; DNA; 21 BP.  
AC AEC02566;  
XX  
DT 03-NOV-2005 (first entry)  
XX  
XX Human IGE short interfering nucleic acid SEQ ID NO 169.  
DE  
XX  
XX antiallergic; antiinflammatory; antiasthmatic; dermatological;  
KM immunosuppressive; expression; RNA interference; allergy;  
KM atopic dermatitis; urticaria; dermatological; dermatological disease;  
KM immediate type hypersensitivity; immunosuppressive; asthma;  
KM antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;  
KM ear, nose, throat disease; inflammation; respiratory disease;  
KM immune disorder; IGE; short interfering nucleic acid; siRNA;  
KM gene silencing; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2005080410-A1.  
PN  
XX 01-SEP-2005.  
PD  
XX 21-FEB-2005; 2005WO-NZ000021.  
PF  
XX 20-FEB-2004; 2004US-0546434P.  
PR  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
PA  
XX Watson JD, Murison GJ, Grigor MR, Havukkala IU, Munro G;  
PI Abernethy N, Webster G;  
XX  
XX WPI: 2005-591970/60.  
DR  
XX

PT New composition comprises small interfering nucleic acid molecule (siNA)  
PT capable of reducing expression of a target gene that is active in a IGE-  
PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic  
PT dermatitis.

PS Disclosure; SEQ ID NO 169; 178bp; English.

CC The invention describes a composition comprising a small interfering  
CC nucleic acid molecule (siNA) capable of reducing expression of a target  
CC gene that is active in a IGE-mediated disorder, a genetic construct that  
CC expresses the siNA, and a binding agent that specifically binds to a  
CC target antigen expressed on the surface of the cell. Also described are:  
CC a method for the treatment of an IGE-mediated disorder in a patient;  
CC prevention of IGE-mediated disorder in a patient; reduction of  
CC eosinophilia in a patient; modulating an IGE-mediated immune response to  
CC a specific antigen in a patient; and preventing or reducing the severity  
CC of an immune response to a specific antigen in a patient. The composition  
CC is useful in the preparation of a medicament useful for the treatment of  
CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,  
CC urticaria, atopic dermatitis, food allergies, diseases that benefit from  
CC the reduction of eosinophilia in the tissues of the respiratory system,  
CC or disorders having hypersensitivity immune reaction. This sequence  
CC represents a siNA for suppression of human IGE expression.

XX  
SQ Sequence 21 BP; 4 A; 2 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 6.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 42;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCTGGGTCATGGGGC 18

Db 4 TGTCTGGGTCATGGAGGC 21

Search completed: October 2, 2006, 15:45:39  
Job time : 0.001 secs

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107 17.2 7.3 24 1 US-10-310-914A-66335 Sequence 66335, A
108 16.8 7.1 20 1 US-10-298-953-44 Sequence 44, Appl
109 16.8 7.1 20 1 US-10-310-914A-661149 Sequence 661149,
110 16.8 7.1 20 1 US-10-310-914A-845542 Sequence 845542,
111 16.8 7.1 20 1 US-10-310-914A-1073095 Sequence 1073095,
112 16.8 7.1 20 1 US-10-310-914A-1242020 Sequence 1242020,
113 16.8 7.1 21 1 US-10-847-918-1184 Sequence 1184, Ap
114 16.8 7.1 21 1 US-10-847-918-1853 Sequence 1853, Ap
115 16.8 7.1 21 1 US-10-847-918-1942 Sequence 1942, Ap
116 16.8 7.1 21 1 US-10-847-918-1944 Sequence 1944, Ap
117 16.8 7.1 21 1 US-10-847-918-2092 Sequence 2092, Ap
118 16.8 7.1 21 1 US-10-310-914A-828967 Sequence 828967,
119 16.8 7.1 21 1 US-10-310-914A-1009274 Sequence 1009274,
120 16.8 7.1 21 1 US-10-310-914A-1371246 Sequence 1371246,
121 16.8 7.1 24 1 US-10-310-914A-74338 Sequence 74338, A
122 16.8 7.1 24 1 US-10-416-122-2 Sequence 2, Appli
123 16.8 7.0 23 1 US-10-708-204-3803 Sequence 3803, Ap
124 16.6 7.0 23 1 US-10-310-914A-287417 Sequence 287417,
125 16.6 7.0 23 1 US-10-310-914A-360372 Sequence 360372,
126 16.6 7.0 23 1 US-10-310-914A-651766 Sequence 651766,
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128 16.6 7.0 23 1 US-10-310-914A-967480 Sequence 967480,
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130 16.4 6.9 18 1 US-10-310-914A-115988 Sequence 115988,
131 16.4 6.9 18 1 US-10-310-914A-1053329 Sequence 1053329,
132 16.4 6.9 19 1 US-10-727-780A-425 Sequence 425, App
133 16.4 6.9 19 1 US-10-310-914A-1053330 Sequence 1053330,
134 16.4 6.9 19 1 US-11-083-784-134328 Sequence 134328,
135 16.4 6.9 19 1 US-11-083-784-134365 Sequence 134365,
136 16.4 6.9 19 1 US-11-083-784-863172 Sequence 863172,
137 16.4 6.9 19 1 US-11-083-784-914575 Sequence 914575,
138 16.4 6.9 19 1 US-11-083-784-1250582 Sequence 1250582,
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140 16.4 6.9 19 1 US-11-101-244-134365 Sequence 134365,
141 16.4 6.9 19 1 US-11-101-244-863172 Sequence 863172,
142 16.4 6.9 19 1 US-11-101-244-914575 Sequence 914575,
143 16.4 6.9 19 1 US-11-101-244-1250582 Sequence 1250582,
144 16.4 6.9 21 1 US-10-310-914A-31831 Sequence 31831,
145 16.2 6.9 21 1 US-10-708-204-3346 Sequence 3346, Ap
146 16.2 6.9 21 1 US-10-310-914A-59888 Sequence 59888, A
147 16.2 6.9 21 1 US-10-310-914A-95531 Sequence 95531, A
148 16.2 6.9 21 1 US-10-310-914A-174457 Sequence 174457,
149 16.2 6.9 21 1 US-10-310-914A-612161 Sequence 612161,
150 16.2 6.9 21 1 US-10-310-914A-628516 Sequence 628516,
151 16.2 6.9 21 1 US-10-310-914A-969044 Sequence 969044,
152 16.2 6.9 21 1 US-10-310-914A-1111794 Sequence 1111794,
153 16.2 6.9 21 1 US-10-310-914A-1227944 Sequence 1227944,
154 16.2 6.9 22 1 US-10-310-914A-97305 Sequence 97305, A
155 16.2 6.9 22 1 US-10-310-914A-360369 Sequence 360369,
156 16.2 6.9 22 1 US-10-310-914A-875345 Sequence 875345,
157 16.2 6.9 22 1 US-10-310-914A-910065 Sequence 910065,
158 16.2 6.9 23 1 US-10-092-900A-521 Sequence 521, App
159 16.2 6.9 23 1 US-10-310-914A-596179 Sequence 596179,
160 16.2 6.9 23 1 US-10-310-914A-1171021 Sequence 1171021,
161 16 6.8 18 1 US-10-310-914A-1037134 Sequence 1037134,
162 16 6.8 19 1 US-11-083-784-508230 Sequence 508230,
163 16 6.8 19 1 US-11-101-244-508230 Sequence 508230,
164 16 6.8 20 1 US-09-791-942-85 Sequence 85, Appl
165 16 6.8 20 1 US-10-415-463-85 Sequence 85, Appl
166 16 6.8 20 1 US-10-476-264-285 Sequence 285, App
167 16 6.8 22 1 US-10-310-914A-1037133 Sequence 1037133,

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## ALIGNMENTS

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RESULT 1
US-10-891-260-437
; Sequence 437, Application US/10891260
; Publication No. US20050227244A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Matsuzaki, Hajime

```

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; APPLICANT: Mei, Rui
; TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
; FILE REFERENCE: 3522.3
; CURRENT APPLICATION NUMBER: US/10/891,260
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 10/681,773
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 10244
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 437
; LENGTH: 33
; TYPE: DNA
; ORGANISM: homo sapien
US-10-891-260-437

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Query Match          9.8%; Score 23.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 25; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy      14  |||||
Db      1  GGGGCGAGATCCCTCATGATGATTAGTGC 43
          GGGGCGAGATCCCTTACRAATGGCTTGTC 30

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RESULT 2
US-10-310-914A-1140145/c
; Sequence 1140145, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuak
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1140145
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1140145

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Query Match          9.4%; Score 22.2; DB 1; Length 28;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      13  |||||
Db      27  GAGGCGAGATCCCTTATGATGTTCA 1

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RESULT 3
US-11-060-756-81484/c
; Sequence 81484, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81484

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Best Local Similarity 91.7%; Pred. No. 24;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 155 CTTCTGCCATGATTTAAGATTC 178  
Db 25 CTTCTGCCATGATTTAAGATTC 2

RESULT 9  
US-11-060-756-81501/c  
; Sequence 81501, Application US/11060756  
; Publication No. US2005021354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81501  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-81501

Query Match 8.6%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 24;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 154 CTTCTGCCATGATTTAAGATTC 177  
Db 24 CTTCTGCCATGATTTAAGATTC 1

RESULT 10  
US-10-310-914A-596177  
; Sequence 596177, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 596177  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-596177

Query Match 8.6%; Score 20.4; DB 1; Length 24;  
Best Local Similarity 63.6%; Pred. No. 26;  
Matches 14; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 139 CTTCTGCCATGATTTAAGATTC 160  
Db 3 CTTCTGCCATGATTTAAGATTC 24

RESULT 11  
US-10-310-914A-116013/c  
; Sequence 116013, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 116013  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-116013

Query Match 8.6%; Score 20.4; DB 1; Length 25;  
Best Local Similarity 95.5%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 78 CTTCTGCCATGATTTAAGATTC 99  
Db 25 CTTCTGCCATGATTTAAGATTC 4

RESULT 12  
US-11-060-756-81488/c  
; Sequence 81488, Application US/11060756  
; Publication No. US2005021354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81488  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-81488

Query Match 8.6%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 28;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 151 TCTCTGCCATGATTTAAGATTC 175  
Db 25 TCTCTGCCATGATTTAAGATTC 1

RESULT 13  
US-11-060-756-81497/c  
; Sequence 81497, Application US/11060756  
; Publication No. US2005021354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81497  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-81497

Query Match 8.6%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 28;



```
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 156 TTCGCCATGATTTAAGATTCCAG 180
Db 25 TTCGCCATGATTTAAGATTCCAG 1

RESULT 14
US-11-060-756-81505/C
; Sequence 81505, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; CURRENT APPLICATION NUMBER: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81505
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
US-11-060-756-81505

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 152 CTCCTTCGCCATGATTTAAGATT 176
Db 25 CACCTTCGCCATGATTTAAGATT 1

RESULT 15
US-11-121-849-628945
; Sequence 628945, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: Microarrays
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 628945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-628945

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 195 GCAATGCTAACGCCATGCTCTTGG 219
Db 1 GCAATGCTAACGCCATGCTCTTGG 25

RESULT 16
US-11-121-849-630324
; Sequence 630324, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
```

```
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 630324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-630324

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 195 GCAATGCTAACGCCATGCTCTTGG 219
Db 1 GCAATGCTAACGCCATGCTCTTGG 25

RESULT 17
US-10-310-914A-661150/C
; Sequence 661150, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661150
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661150

Query Match 8.4%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 65 GTTACGAGAGAGCTGTTGTTT 87
Db 23 GTTACGAGAGAGCTGTTGTTT 1

RESULT 18
US-10-310-914A-1073215/C
; Sequence 1073215, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073215
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073215

Query Match 8.4%; Score 19.8; DB 1; Length 25;
```

Best Local Similarity 91.3%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 CAGATCCCTCATGATGTTAG 40  
Db 25 CAGATCCCTCATGATGTTAG 3

## RESULT 19

US-11-121-849-597791/C  
; Sequence 597791, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 597791  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-597791

Query Match  
Best Local Similarity 91.3%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 48 CCCTTGCGATGATGTTAC 70  
Db 25 CCCTTGCGATGATGTTAC 3

## RESULT 20

US-11-121-849-602992  
; Sequence 602992, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 602992  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-602992

Query Match  
Best Local Similarity 91.3%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 CAGATCCCTCATGATGTTAG 40  
Db 1 CAGATCCCTCATGATGTTAG 23

## RESULT 21

US-11-060-756-81510/C  
; Sequence 81510, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 81510  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-81510

Query Match  
Best Local Similarity 87.5%; Pred. No. 35;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 157 TCTGCCATGATTTAGATTCAG 180  
Db 25 TCTGCCATGATTTAGATTCAG 2

## RESULT 22

US-11-121-849-149128  
; Sequence 149128, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 149128  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-149128

Query Match  
Best Local Similarity 87.5%; Pred. No. 35;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 40 GTGCCATCCCTTGATGATG 63  
Db 2 GTGCCATCCCTTGATGATG 25

## RESULT 23

US-11-121-849-595763/C  
; Sequence 595763, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 595763  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien

US-11-121-849-595763

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches	21; Conservative	0; Mismatches	3; Indels	0; Gaps

Qy 64 AGTTCACGTGAGAGCTGGTGT 87  
Db 25 AGTCTCTGTGAGAGCTGGCTTT 2

RESULT 24  
US-11-121

```

US-11-121-849-595764/C
? Sequence 595764, Application US/11121849
? Publication No. US20050272080A1
? GENERAL INFORMATION:
?   APPLICANT: John Palma
?   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
?   TITLE OF INVENTION: Microarrays
?   FILE REFERENCE: 3684.1
?   CURRENT APPLICATION NUMBER: US/11/121,849
?   CURRENT FILING DATE: 2005-05-03
?   PRIOR APPLICATION NUMBER: 60/567,949
?   PRIOR FILING DATE: 2004-05-03
?   NUMBER OF SEQ ID NOS: 673904
?   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
?   SEQ ID NO 595764
?   LENGTH: 25
?   TYPE: DNA
?   ORGANISM: Homo sapien
US-11-121-849-595764

```

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY	60	AGTGAGTTCACGTGAGAGCTGGTT	83
Db	24	AGTGAGTCTTGTGAGAGCTGGCT	1

```

RESULT 25
US-11-121-849-668361/c
; Sequence 668361. Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION;
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded s
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-668361

```

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

RESULT 26  
US-11-121-849-673887

; Sequence 673887, Application US/11121849  
; Publication No. US20050272080A1  
; Publication No. 11121849

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 673887

```

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

OY      64 AGTTCACGTGAGAGCTGGTTGTTT    87  
         |||||  
Db      1 AGTTCTCCTGAGAGCTAGTTGTTT    24

```

RESULT 27
US-10-310-914A-661230/C
; Sequence 661230, Application US/10310914A
; Publication NO. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPU501
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661230
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661230

```

Query Match	8.0%	Score 18.8;	DB 1;	Length 22;
Best Local Similarity	90.9%	Pred. No. 37;		
Matches 20; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```

Qy      71 GTGAGAGCTGGTGTGTTGAAG 92
          |||||
Db      22 GTGAGATCTGCTGTTAAAG 1

```

```

RESULT 28
US-10-310-914A-66369
; Sequence 66369, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200:CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66369
; LENGTH: 23

```

TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-66369

Query Match 8.0%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 63.6%; Pred. No. 38;  
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTTCCTTCCTC 158  
DB 1 CGCCGCGCCCTCCGCGCCTC 22

## RESULT 29

US-10-310-914A-99099  
Sequence 99099, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 99099  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-99099

Query Match 8.0%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 59.1%; Pred. No. 38;  
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 140 CTGCTCCCTTCCTTCCTTCG 161  
DB 1 CUGCUCGCGCGCUCGUCUCG 22

RESULT 30  
US-10-310-914A-1158304  
Sequence 1158304, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1158304  
LENGTH: 24  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1158304

Query Match 8.0%; Score 18.8; DB 1; Length 24;  
Best Local Similarity 59.1%; Pred. No. 38;  
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 139 CCGTCCCTTCCTTCCTTCG 160  
DB 3 CCUCGUCGCGCUCGUCGUCG 24

RESULT 31  
US-10-719-900-570264

Sequence 570264, Application US/107199300  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT FILING DATE: 2003-11-20  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 570264  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-570264

Query Match 8.0%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 39;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 115 CTGCTCCACTCTTCGATGAGA 136  
DB 2 CTGACCCACTCTTCGAGAAGA 23

RESULT 32  
US-10-956-157-161277/C  
Sequence 161277, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Mounes, William  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 319805  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 161277  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Probe Sequence  
US-10-956-157-161277

Query Match 8.0%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 39;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 GCAGATCCCTCATGATGCTT 38  
DB 22 GCAGATCCTTCATGATGCTT 1

RESULT 33  
US-10-310-914A-845546/C  
Sequence 845546, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 845546  
LENGTH: 25  
TYPE: RNA

ORGANISM: Human  
US-10-310-914A-845546

Query Match 8.0%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 39;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 139 CCTGCTCCCTTCCTTCCTTG 160  
Db 22 CCTGCTCCCTTCCTTCCTTG 1

RESULT 34  
US-10-681-773-20812

Sequence 20812, Application US/10681773  
Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuzaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 20812

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-20812

Query Match 7.9%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 41;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 19 AGATCCCTCATGATGTTTAGTGC 43  
Db 1 AGATCCCTTACGAATGGCTTGTC 25

RESULT 35  
US-10-681-773-24075/c

Sequence 24075, Application US/10681773

Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuzaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24075

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-24075

Query Match 7.9%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 41;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 73 GAGAGCTGTTGTTGAAGACCT 97  
Db 25 GAGAACTAGTTGTTGAAGACCT 1

RESULT 36  
US-10-681-773-41906

Sequence 41906, Application US/10681773

Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuzaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 41906

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-41906

Query Match 7.9%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 41;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 18 CAGATCCCTCATGATGTTTAGTGC 42  
Db 1 CAGATCCCTTACGAATGGCTTGTC 25

RESULT 37  
US-10-681-773-42861/c

Sequence 42861, Application US/10681773

Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuzaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 42861

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-42861

Query Match 7.9%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 41;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 74 AGAGCTGTTGTTGAAGACCTG 98  
Db 25 AGAACTAGTTGTTGAAGACCTG 1

```
RESULT 38
US-10-681-773-70955
; Sequence 70955, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-70955
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      17 GCAGATCCCTCATGATGCTTTAGT 41
Db      1 GCAGATCCCTTACGATGCGTTGCT 25
```

```
RESULT 39
US-10-681-773-77134
; Sequence 77134, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-77134
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      16 GGCAGATCCCTCATGATGCTTTAG 40
Db      1 GGCAGATCCCTTACGATGCGTTG 25
```

```
RESULT 40
US-10-681-773-77826/c
; Sequence 77826, Application US/10681773
```

```
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77826
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-77826
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      72 TGAGAGCTGCTGTTGAAAGAGCC 96
Db      25 TGAGAACTAGTGTGTGAAAGAGCC 1
```

```
RESULT 41
US-10-956-157-55282/c
; Sequence 55282, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-55282
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      149 CTTCTCCTCTGCCATGATTTTAAG 173
Db      25 CTTCACTTCCACCATGATTTCTAAG 1
```

```
RESULT 42
US-10-956-157-131003
; Sequence 131003, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
```

```

; SOFTWARE: Patentin version 3.2
; SEQ ID NO 131003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-131003

```

Query Match	7.9%	Score 18.6;	DB 1;	Length 25;
Best Local Similarity	84.0%;	Pred. No. 41;		
Matches	21; Conservative	0; Mismatches	4; Indels	0; Gaps 0;

QY 210 ATGCTTCTGTCTGTCTGCAAAAC 234  
 Db 1 ATGCTTCTGTACAGCTGCAAAAC 25

RESULT 43  
US-10-956-157-199403  
; Sequence 199403, Application US/1095615  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; ADDITIONAL INFORMATION:

1 APPLICANT: Mounts, William  
2  
3 TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
4  
5 TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
6  
7 FILE REFERENCE: 031896-043000 (AM 101081)  
8  
9 CURRENT APPLICATION NUMBER: US/10/956.157  
10  
11 CURRENT FILING DATE: 2004-10-04  
12  
13 NUMBER OF SEQ ID NOS: 319805  
14  
15 SOFTWARE: PatentIn version 3.2

```

; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199403

```

Query Match	7.9%	Score 18.6;	DB 1;	Length 25;
Best Local Similarity	84.0%;	Pred. No. 41;		
Matches	21;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0;

OY		154 CCTTCTGCCATGATTTTAAGATTCC	178
Db	1	CCTTCTGCCGTGATTGTCA G T T C C	25

RESULT 44  
US-11-060-756-81506/C  
; Sequence 81506, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth

APPLICANT: Mounts, William Martin  
 TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drugs  
 TITLE OF INVENTION: Target Genes  
 FILE REFERENCE: AM101083 (031896-042000)  
 CURRENT APPLICATION NUMBER: US/11/060,756  
 CURRENT FILING DATE: 2005-02-18  
 NUMBER OF SEQ ID NOS: 303284  
 SOFTWARE: PatentIn version 3.2

```

; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81506

```

Query Match	7.9%	Score 18.6;	DB 1;	Length 25;
Beat Local Similarity	84.0%;	Pred. No. 41;		
Matches	21;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0;

```

QY      158 CTGCCATGATTTTAAGATTCCAGG 182
          |||||
Db      25 CTGCCATGATTGTAAGTTCTGAG 1

```

RESULT 45  
US-11-121-849-584812/c  
; Sequence 584812, Application US/11121845  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; TITLE OF INVENTION:
; FILER REFERENCE: 3684 1

```

; CURRENT APPLICATION NUMBER: US/11/121,845  
 ; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 584812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-584812

```

Query Match	7.9%	Score 18.6;	DB 1;	Length 25;
Best Local Similarity	84.0%;	Pred. No. 41;		
Matches	21; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;

Oy 67 TCACGTGAGAGCTGGTTGTTGAA 91  
 |||||  
 Db 25 TCACCTGAGAGCTGATTGCTTAAA 1

RESULT 46  
US-11-121-849-597792/c  
; Sequence 597792, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION

```

1  APPLICANT: John Palma
2  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
3  TITLE OF INVENTION: Microarrays
4  FILE REFERENCE: 3684.1
5  CURRENT APPLICATION NUMBER: US/11/121,849
6  CURRENT FILING DATE: 2005-05-03
7  PRIOR APPLICATION NUMBER: 60/567,949
8  PRIOR FILING DATE: 2004-05-03

```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.0
; SEQ ID NO: 597792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-597792
```

Query Match	7.9%	Score 18.6;	DB 1;	Length 25;
Best Local Similarity	84.0%	Pred. No. 41;		
Matches 21; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```

Oy      24  CCTCATGAATGGTTTAGTGCCATCC  48
          ||||| | | | | | | | |
Db      25  CCTCATGAGTACTTAGTGCCACCC  1

```

RESULT 47  
US-11-121-849-637715  
; Sequence 637715, Application US/11121849  
; Publication No. US20050272080A1  
Current: INFORMATION

```

: TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
:
: TITLE OF INVENTION: Microarrays
:
: FILE REFERENCE: 3684.1
:
: CURRENT APPLICATION NUMBER: US/11/121,849
:
: CURRENT FILING DATE: 2005-05-03
:
: PRIOR APPLICATION NUMBER: 60/567,949
:

```

```

; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 637715
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-637715

```

```

Query Match      7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy      24 CCTCATGATGTTAGTGCATCC 48
      1 CCTCATGATGTTAGTGCATCC 25

```

```

RESULT 48

```

```

US-11-121-849-638121
; Sequence 638121, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 638121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-638121

```

```

Query Match      7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy      24 CCTCATGATGTTAGTGCATCC 48
      1 CCTCATGATGTTAGTGCATCC 25

```

```

RESULT 49

```

```

US-11-121-849-663681/C
; Sequence 663681, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 663681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-663681

```

```

Query Match      7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy      24 CCTCATGATGTTAGTGCATCC 48
      1 CCTCATGATGTTAGTGCATCC 25

```

```

RESULT 49

```

```

US-11-121-849-663681/C
; Sequence 663681, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 663681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-663681

```

```

Query Match      7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy      79 TGGTTGTTGAAGAGCTGCCCC 103
      25 TGGCTTTGAAGAGAGCTGCGACC 1

```

```

RESULT 50

```

```

US-10-310-914A-131336
; Sequence 131336, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131336
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-131336

```

```

Query Match      7.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 40;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      105 TCTCATCTCTCTCTCTCCAC 124
      1 UCUCANUCUCUCUCUCAC 20

```

```

RESULT 51

```

```

US-10-310-914A-131349
; Sequence 131349, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131349
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-131349

```

```

Query Match      7.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 40;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      105 TCTCATCTCTCTCTCTCCAC 124
      1 UCUCANUCUCUCUCUCAC 20

```

```

RESULT 51

```

```

US-10-310-914A-131349
; Sequence 131349, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131349
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-131349

```

```

Query Match      7.8%; Score 18.4; DB 1; Length 24;
Best Local Similarity 65.0%; Pred. No. 42;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      105 TCTCATCTCTCTCTCTCCAC 124
      2 UCUCANUCUCUCUCUCAC 21

```

```

RESULT 52

```

```

US-10-956-157-180126
; Sequence 180126, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)

```



```
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180126
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-180126
```

```
Query Match          7.8%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      216 CTTGTTCTGCTCGCAAACT 235
Db      1 CTTGTTCTGCTCGCAAACT 20
```

```
RESULT 53
US-10-310-914A-116036/c
; Sequence 116036, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Benitwich, Isaac
; APPLICANT: Shlier, Kynzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1398402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116036
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116036
```

```
Query Match          7.7%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      42 GCCATCCCTTGCTGATGAGTGA 64
Db      23 GCCATCCCTGATGATGAGTGA 1
```

```
RESULT 54
US-10-310-914A-453805
; Sequence 453805, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Benitwich, Isaac
; APPLICANT: Shlier, Kynzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1398402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453805
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-453805
```

```
Query Match          7.7%; Score 18.2; DB 1; Length 24;
Best Local Similarity 65.2%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      134 AGACACCTGCTCCCTTCTCTCT 156
```

```
Db      2 AGCCUCGAGCUCGCCUCUCUCU 24
```

```
RESULT 55
US-10-681-773-106005/c
; Sequence 106005, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106005
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-106005
```

```
Query Match          7.7%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      78 CTGTTGTTGAAAGACCTGCGC 100
Db      24 CTAGTTGTTGAAAGACCTGCGC 2
```

```
RESULT 56
US-10-719-900-221757
; Sequence 221757, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 221757
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-221757
```

```
Query Match          7.7%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      64 AGTTCACGTGAGACGTGTTGTT 86
Db      1 AGTTCACGTGAGACGTGTTCTT 23
```

```
RESULT 57
US-10-956-157-170117/c
; Sequence 170117, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 31805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-170117
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 62 TGAGTTCACGTGAGAGCTGGTTG 84
Db 23 TGAGTTCACGCAGATCTGGTTG 1
```

```

RESULT 58
US-10-310-914A-715048/c
; Sequence 715048, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Krutac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 715048
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-715048
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 70 CGTGAGCTGGTGTGTTGAAG 92
Db 23 CGTGAGCTGGTGTGTTGGCAG 1
```

```

RESULT 59
US-11-121-849-297414/c
; Sequence 297414, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 297414
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-297414
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 5 TGGTCATGGGGCAGATCCCTC 27
Db 23 TAGGTCATAGGGCAGATCCCTC 1
```

```

RESULT 60
US-10-310-914A-1140091/c
; Sequence 1140091, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Krutac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1140091
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1140091
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 45 ATCCCTGGTGGTGGTGGT 62
Db 18 ATCCCTGGTGGTGGTGGT 1
```

```

RESULT 61
US-10-847-918-1939/c
; Sequence 1939, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeck
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1939
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-1939
```

```

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 149 CTCTCTCTCTGCGCATGATT 169
Db 21 CTCTCTCTCTGCGCATGATT 1
```

```

RESULT 62
US-10-847-918-1941
```

```
; Sequence 1941, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1941
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-1941

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 42.9%; Pred. No. 47;
Matches 9; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

Qy      149 CTTCTCCTTCTGCCATGATT 169
Db      1 CUUCUGUCUGCCAUUUUU 21

RESULT 63
US-10-847-918-2094
; Sequence 2094, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2094
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-2094

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 38.1%; Pred. No. 47;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy      150 TTCCTCTCTGCCATGATT 170
Db      1 UUCUGUCUGCCAUUUUU 21

RESULT 64
US-10-310-914A-116023/c
; Sequence 116023, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
```

```
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1386402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116023
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116023

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 GTCATGGGGCGAGATCCTCA 28
Db      21 GTCATGGGGCGAGATCCTTA 1

RESULT 65
US-10-310-914A-845545/c
; Sequence 845545, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1386402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 845545
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-845545

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      140 CTGCTCCCCCTTCTCTCTG 160
Db      21 CTGCTCCCCCTTCTCTCTG 1

RESULT 66
US-10-310-914A-967563/c
; Sequence 967563, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1386402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 967563
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-967563

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      72  TGAGAGCTGGTTGTTTGAAG  92
          ||||| ||||| ||||| |||||
Db      21  TGAGATCTGTTTGTGAAG  1
```

```

RESULT 67
US-10-310-914A-1073142/c
: Sequence 1073142, Application US/10310914A
: Publication NO. US20060003322A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Isaac
: APPLICANT: Shlier, Kyuzat
: TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
: FILE REFERENCE: 06087.0200.CPUS01
: CURRENT APPLICATION NUMBER: US/10/310,914A
: CURRENT FILING DATE: 2002-12-06
: NUMBER OF SEQ ID NOS: 1388402
: SOFTWARE: Patent in version 3.3
: SEQ ID NO 1073142
: LENGTH: 21
: TYPE: RNA
: ORGANISM: Human
: US-10-310-914A-1073142

```

```

RESULT 68
US-10-310-914A-1073155/c
? Sequence 1073155, Application US/10310914A
? Publication No. US2006000322A1
? GENERAL INFORMATION:
? APPLICANT: Bentwich, Isaac
? APPLICANT: Shlier, Kvuazat
? TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
? TITLE OF INVENTION: uses thereof
? FILE REFERENCE: 06087.0200.CPUS01
? LENGTH: 21
? TYPE: RNA
? ORGANISM: Human
US-10-310-914A-1073155

Query Match      7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred.No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY          20   GATCCCTCATGAAATGGTTAG 40
                |||||
Db           21   GATCCTCATGATGGCTTGG 1

RESULT 69
US-10-310-914A-1295208/c
? Sequence 1295208, Application US/10310914A
? Publication No. US2006000322A1
? GENERAL INFORMATION:
? APPLICANT: Bentwich, Isaac
? APPLICANT: Shlier, Kvuazat
? TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
? TITLE OF INVENTION: uses thereof
? FILE REFERENCE: 06087.0200.CPUS01

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; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295208

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ORGANISM: Human  
US-10-310-914A-1295208

```

RESULT 70
US-11-063-391-290
; Sequence 290. Application US/11063391
; Publication No. US20050202077A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Marrison, J Greg
; APPLICANT: Grigor, Murray R
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Munro, Grant
; APPLICANT: Adernechy, Nevlin
; APPLICANT: Webster, Gill
; TITLE OF INVENTION: Targeted delivery of RNA interference
; TITLE OF INVENTION: molecules
; FILE REFERENCE: 11000.1100U
; CURRENT APPLICATION NUMBER: US/11/063,391
; CURRENT FILING DATE: 2005-02-22
; NUMBER OF SEQ ID NOS: 980
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-11-063-391-290

```

```

RESULT 71
US-10-310-914A-628574
; Sequence 628574, Application US/10310914A
; Publication No. US20060003222A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CRU501
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628574
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628574

```

Query Match 7.5% Score 17.8; DB 1; Length 22;  
Best Local Similarity 57.1%; Pred. No. 47;  
Matches 12; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 113 TCCTGCTCCCACTCTTGATG 133  
DB 1 UCCUGCUCACACUUCUGCUG 21

RESULT 72  
US-10-310-914A-1180683/c  
; Sequence 1180683, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Biointentionally detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1180683  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1180683

Query Match 7.5% Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 47;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 153 TCCTTCTGCCATGATTTTAA 173  
DB 22 TCCTTCTGCCATGATTTGAG 2

RESULT 73  
US-10-956-157-281991  
; Sequence 281991, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeath  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956.157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 281991  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-281991

Query Match 7.5% Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 72 TGAGAGCTGCTGTTTGAAG 92  
DB 1 TGAGAGTGTGTTGTTTAAAG 21

RESULT 74  
US-10-310-914A-399112  
; Sequence 399112, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Biointentionally detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 399112  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-399112

Query Match 7.5% Score 17.8; DB 1; Length 25;  
Best Local Similarity 81.0%; Pred. No. 49;  
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 178 CAGGACTTCACAGAGCAA 198  
DB 4 CAGGCTTCCACAGAGCAA 24

RESULT 75  
US-11-121-849-152798/c  
; Sequence 152798, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121.849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 152798  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-152798

Query Match 7.5% Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 178 CAGGACTTCACAGAGCAA 198  
DB 25 CAGGCTTCCACAGAGCAA 5

RESULT 76  
US-10-310-914A-1073186/c  
; Sequence 1073186, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Biointentionally detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1073186  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1073186

Query Match 7.5%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 42 GCCATCCCTTGGTGAAGTGC 65  
Db 24 GCCATCCCTTGGTGAAGTGC 1

## RESULT 77

US-10-310-914A-1295216/C  
; Sequence 1295216, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kyzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200,CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295216  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1295216

Query Match 7.5%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 7 GGTGATGGGGGAGATCCCTCATG 30  
Db 24 GGTGATGGGGGAGATCCCTCATG 1

## RESULT 78

US-10-681-773-23765/C  
; Sequence 23765, Application US/10681773  
; Publication No. US20040146890A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsumaki, Hajime  
; APPLICANT: Mei, Rui  
; APPLICANT: Shen, Mei-Mei  
; APPLICANT: Kennedy, Giulia  
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
; FILE REFERENCE: 3522.2  
; CURRENT APPLICATION NUMBER: US/10/681,773  
; CURRENT FILING DATE: 2003-10-07  
; PRIOR APPLICATION NUMBER: 60/470,475  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 60/417,190  
; PRIOR FILING DATE: 2002-10-08  
; NUMBER OF SEQ ID NOS: 124031  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 23765  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-681-773-23765

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 155 CTCTGCGATGATTTAAGATTC 178  
Db 25 CTCTGCGATGATTTAAGATTC 2

## RESULT 79

US-10-681-773-38235/C  
; Sequence 38235, Application US/10681773  
; Publication No. US20040146890A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsumaki, Hajime  
; APPLICANT: Mei, Rui  
; APPLICANT: Shen, Mei-Mei  
; APPLICANT: Kennedy, Giulia  
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
; FILE REFERENCE: 3522.2  
; CURRENT APPLICATION NUMBER: US/10/681,773  
; CURRENT FILING DATE: 2003-10-07  
; PRIOR APPLICATION NUMBER: 60/470,475  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 60/417,190  
; PRIOR FILING DATE: 2002-10-08  
; NUMBER OF SEQ ID NOS: 124031  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 38235  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-681-773-38235

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 152 CTCTGCGATGATTTAAGAT 175  
Db 25 CACCTCTGCGATGATTCAGTT 2

## RESULT 80

US-10-719-900-320328  
; Sequence 320328, Application US/10719900  
; Publication No. US2005026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 320328  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-320328

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 178 CAGGACTTCACAAGAAGAAATG 201  
Db 1 CAGGACTTCACAAGAAGTAATTTG 24

## RESULT 81

US-10-956-157-55283/C  
; Sequence 55283, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mouna, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157

US-10-956-157-55283/C  
; Sequence 55283, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mouna, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55283  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-55283

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 149 CTTCTCTTCTGCGCATGATTTAA 172  
Db 24 CTTCTCTTCTGCGCATGATTTAA 1

RESULT 82

US-10-956-157-55284/C  
; Sequence 55284, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55284  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-55284

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 150 TTCTCTCTGCGCATGATTTAA 173  
Db 25 TTCTCTCTGCGCATGATTTAA 2

RESULT 83

US-10-956-157-123288  
; Sequence 123288, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 123288  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-123288

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 21 ATCCCTCATGATGTTAGTCC 44  
Db 21 ATCCCTCATGATGTTAGTCC 44

Db 1 ATCCCTCATGATGTTAGTCC 24

RESULT 84

US-10-956-157-199404  
; Sequence 199404, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 199404  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-199404

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 154 CTTCTCTTCTGCGCATGATTTAA 177  
Db 1 CTTCTCTTCTGCGCATGATTTAA 24

RESULT 85

US-10-843-527-11826  
; Sequence 11826, Application US/10843527  
; Publication No. US20050136395A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: Eric Schell  
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus  
; FILE REFERENCE: 3602.1  
; CURRENT FILING DATE: 2004-05-10  
; PRIOR FILING DATE: 2003-05-08  
; NUMBER OF SEQ ID NOS: 238196  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 11826  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: SARS Virus  
US-10-843-527-11826

Query Match 7.5%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 137 CACCTGCTCCCTCTCTCTCTG 160  
Db 2 CACCTGCTCCCTCTCTCTCTG 25

RESULT 86

US-10-843-527-224887/C  
; Sequence 224887, Application US/10843527  
; Publication No. US20050136395A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: Eric Schell  
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus  
; FILE REFERENCE: 3602.1  
; CURRENT FILING DATE: 2004-05-10

```
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-224887
```

```
Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      137 CACCTGCTCCCTTCCTCTCTG 160
Db      24 CAACTCTTCTCTCTCTCTCTG 1
```

```
RESULT 87
US-10-932-182A-168000/c
; Sequence 168000, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-168000
```

```
Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      174 ATCCAGGAGCTTCAACAAGACGA 197
Db      25 ATACCAGGAGCTGCAAAAAGCA 2
```

```
RESULT 88
US-11-036-317-439119/c
; Sequence 439119, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439119
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-439119
```

```
Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
```

```
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy      83 TGTTGAAGAGCCTGGCCCCCTC 106
Db      24 TATTGAAGAGACTAGCGCCCTC 1
```

```
RESULT 89
US-11-036-317-706660
; Sequence 706660, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 706660
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-706660
```

```
Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      16 GGCAGATCCTCATGAATGTTTA 39
Db      1 GGCAGATGCTGAGAGATGTTTA 24
```

```
RESULT 90
US-11-036-317-986030/c
; Sequence 986030, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 986030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-986030
```

```
Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      37 TTAGTGCATCCCTTGATGATGA 60
Db      25 TGAATGTCGTCCTTGGGATGA 2
```

```
RESULT 91
US-11-121-849-370/c
; Sequence 370, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
```



```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-370

Query Match      7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 92
US-11-121-849-588191
; Sequence 588191, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 588191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-588191

Query Match      7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      141 TGCTCCCGCTCTCTGCGCAT 164
Db      2 TGCTTCCCTTCGCTCTGCGCAT 25

RESULT 93
US-11-121-849-668370/c
; Sequence 668370, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-668370

Query Match      7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 94
US-11-121-849-668624/c
; Sequence 668624, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-668624

Query Match      7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 95
US-11-083-784-292730/c
; Sequence 292730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 292730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-292730

Query Match      7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy 110 TTCTCCTGCTGCCACTCTT 128  
 Db 19 TTCTCCTGACCCACTCTT 1

## RESULT 96

US-11-083-784-1546724/c  
 ; Sequence 1546724, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1546724  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1546724

Query Match 7.4%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 49;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 150 TTCTCCTTTCGCCATGATT 168  
 Db 19 TTCACCTTTCGCCATGATT 1

## RESULT 97

US-11-101-244-292730/c  
 ; Sequence 292730, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 292730  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-292730

Query Match 7.4%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 49;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 110 TTCTCCTGCTGCCACTCTT 128  
 Db 19 TTCTCCTGACCCACTCTT 1

## RESULT 98

US-11-101-244-1546724/c  
 ; Sequence 1546724, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1546724  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-1546724

Query Match 7.4%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 49;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 150 TTCTCCTTTCGCCATGATT 168  
 Db 19 TTCACCTTTCGCCATGATT 1

## RESULT 99

US-10-310-914A-1158279  
 ; Sequence 1158279, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shlier, Kivuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: Patent version 3.3  
 ; SEQ ID NO 1158279  
 ; LENGTH: 20  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-1158279

Query Match 7.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 57.9%; Pred. No. 50;  
 Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
 Oy 22 TCCCTCATGATGTTAG 40  
 Db 1 UCCUUCAGAUUGUUG 19

## RESULT 100

```
US-10-310-914A-115919/c
; Sequence 115919, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115919
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-115919

Query Match      7.3%  Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  TGCTGGGTCATGGGGCGCAGAT 22
Db      22  TATTGGGTCATGGGGCGCGAT 1

RESULT 101
US-10-310-914A-969089/c
; Sequence 969089, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969089
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969089

Query Match      7.3%  Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      71  GTGAGAGCTGTTGTTTGAAG 92
Db      22  GTGAGATCTGTTAGTTAAAG 1

RESULT 102
US-10-310-914A-1036172
; Sequence 1036172, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1036172
; LENGTH: 22
```

```
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1036172

Query Match      7.3%  Score 17.2; DB 1; Length 22;
Best Local Similarity 59.1%; Pred. No. 54;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      103  CCTGCATTCCTCCGCCAC 124
Db      1  CCUCUCGUCUCGUCGCAAC 22

RESULT 103
US-10-310-914A-1087700/c
; Sequence 1087700, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087700
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087700

Query Match      7.3%  Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      24  CCTCATGAATGTTATGCCA 45
Db      22  CCTCAGATGATTAATGCCA 1

RESULT 104
US-10-310-914A-273857/c
; Sequence 273857, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273857
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-273857

Query Match      7.3%  Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      137  CACCGCTCCCCCTTCCTTC 158
Db      23  CACCTCTTCCCTTCCTTC 2

RESULT 105
US-10-310-914A-1158269
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; Sequence 1158289, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1158289
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1158289

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 23;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 157 TCTGCCATGATTTTAAAGATTC 178
DB 1 UCUGCCAGUAGUAGUAGUAGUCC 22

RESULT 106
US-10-310-914A-32934/C
; Sequence 32934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32934
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-32934

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGCTGTTGAAG 92
DB 22 GTGGGATCTGCTGTTAAAG 1

RESULT 107
US-10-310-914A-66335
; Sequence 66335, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66335
; LENGTH: 24
; TYPE: RNA

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; ORGANISM: Human
US-10-310-914A-66335

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 24;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 73 GAGAGCTGCTGTTGAAGAG 94
DB 3 GAGAUUCGUGUUGUAAAAGUG 24

RESULT 108
US-10-298-953-44
; Sequence 44, Application US/10298953
; Publication No. US20040097444A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF SERINE/THREONINE KINASE 16 EXPRESSION
; FILE REFERENCE: HTS-0109
; CURRENT APPLICATION NUMBER: US/10/298,953
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-953-44

Query Match
Best Local Similarity 7.1%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 106 CTCATTCTCCTGCTCCACT 125
DB 1 CACATCTCCTGCTCCCAAT 20

RESULT 109
US-10-310-914A-661149/C
; Sequence 661149, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661149
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661149

Query Match
Best Local Similarity 7.1%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 68 CACGTGAGAGCTGCTGTTT 87
DB 20 CTCGTGAGATCTGCTGTTT 1

RESULT 110
US-10-310-914A-845542/C
; Sequence 845542, Application US/10310914A
; Publication No. US20060003322A1

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; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 845542
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-845542

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      146 CCCCTTCCTTCCTTCGCGATG 165
DB      20 CCCCTTCGCTTCCTTCGCGGTG 1

RESULT 111
US-10-310-914A-1073095/c
; Sequence 1073095, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073095
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073095

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      140 CTGCTCCCTTCCTTCCTTCT 159
DB      20 CTGCTCCCTTCCTTCCTTCT 1

RESULT 112
US-10-310-914A-1242020/c
; Sequence 1242020, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1242020
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1242020

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      140 CTGCTCCCTTCCTTCCTTCT 159
DB      20 CTGCTCCCTTCCTTCCTTCT 1

RESULT 113
US-10-847-918-1184/c
; Sequence 1184, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1184
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-1184

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      171 AAGATTCAGGAGCTTCACA 190
DB      20 AAGATTCAGGAGCTTCACA 1

RESULT 114
US-10-847-918-1853/c
; Sequence 1853, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1853
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-1853

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      171 AAGATTCAGGAGCTTCACA 190
DB      20 AAGATTCAGGAGCTTCACA 190

US-10-310-914A-1242020
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Db      20 AGATTCAGGCGCTTCA 1

RESULT 115
US-10-847-918-1942/c
; Sequence 1942, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1942
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-1942

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      149 CTCTCCTTCGCCATGATT 168
Db      20 CTCTGTCTCGCATGATT 1

RESULT 116
US-10-847-918-1944
; Sequence 1944, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1944
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1-antisense strand
US-10-847-918-1944

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 45.0%; Pred. No. 59;
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Cy      149 CTCTCCTTCGCCATGATT 168
Db      2 CUCUCUUCUCGCCAUGAUU 21

RESULT 117
US-10-847-918-2092/c
; Sequence 2092, Application US/10847918
; Publication No. US20050119210A1

; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2092
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-2092

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      150 TTCTCCTTCGCCATGATT 169
Db      21 TTCTGTCTCGCATGATT 2

RESULT 118
US-10-310-914A-828967/c
; Sequence 828967, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, KvuZac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 828967
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-828967

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      139 CTGCTCCCTTCCTTCCTTC 158
Db      20 CTCTCCTCCCTTCCTTCCTCC 1

RESULT 119
US-10-310-914A-1009274/c
; Sequence 1009274, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, KvuZac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1009274

```

LENGTH: 21  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-1009274

Query Match 7.1%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 59;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 179 AGGACTTCACAGAGCA 198  
 Db 20 AGGACTTCACAGAGCA 1

RESULT 120  
 US-10-310-914A-1371246/c  
 ; Sequence 1371246, Application US/10310914A  
 ; Publication No. US2006000322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benetwich, Isaac  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1371246  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-1371246

Query Match 7.1%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 59;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 137 CACCTGCTCCCTCTCTCT 156  
 Db 20 CTCCTGATCCCCCTCTCT 1

RESULT 121  
 US-10-310-914A-74338/c  
 ; Sequence 74338, Application US/10310914A  
 ; Publication No. US2006000322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benetwich, Isaac  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 74338  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-74338

Query Match 7.1%; Score 16.8; DB 1; Length 23;  
 Best Local Similarity 90.0%; Pred. No. 61;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 208 CCAGCTCTGTTCTGCT 227  
 Db 22 CCAGCTCTGTTCTGCT 3

RESULT 122

US-10-416-122-2  
 ; Sequence 2, Application US/10416122  
 ; Publication No. US20040072199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brem, Gottfried  
 ; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF  
 ; TITLE OF INVENTION: DNA-CONTAINING SAMPLES BY MEANS OF OLIGONUCLEOTIDES  
 ; FILE REFERENCE: KLAUS1.001APC  
 ; CURRENT APPLICATION NUMBER: US/10/416,122  
 ; CURRENT FILING DATE: 2003-10-24  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/12880  
 ; PRIOR FILING DATE: 2001-11-07  
 ; PRIOR APPLICATION NUMBER: DE 100 55 368.0  
 ; PRIOR FILING DATE: 2000-11-08  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic oligonucleotide  
 US-10-416-122-2

Query Match 7.1%; Score 16.8; DB 1; Length 24;  
 Best Local Similarity 90.0%; Pred. No. 61;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTGCTCCCTCTCTCTCT 159  
 Db 5 CTGCTCCCTCTCTCTCT 24

RESULT 123  
 US-10-708-204-3803  
 ; Sequence 3803, Application US/10708204  
 ; Publication No. US20050222399A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES  
 ; FILE REFERENCE: 55033  
 ; CURRENT APPLICATION NUMBER: US/10/708,204  
 ; CURRENT FILING DATE: 2004-02-16  
 ; NUMBER OF SEQ ID NOS: 7351  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 3803  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-708-204-3803

Query Match 7.0%; Score 16.6; DB 1; Length 23;  
 Best Local Similarity 65.2%; Pred. No. 64;  
 Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 57 ATGAGTAGATTCACGTGAGAGCT 79  
 Db 1 AUCAGUGAGCUCAGAGAGAGCU 23

RESULT 124  
 US-10-310-914A-287417/c  
 ; Sequence 287417, Application US/10310914A  
 ; Publication No. US2006000322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benetwich, Isaac  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A

```
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patentln version 3.3
/ SEQ ID NO 287417
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-287417

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 100 CCCCTCTCATTTCTCTGCTCCC 122
Db 23 CCACCCCTCTTTCTCCGGCTCCC 1

RESULT 125
US-10-310-914A-360372/c
/ Sequence 360372, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kvuzaat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patentln version 3.3
/ SEQ ID NO 360372
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-360372

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 CCTCTCATTTCTCTGCTCCCAC 124
Db 23 CCTCTCTCTTCCCTCCTCCCCC 1

RESULT 126
US-10-310-914A-651766/c
/ Sequence 651766, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kvuzaat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patentln version 3.3
/ SEQ ID NO 651766
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-651766

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 65 GTTCACTGAGAGCTGTTGTTT 87
|||||
```

```
Db 23 GTTCTCATGAGATCTGTTT 1

RESULT 127
US-10-310-914A-819312/c
/ Sequence 819312, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kvuzaat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patentln version 3.3
/ SEQ ID NO 819312
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-819312

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 103 CCTCTCATTTCTCTGCTCCCACT 125
Db 23 CCTCTCATTTCTCTCCCTCCCAAT 1

RESULT 128
US-10-310-914A-967480/c
/ Sequence 967480, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kvuzaat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patentln version 3.3
/ SEQ ID NO 967480
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-967480

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 65 GTTCACTGAGAGCTGTTGTTT 87
Db 23 GTTCTCATGAGATCTGTTT 1

RESULT 129
US-10-310-914A-1186008/c
/ Sequence 1186008, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kvuzaat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
```



```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1186008
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1186008
```

```
Query Match          7.0%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      76 AGCTGCTGTTGAAGAGACCTG 98
Db      23 AGACGCTGTTTAAAGAGCTCG 1
```

```
RESULT 130
US-10-310-914A-115988/C
; Sequence 115988, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 115988
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-115988
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      75 GAGCTGCTGTTGTTGAAG 92
Db      18 GAGCTGCTGTTGTTAAAG 1
```

```
RESULT 131
US-10-310-914A-1053329/C
; Sequence 1053329, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1053329
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053329
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      146 CCCCTTCCTCTTGCCA 163
Db      18 CCCCTTCCTCTTGCCA 1
```

```
RESULT 132
US-10-727-780A-425/C
; Sequence 425, Application US/10727780A
; Publication No. US20050233329A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Vaish, Narendra
; APPLICANT: Zimen, Shawn
; APPLICANT: McSwigen, James
; APPLICANT: Sigma Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT APPLICATION NUMBER: US/10/727.780A
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 425
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-727-780A-425
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      148 CCTCTCCTCTGCGCATG 165
Db      19 CCTCTCCTCTGCGCATG 2
```

```
RESULT 133
US-10-310-914A-1053330/C
; Sequence 1053330, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1053330
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053330
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      146 CCCCTTCCTCTTGCCA 163
Db      18 CCCCTTCCTCTTGCCA 1
```

```
RESULT 134
US-11-083-784-134328/C
; Sequence 134328, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 134328
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-134328
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      107 TCATTCCTGCTGCCAC 124
Db      19 TCATTCCTGCTGCCAC 2
```

```
RESULT 135
US-11-083-784-134365/c
; Sequence 134365, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 134365
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-134365
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTGCTCCC 122
Db      18 TCTCATTCCTGCTCCC 1
```

```
RESULT 136
US-11-083-784-863172/c
; Sequence 863172, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 863172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-863172
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTGCTCCC 122
Db      19 TCTCATTCCTGCTCCC 2
```

```
RESULT 137
US-11-083-784-914575/c
; Sequence 914575, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 914575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-914575
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      150 TTCTCCTTCTGCCATGAT 167
Db      19 TTCTCCTTCTGCCATGAT 2
```

```
RESULT 138
US-11-083-784-1250582
; Sequence 1250582, Application US/11083784
```

Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1250582  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1250582

Query Match 6.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 55.6%; Pred. No. 63;  
Matches 10; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Oy 70 CGTGAGAGCTGGTGT 87  
||:|||||:||||:|  
Db 1 CGUGAGUCGUGUUU 18

RESULT 139  
US-11-101-244-134328/c  
Sequence 134328, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 134328  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-134328

Query Match 6.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 107 TCATTCTCTGCTCCAC 124  
|||||  
Db 19 TCATTCTCTGCTCCAC 2

RESULT 140  
US-11-101-244-134365/c

Sequence 134365, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 134365  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-134365

Query Match 6.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 105 TCTCATTTCTCTGCTCC 122  
|||||  
Db 18 TCTCATTTCTCTGCTCC 1

RESULT 141  
US-11-101-244-863172/c  
Sequence 863172, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 863172  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-863172

Query Match 6.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 105 TCTCATTTCTCTGCTCC 122  
|||||  
Db 19 TCTCATTTCTCTGCTCC 2

RESULT 142  
US-11-101-244-914575/c  
Sequence 914575, Application US/11101244

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsdale, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 914575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-914575
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 150 TTCTCTTCTTCTCCATGAT 167
Db 19 TTTCTCTTCTGCGCATGAT 2
```

```
RESULT 143
US-11-101-244-1250582
; Sequence 1250582, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsdale, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1250582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1250582
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 10; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 70 CGTGAGACCTGCTGTTT 87
Db 1 CGUGAGACUCGUGUGUUU 18
```

```
RESULT 144
US-10-310-914A-313831
; Sequence 313831, Application US/10310914A
; Publication No. US20060003322A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyasat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 313831
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-313831
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 61.1%; Pred. No. 65;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 140 CTGCTCCCTCTCTCCTT 157
Db 3 CUGCUCCTCCCGCUCCTU 20
```

```
RESULT 145
US-10-708-204-3346/C
; Sequence 3346, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3346
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-3346
```

```
Query Match 6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 135 GACACCTGCTCCCTCTTCC 155
Db 21 GACCCCTGTTCTCCTTCTCC 1
```

```
RESULT 146
US-10-310-914A-59888/C
; Sequence 59888, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyasat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59888
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-59888
```

```
Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      94 GCGTCGCCCTCTCTCTCTC 114
DB      21 GCGTCGCCCTCTCTCTCTC 1

RESULT 147
US-10-310-914A-95531/c
; Sequence 95531, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95531
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-95531

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      142 GCTCCCTCTCTCTCTCTGCC 162
DB      21 GCTCCCTCTCTCTCTCTGCC 1

RESULT 148
US-10-310-914A-174457
; Sequence 174457, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174457
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-174457

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      79 TGCTGTTTGAAGAGCCTGG 99
DB      1 UGGGUCUUUGAAGAGCCTGG 21

RESULT 149
US-10-310-914A-612161
; Sequence 612161, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 612161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-612161

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      24 CCGATGAAAGTGTAGGCC 44
DB      1 CCUCAGAAAGCUCUGGCC 21

RESULT 150
US-10-310-914A-628516
; Sequence 628516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628516
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628516

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      108 CATCTCTGCTCCACTCTT 128
DB      1 CAGGUCCTGCTCCACTCTT 21

RESULT 151
US-10-310-914A-969044/c
; Sequence 969044, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969044
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969044
```

Query Match	6.9%	Score 16.2;	DB 1;	Length 21;
Best Local Similarity	85.7%	Pred. No. 68;		
Matches 18;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy	140	CTGCTCCCCCTTCTCCTTCTG	160
Db	21	CTGCTCCCACTTTGCCTTCTG	1

RESULT 152  
US-10-310-

```

US-10-310-914A-1111794/c
: Sequence 1111794, Application US/10310914A
: Publication No. US20060003322A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Bentwich, Isaac
:
: TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
: TITLE OF INVENTION: uses thereof
:
: FILE REFERENCE: 06087.0200.CPUS01
:
: CURRENT APPLICATION NUMBER: US/10/310,914A
:
: CURRENT FILING DATE: 2002-12-06
:
: NUMBER OF SEQ ID NOS: 1388402
:
: SOFTWARE: PatentIn version 3.3
:
: SEQ ID NO 1111794
:
: LENGTH: 21
:
: TYPE: RNA
:
: ORGANISM: Human
:
: US-10-310-914A-1111794

```

RESULT 153  
US-10-310-

```

US-10-310-914A-1227944
; Sequence 1227944, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentzwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200, CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1227944
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1227944

```

**RESULT 154**

US-10-310-914A-97305/C  
; Sequence 97305, Application US/10310914A  
; Publication NO. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

```

; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97305
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-97305

```

RESULT 155

```

US-10-310-914A-360369/c
; Sequence 360369, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Benitwch, Isaac
; APPLICANT: Shiler, Krznac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 360369
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-360369

```

RESULT 156

```

US-10-310-914A-875345
; Sequence 875345, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiner, Kyuzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 875345
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-875345

```

Query Match

Best Local Similarity 71.4%; Pred. No. 69;  
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 53 GGTGATGACTGAGTTCACCTG 73  
||:|||||:|||||:|||||:  
Db 2 GGUGAGAGGAGGAGCUCACUG 22

## RESULT 157

US-10-310-914A-910065/c

; Sequence 910065, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shlier, Kiyazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 910065

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-910065

Query Match 6.9%; Score 16.2; DB 1; Length 22;

Best Local Similarity 85.7%; Pred. No. 69;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 143 CTCCTCTCTCTCTCTCTGCA 163  
|||||:|||||:|||||:|||||:  
Db 21 CTCCTCTCTCTCTCTCTCA 1

## RESULT 158

US-10-092-900A-521

; Sequence 521, Application US/10092900A

; Publication No. US20040043382A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Taupier Jr., Raymond J.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Li, Li

; APPLICANT: Zernhusen, Bryan D.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: Gorman, Linda

; APPLICANT: Miller, Charles E.

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Paturajan, Meera

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Verneet, Corine A.M.

; APPLICANT: Guo, Xiaojia Sasna

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Casman, Steacie J.

; APPLICANT: Malyanekar, Uriel M.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Liu, Yi

; APPLICANT: Anderson, David W.

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Carterton, Elna

; APPLICANT: Leite, Mario W.

; APPLICANT: Zhong, Haihong

; APPLICANT: Aliebrook, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-290C

; CURRENT APPLICATION NUMBER: US/10/092,900A

; PRIOR FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: USSN 60/274,322

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/283,675

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: USSN 60/338,092

; PRIOR FILING DATE: 2001-12-03

; PRIOR APPLICATION NUMBER: USSN 60/274,281

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/274,191

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/325,681

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: USSN 60/304,354

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: USSN 60/279,995

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: USSN 60/294,899

; PRIOR FILING DATE: 2001-05-31

; PRIOR APPLICATION NUMBER: USSN 60/287,424

; PRIOR FILING DATE: 2001-04-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 768

; SEQ ID NO 521

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

US-10-092-900A-521

Query Match 6.9%; Score 16.2; DB 1; Length 23;

Best Local Similarity 85.7%; Pred. No. 70;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 100 CCCCCTCTCTCTCTCTCTC 120  
|||||:|||||:|||||:|||||:  
Db 2 CCGCCTCTCTCTCTCTCTC 22

## RESULT 159

US-10-310-914A-596179

; Sequence 596179, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shlier, Kiyazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 596179

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-596179

Query Match 6.9%; Score 16.2; DB 1; Length 23;

Best Local Similarity 61.9%; Pred. No. 70;

Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 20 GATCCCTGATGAATGCTTAG 40  
||:|||||:|||||:|||||:  
Db 3 GAUCCCTCAUGAUGCCUGG 23

## RESULT 160

```

US-10-310-914A-1171021/C
; Sequence 1171021, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1171021
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1171021

```

```

Query Match          6.8%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      154 CCTTCTGCCATGATTTAAGA 174
Db      21 CCTTCTACCATGACTGTAGA 1

```

```

RESULT 161
US-10-310-914A-1037134/C
; Sequence 1037134, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1037134
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1037134

```

```

Query Match          6.8%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      143 CTCGCCCTTCCTCTTC 158
Db      18 CTCGCCCTTCCTCTTC 3

```

```

RESULT 162
US-11-083-784-508230/C
; Sequence 508230, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; NUMBER OF SEQ ID NOS: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

```

```

; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 508230
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-508230

```

```

Query Match          6.8%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      105 TCTCATTTCTCTGCTC 120
Db      19 TCTCATTTCTCTGCTC 4

```

```

RESULT 163
US-11-101-244-508230/C
; Sequence 508230, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 508230
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-508230

```

```

Query Match          6.8%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      105 TCTCATTTCTCTGCTC 120
Db      19 TCTCATTTCTCTGCTC 4

```

```

RESULT 164
US-09-791-942-85
; Sequence 85, Application US/09791942
; Patent No. US2002014716A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Kothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0099
; CURRENT APPLICATION NUMBER: US/09/791,942
; NUMBER OF SEQ ID NOS: 2001-02-22
; SEQ ID NO 85

```



```
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-942-85
```

```
Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTCGCTC 120
          |||||
Db      3 TCTCATTCCTCGCTC 18
```

```
RESULT 165
US-10-415-463-85
; Sequence 85, Application US/10415463
; Publication No. US20040110705A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RSP-0198
; CURRENT APPLICATION NUMBER: US/10/415,463
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 09/702,251
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-415-463-85
```

```
Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTCGCTC 120
          |||||
Db      3 TCTCATTCCTCGCTC 18
```

```
RESULT 166
US-10-476-264-285/C
; Sequence 285, Application US/10476264
; Publication No. US20050123910A1
; GENERAL INFORMATION:
; APPLICANT: Cookson, William Omond Charles Michael
; APPLICANT: Moffat, Miriam Fleur
; APPLICANT: Allen, Maxine
; APPLICANT: Lench, Nick
; TITLE OF INVENTION: Enzyme and SNP marker for disease
; FILE REFERENCE: 16721-002US1
; CURRENT APPLICATION NUMBER: US/10/476,264
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: PCT/GB02/01887
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: GB0110044.5
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0110046.0
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0124594.3
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: GB0124575.2
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 421
; SOFTWARE: PatentIn version 3.1
```

```
/ SEQ ID NO 285
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-10-476-264-285
```

```
Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      191 AGAGCAATGCTAAC 206
          |||||
Db      18 AGAGCAATGCTAAC 3
```

```
RESULT 167
US-10-310-914A-1037133/C
; Sequence 1037133, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1037133
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1037133
```

```
Query Match          6.8%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      143 CTCCCCCTTCCTTC 158
          |||||
Db      19 CTCCCCCTTCCTTC 4
```

```
Search completed: October 2, 2006, 15:43:17
Job time : 0.001 secs
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